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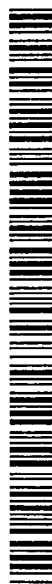
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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE  
EXPRESSION IN HUMAN ADULT LIVER

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene  
expression in a sample derived from human adult liver is described. Also described are single exon nucleic acid probes expressed in  
the adult liver and their use in methods for detecting gene expression.

WO 01/57273 A2



HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL  
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER

CROSS REFERENCE TO RELATED APPLICATIONS

5

The present application is a continuation-in-part of U.S.  
patent application serial nos. 09/632,366, filed August 3,  
2000 and 09/608,408, filed June 30, 2000; claims the  
benefit under 35 U.S.C. s 119(e) of U.S. provisional patent  
10 application serial nos. 60/236,359, filed September 27,  
2000, 60/234,687, filed September 21, 2000, 60/207,456,  
filed May 26, 2000, and 60/180,312, filed February 4, 2000;  
and further claims the benefit under 35 U.S.C. s 119(a) of  
UK patent application no. 0024263.6, filed October 4, 2000,  
15 the disclosures of which are incorporated herein by  
reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY  
REFERENCE THEREOF

20

The present application includes a Sequence Listing in  
electronic format, filed pursuant to PCT Administrative  
Instructions 801 - 806 on a single CD-R disc, in  
triplicate, containing a file named pto\_ADULT\_LIVER.txt,  
25 created 24 January 2001, having 26,335,065 bytes. The  
Sequence Listing contained in said file on said disc is  
incorporated herein by reference in its entirety.

Field of the Invention

30

The present invention relates to genome-derived  
single exon microarrays useful for verifying the expression  
of regions of genomic DNA predicted to encode protein. In  
particular, the present invention relates to unique genome-  
35 derived single exon nucleic acid probes expressed in human

adult liver and single exon nucleic acid microarrays that include such probes.

#### Background of the Invention

5           For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger *et al.*, *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert *et al.*, *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to  
10 further the understanding of proteins – known or suspected – about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent  
15 biological understanding.

          For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via  
20 T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick *et al.*, *Nature* 308(5955):153-8 (1984).

          More recently, however, the development of high  
25 throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes understanding of the basic biology of the encoded protein  
30 product.

          One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences – that is, those accessible through isolation of mRNA – are of greatest initial interest. This "expressed  
35 sequence tag" ("EST") approach has already yielded vast

amounts of sequence data (see for example Adams et al.,  
Science 252:1651 (1991); Williamson, *Drug Discov. Today*  
4:115 (1999)). For nucleic acids sequenced by this  
approach, often the only biological information that is  
5 known *a priori* with any certainty is the likelihood of  
biologic expression itself. By virtue of the species and  
tissue from which the mRNA had originally been obtained,  
most such sequences are also annotated with the identity of  
the species and at least one tissue in which expression  
10 appears likely.

More recently, the pace of genomic sequencing has  
accelerated dramatically. When genomic DNA serves as the  
initial substrate for sequencing efforts, expression cannot  
be presumed; often the only *a priori* biological information  
15 about the sequence includes the species and chromosome (and  
perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence  
accumulation by directed, EST, and genomic sequencing  
approaches - and in particular, with the accumulation of  
20 sequence information from multiple genera, from multiple  
species within genera, and from multiple individuals within  
a species - there is an increasing need for methods that  
rapidly and effectively permit the functions of nucleic  
sequences to be elucidated. And as such functional  
25 information accumulates, there is a further need for  
methods of storing such functional information in  
meaningful and useful relationship to the sequence itself;  
that is, there is an increasing need for means and  
apparatus for annotating raw sequence data with known or  
30 predicted functional information.

Although the increase in the pace of genomic  
sequencing is due in large part to technological changes in  
sequencing strategies and instrumentation, Service, *Science*  
280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),  
35 there is an important functional motivation as well.



While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. *C. elegans* Sequencing Consortium, *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and most importantly, but not exclusively, regions that function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al., *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al.,

*Ismb* 5:294-302 (1997); and GENESCAN, Burge *et al.*, *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known, however, to give high false positive rates. Burset *et al.*,  
5 *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence. Ansari-Lari *et al.*, *Genome Res.* 8(1):29-40 (1998)

Identification of functional genes from genomic  
10 data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may need to be revised substantially downwards. *Nature*  
15 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically – and specifically, that permit the expression of regions predicted to encode protein – readily  
20 to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in Schena (ed.), DNA Microarrays : A Practical Approach  
25 (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

30 It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon *et al.*, *Genomics* 33(1):151-2 (1996), or from the construction of "problem specific" libraries  
35 targeted at a particular biological question, R.S. Thomas

et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

5           The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single  
10 exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally been used to probe gene expression from more complex  
15 eukaryotic genomes, and in particular from those averaging more than one intron per gene.

Diseases of the liver are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these  
20 diseases; although causative mutations in single genes have been identified for some, these disorders are believed for the most part to have polygenic etiologies. There is a need for methods and apparatus that permit prediction, diagnosis  
25 and prognosis of diseases of the liver particularly those diseases with polygenic etiologies.

#### Summary of the Invention

30           The present invention solves these and other problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional information derived from genomic sequence. The present invention also provides apparatus for verifying the  
35 expression of putative genes identified within genomic

sequence.

In particular, the invention provides novel genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human adult liver, comprising a plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 13,109 or a complementary sequence, or a portion of such a sequence.

By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably amplifiable.

In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality of probes is amplifiable using at least one common primer. Preferably, each of said plurality of probes is amplifiable using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

Suitably, said set of single exon nucleic acid

probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 25,995 or a complimentary sequence, or a portion of such a sequence.

5                    Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, preferably at least 400bp and, most preferably, 500 bp.

10                   In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said  
15 single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

                    In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is preferred that at least 50%, suitably at least 60%, most  
20 suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

                    Preferably, a spatially-addressable set of single  
25 exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

                    Suitable substrates include a filter membrane which may, preferably, be nitrocellulose or nylon. The  
30 nylon may preferably, be positively-charged. Other suitable substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride,  
35 polytetrafluoroethylene, polystyrene, polycarbonate,

polyacetal, polysulfone, celluloseacetate,  
cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is provided a microarray comprising a spatially addressable  
5 set of single exon nucleic acid probes in accordance with the first aspect of the invention.

In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or  
10 more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In another aspect, the invention provides genome-  
15 derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray. In particular embodiments of this aspect, the present invention provides human single-exon probes that include specifically-hybridizable fragments of  
20 SEQ ID Nos. 13,110 - 25,995, wherein the fragment hybridizes at high stringency to an expressed human gene. In particular embodiments, the invention provides single exon probes comprising SEQ ID Nos. 1 - 13,109.

Accordingly, in a third aspect of the invention,  
25 there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human adult liver which is a nucleic acid molecule comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 13,109 or a complementary sequence or a  
30 fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human adult liver.

In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a  
35 nucleotide sequence as set out in any of SEQ ID NOs.:

13,110 - 25,995 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring  
5 human gene expression in a sample derived from human adult liver which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 25,996 - 38,578 or a complementary sequence or a fragment thereof wherein said probe  
10 hybridizes at high stringency to a nucleic acid expressed in the human adult liver.

Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous  
15 nucleotides of said SEQ ID NO:. It is preferred that the single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

20 In another preferred embodiment, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb,  
25 preferably 15kb, more preferably 20kb or, most preferably, no more than 20kb in length.

Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or  
30 PNA.

In another embodiment of either the third or fourth aspect of the invention, a single exon nucleic acid probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first  
35 member of a specific binding pair. Suitable fluorescent

labels include dyes such as cyanine dyes, preferably Cy3 and Cy5 although other suitable dyes will be known to those skilled in the art.

In a particularly preferred embodiment, a single  
5 exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks  
10 homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition, comprising:

the single exon nucleic acid probe in accordance  
15 with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is  
20 provided a method of measuring gene expression in a sample derived from human adult liver, comprising:

contacting the single exon microarray in accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said  
25 first collection of nucleic acids derived from mRNA of human adult liver; and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is  
30 provided a method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably  
35 labeled nucleic acids to a single exon probe,



wherein said detectably labeled nucleic acids are derived from mRNA from the adult liver of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a single exon microarray in accordance with the first aspect of the invention, and said fragment is selectively hybridizable at high stringency.

In a eighth aspect of the invention, there is provided a method of assigning exons to a single gene, comprising:

identifying a plurality of exons from genomic sequence in accordance with the seventh aspect of the invention; and then measuring the expression of each of said exons in a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

In an ninth aspect of the invention, there is provided a nucleic acid sequence as set out in any of SEQ ID NOS: 1 - 25,995 wherein said sequence encodes a peptide.

In a tenth aspect of the invention, there is provided a peptide encoded by a sequence comprising a sequence as set out in any of SEQ ID NOS: 13,110 - 25,995, or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be encoded by a sequence comprising a sequence set out in any of SEQ ID NOS.: 1 - 13,109.

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ

ID NOS.: 25,996 - 38,578.

Accordingly in a eleventh aspect of the invention there is provided a peptide comprising a sequence as set out in any of SEQ ID NOs: 25,996 - 38,578, or fragment  
5 thereof.

In another aspect, the invention provides means for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display  
10 can be used as a preferred graphical user interface for electronic search, query, and analysis of such annotated sequence.

## 15 Detailed Description of the Invention

### Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound  
20 collection of plural nucleic acids, hybridization to each of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase  
25 "nucleic acid microarray" include all the devices so called in Schena (ed.), DNA Microarrays: A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and  
30 Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376). As so defined, the term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably  
35 disposed on a plurality of beads, rather than on a unitary

planar substrate, as is described, *inter alia*, in Brenner  
et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000);  
in such case, the term "microarray" and phrase "nucleic  
acid microarray" refer to the plurality of beads in  
5 aggregate.

As used herein with respect to a nucleic acid  
microarray, the term "probe" refers to the nucleic acid  
that is, or is intended to be, bound to the substrate; in  
such context, the term "target" thus refers to nucleic acid  
10 intended to be bound thereto by Watson-Crick  
complementarity. As used herein with respect to solution  
phase hybridization, the term "probe" refers to the nucleic  
acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising  
15 SEQ ID NO.", and variants thereof, intends a nucleic acid  
probe, at least a portion of which probe has either (i) the  
sequence directly as given in the referenced SEQ ID NO., or  
(ii) a sequence complementary to the sequence as given in  
the referenced SEQ ID NO., the choice as between sequence  
20 directly as given and complement thereof dictated by the  
requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and  
the equivalent acronym "ORF" refer to that portion of an  
exon that can be translated in its entirety into a sequence  
25 of contiguous amino acids i.e. a nucleic acid sequence  
that, in at least one reading frame, does not possess stop  
codons; the term does not require that the ORF encode the  
entirety of a natural protein.

As used herein, the term "amplicon" refers to a  
30 PCR product amplified from human genomic DNA, containing  
the predicted exon.

As used herein the term "exon" refers to the  
consensus prediction of the various exon and gene  
predicting algorithms i.e. a nucleic acid sequence  
35 bioinformatically predicted to encode a portion of a

natural protein.

As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a portion thereof set out in exon SEQ ID NOS.: The codons encoding the peptide are wholly contained within the exon.

As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a combination of those sequences. A fragment unique to a nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF present within the probe, or its complement, is present within a target mRNA.

As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another of a given sequence under "stringent conditions" it is meant that it is homologous to the given sequence.

As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit specific binding when they exhibit avidity of at least  $10^7$ , preferably at least  $10^8$ , more preferably at least  $10^9$  liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

As used herein with respect to the visual display of annotated genomic sequence, the term "rectangle" means any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual

object of the display.

As used herein, a "Mondrian" means a visual display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional  
5 information.

#### Brief Description of the Drawings

10 The present invention is further illustrated with reference to the following non-limiting figures and examples in which:

FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the  
15 functional activity of such regions experimentally, and associating and displaying the data so obtained in meaningful and useful relationship to the original sequence data;

FIG. 2 further elaborates that portion of the  
20 process schematized in FIG. 1 for predicting functional regions from genomic sequence;

FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

25 FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length shown in black and PCR product length shown in dotted lines;

FIG. 6 is a histogram showing the distribution,  
30 among exons predicted according to the methods described, of expression as measured using simultaneous two color hybridization to a genome-derived single exon microarray. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or  
35 more but not all tested tissues ("1" - "9"), or expressed

in all tissues tested ("10");

FIG. 7 is a pictorial representation of the expression of verified sequences that showed expression with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by microarray hybridization in each of the 10 measured tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than  $1e^{-30}$  ( $1 \times 10^{-30}$ ) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than  $1e^{-30}$  ( $1 \times 10^{-30}$ ) ("known");

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

Methods and Apparatus for Predicting, Confirming, Annotating, and Displaying Functional Regions From Genomic Sequence Data

FIG. 1 is a flow chart illustrating in broad outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained

in meaningful and useful relationship to the original sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100 in the present invention include GenBank, and particularly include several divisions thereof, including the htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the National Institutes of Health and is maintained by the

National Center for Biotechnology Information (NCBI).  
Databases of genomic sequence from species other than  
human, such as mouse, rat, Arabidopsis, *C. elegans*, *C.*  
*briggsii*, *Drosophila*, zebra fish, and other higher  
5 eukaryotic organisms will also prove useful as genomic  
sequence database 100.

Genomic sequence obtained by query of genomic  
sequence database 100 is then input into one or more  
processes 200 for identification of regions therein that  
10 are predicted to have a biological function as specified by  
the user. Such functions include, but are not limited to,  
encoding protein, regulating transcription, regulating  
message transport after transcription into mRNA, regulating  
message splicing after transcription into mRNA, of  
15 regulating message degradation after transcription into  
mRNA, and the like. Other functions include directing  
somatic recombination events, contributing to chromosomal  
stability or movement, contributing to allelic exclusion or  
X chromosome inactivation, and the like.

20 The particular genomic sequence to be input into  
process 200 will depend upon the function for which  
relevant sequence is to be identified as well as upon the  
approach chosen for such identification. Process step 200  
can be iterated to identify different functions within a  
25 given genomic region. In such case, the input often will  
be different for the several iterations.

Sequences predicted to have the requisite  
function by process 200 are then input into process 300,  
where a subset of the input sequences suitable for  
30 experimental confirmation is identified. Experimental  
confirmation can involve physical and/or bioinformatic  
assay. Where the subsequent experimental assay is  
bioinformatic, rather than physical, there are fewer  
constraints on the sequences that can be tested, and in  
35 this latter case therefore process 300 can output the



entirety of the input sequence.

The subset of sequences output from process 300 is then used in process 400 for experimental verification and characterization of the function predicted in  
5 process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can  
10 be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a  
15 combination thereof, or by other means well known within the database arts. The data can even be submitted for incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation  
20 can be input into process 500 from external sources 600.

The annotated data is then displayed in process 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magnetooptical disk, flash memory, or the  
25 like.

FIG. 1 shows that the experimental data output from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an  
30 experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly  
35 to the succeeding process, or stored in permanent or

interim form prior to passage to the succeeding process. Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps can be automated.

5               FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to process 200.

Genomic sequence database 100 is first queried 20 for genomic sequence.

10              The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be identified.

For example, genomic sequences that function to encode protein can be identified *inter alia* using gene  
15 prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding  
20 regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences  
25 and identify regions of least variability.

The exact content of query 20 will also depend upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be  
30 determined is protein coding regions in human genomic sequence, the query will accordingly require that the sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements  
35 of the subsequent analytical method. Alternatively, or in

addition, such operative criteria can be enforced in subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate  
5 criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

10 Such criteria can, for example, consist of a required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any  
15 given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

20 Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given  
25 BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated  
30 into the query can be the date, or range of dates, of sequence accession. Although the process has been described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are  
35 typically updated on a frequent, even hourly, basis. Thus,

as further described in Examples 1 and 2, *infra*, it is possible to query the database for newly added sequence, either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods  
5 and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic, temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the  
10 presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for  
15 sequences that function to encode protein, readily identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery  
20 can be performed using genomic sequence from species other than human.

If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query,  
25 depending in part upon the query language, the complexity of the query, and other considerations well known in the database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by  
30 process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to report and termination of the initial inquiry, a new query 20 can be generated that takes into account the initial negative result.

35 When query 20 returns sequence meeting the query

criteria, the returned sequence is then passed to optional preprocessing 24, suitable and specific for the desired analytical approach and the particular analytical methods thereof to be used in process 25.

5               Preprocessing 24 can include processes suitable for many approaches and methods thereof, as well as processes specifically suited for the intended subsequent analysis.

              Preprocessing 24 suitable for most approaches and  
10 methods will include elimination of sequence irrelevant to, or that would interfere with, the subsequent analysis. Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like.  
15 Such removal can readily be performed by identification and subsequent masking of the undesired sequence.

              Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence,  
20 vector sequence, artificial sequence, and other artifactual sequence. Such comparison can readily be done using programs well known in the art, such as CROSS\_MATCH, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

25               Alternatively, or in addition, undesirable, including artifactual, sequence can be identified algorithmically without comparison to external databases and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies  
30 a significantly higher than average density of known restriction sites. As another example, vector sequence can be identified by algorithms that identify nucleotide or codon usage at variance with that of the bulk of the genomic sequence.

35               Once identified, undesired sequence can be

removed. Removal can usefully be done by masking the undesired sequence as, for example, by converting the specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X".

- 5 Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence, leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of  
10 highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can  
15 also or alternatively be valued by presence in the longest contig.

Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25.  
20 Such formatting can and typically will include, *inter alia*, addition of a unique sequence identifier, either derived from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion  
25 from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the  
30 informational requirements of the methods for effecting such identification, is followed by sequence processing 25, where sequences with the desired function are identified within the genomic sequence.

As mentioned above, such functions can include,  
35 but are not limited to, encoding protein, regulating

transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription, of regulating message degradation, and the like. Other functions include directing somatic  
5 recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for  
10 identifying, from genomic sequence, regions that function to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the  
15 novel single exon microarrays of the present invention, as further described below, the methods herein described become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative  
20 coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more  
25 software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

30 As further described in Example 1, below, gene finding software programs yield a range of results. For the newly accessioned human genomic sequence input in Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region,  
35 2% of the data analyzed; GENEFINDER was second, calling 1%;

and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although  
5 discussed herein particularly with respect to exon calling, consensus among methods will in general increase reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be  
10 repeated with a different method, with consensus among such iterations determined and reported in process 27.

Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as  
15 well as the sequence meeting that consensus, is then stored in process 29a, displayed in process 29b, and/or output to process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated  
20 and reported by process 27. For example, as further described in Example 1, *infra*, process 27 can report consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene  
25 prediction algorithms used. Thus, in Example 1, process 27 reported that GRAIL and GENEFINDER programs agreed on 0.7% of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way,  
30 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

Furthermore, consensus can be required among different approaches to identifying a chosen function.

For example, if the function desired to be  
35 identified is coding of protein sequence, and a first used



approach to exon calling is gene prediction, the process can be repeated on the same input sequence, or subset thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative  
5 sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence, but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

10           Although shown as an iterative process, the multiple analyses required to achieve consensus can be done in series, in parallel, or some combination thereof.

          Predicted functional sequence, optionally representing a consensus among a plurality of methods and  
15 approaches for determination thereof, is passed to process 300 for identification of a subset thereof for functional assay.

          In the preferred embodiment of the methods of the present invention, wherein the function sought to be  
20 identified is protein coding, process 300 is used to identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

          For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into  
25 putative genes. This binning can be based *inter alia* upon consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-  
30 specific ORFs can be chosen for subsequent use in gene expression assay.

          Where such subsequent gene expression assay uses amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative  
35 exon length, sequence GC content, existence of possible

secondary structure, and the like can be used to identify and select those ORFs that appear most likely successfully to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using  
5 amplified product, further considerations involving hybridization stringency can be applied to identify that subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance  
10 of putative exons that span repetitive sequence; such sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested  
15 experimentally, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for  
20 experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred  
25 embodiment of process 400, therefore, the expression of the sequences predicted to encode protein is verified. The combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention  
30 provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of  
35 nucleic acid microarray, the genome-derived single exon

nucleic acid microarrays of the present invention.

Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by  
5 process 300, are amplified from genomic DNA using the polymerase chain reaction (PCR). Although PCR is conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture  
10 the entirety of each predicted ORF in an amplicon with minimal additional (that is, intronic or intergenic) sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying  
15 length.

However, most predicted ORFs are shorter than 500 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the  
20 methods of the present invention have suggested that longer amplicons, at least about 400 or 500 base pairs, are more effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can  
25 alternatively, and preferably, be designed to amplify regions of defined size, preferably at least about 300, 400 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or  
30 intergenic nucleic acid in addition to putative ORF.

Conversely, somewhat fewer than 10% of ORFs predicted from human genomic sequence according to the methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about  
35 300, 400 or 500 bp in length, can be amplified. However, it

has been discovered that the percentage success at amplifying pieces of such ORFs is low, and that such putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

The putative ORFs selected in process 300 are thus input into one or more primer design programs, such as PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>), with a goal of amplifying at least about 500 base pairs of genomic sequence centered within or about ORFs predicted to be no more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased commercially or synthesized by standard techniques.

Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not exceed about 25 nt in length. The "universal" priming sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for

amplification will come from the eukaryotic species from which the genomic sequence data had originally been obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, e.g., Short Protocols in Molecular Biology : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4<sup>th</sup> edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual, 2<sup>nd</sup> edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

Although the intronic and intergenic material flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see

above).

Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include

5 polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can

10 also be used. Typically, the support will be rectangular, although other shapes, particularly circular disks and even spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as

15 described in WO 98/12559.

The amplified nucleic acids can be attached covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by

20 presumed noncovalent interactions, or some combination thereof.

Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version

25 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or can conveniently be purchased from commercial sources (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using

30 ink jet technology.

As is well known in the art, microarrays typically also contain immobilized control nucleic acids. For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of

35 the present invention, a plurality of *E. coli* genes can

readily be used. As further described in Example 1, 16 or 32 *E. coli* genes suffice to provide a robust measure of background noise in such microarrays.

As is well known in the art, the amplified  
5 product disposed in arrays on a support substrate to create a nucleic acid microarray can consist entirely of natural nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as  
10 complementary binding can be obtained in the hybridization. If enzymatic amplification is used to produce the immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

15 Although particularly described herein as using high density microarrays constructed on planar substrates, the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined,  
20 including lower density planar arrays, and microarrays on nonplanar, nonunitary, distributed substrates.

For example, gene expression can be confirmed using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon,  
25 and positively-charged derivatized nylon membranes. Further, gene expression can also be confirmed using nonplanar, bead-based microarrays such as are described in Brenner *et al.*, *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No.  
30 5,736,330. In theory, a packed collection of such beads provides in aggregate a higher density of nucleic acid probe than can be achieved with spotting or lithography techniques on a single planar substrate.

Planar microarrays on solid substrates, however,  
35 provide certain useful advantages, including high

throughput and compatibility with existing readers. For example, each standard microscope slide can include at least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created by *in situ* synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived - either directly or indirectly - from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon *et al.*, or from the *de novo* construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas *et al.*, *Cancer Res.* (in press). Such microarrays are herein collectively denominated "EST microarrays".

Such EST microarrays by definition can measure



expression only of those genes found in EST libraries, shown herein to represent only a fraction of expressed genes. Furthermore, such libraries – and thus microarrays based thereupon – are biased by the tissue or cell type of message origin, by the expression levels of the respective genes within the tissues, and by the ability of the message successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be determined – subsequently arrayed for expression measurements could not, therefore, have been represented as probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the present invention – that is, the one third of sequences that had previously been accessioned in EST or other expression databases – are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA library depends upon the successful reverse transcription, optionally but typically with subsequent successful cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present invention depends upon a successful amplification from genomic material, *a priori* knowledge of the sequence of the desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse

transcription and cloning of unknown message in EST approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-derived single exon microarrays of the present invention lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present invention lack homopolymeric regions consisting of A or T, where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the specificity of hybridization, is occasioned by the typical derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically include a fair amount of vector sequence, more so when the probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector

sequence, having been amplified directly or indirectly from genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage. Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence.

10 With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater

15 specificity during hybridization, since spurious cross-hybridization to a probe vector sequence is reduced.

As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain

20 artificial sequence, derived from vector polylinker multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific

25 primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such

30 "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the genome-derived single exon microarray will include artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon

35 microarray of the present invention can be made without

such sequences, and if so constructed, presents an even smaller amount of nonspecific sequence that would contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially-spliced message, probes disposed upon EST arrays will often include multiple exons. The percentage of such exon-spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized probes. For human genes, the near-complete sequence of human chromosome 22, Dunham et al., *Nature* 402(6761):489-95 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

In contrast, by virtue of their origin from algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus, 5 in contrast to EST microarrays, at least about 50, 60, 70, 75, 80, 85, 95 or 99% of probes deposited in the genome-derived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved 10 using EST microarrays, to use the genome-derived single exon microarrays of the present invention to measure tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of 15 differential splicing to tissue-specific expression patterns.

Furthermore, the exons that are represented in EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used 20 for EST identification are so biased. In contrast, no such 3' or 5' bias necessarily inheres in the selection of exons for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genome- 25 derived single exon microarrays of the present invention typically, but need not necessarily, include intronic and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the 30 exon-including probes on the genome-derived single exon microarrays of the present invention include sequence drawn from noncoding regions. As discussed above, the additional presence of noncoding region does not significantly interfere with measurement of gene expression, and provides 35 the additional opportunity to assay prespliced RNA, and

thus measure such phenomena such as nuclear export control.

The genome-derived single exon microarrays of the present invention are also quite different from *in situ* synthesis microarrays, where probe size is severely  
5 constrained by inadequacies in the photolithographic synthesis process.

Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be  
10 performed at low stringency. In order, therefore, to achieve unambiguous sequence-specific hybridization results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered  
15 (*i.e.*, mismatched) sequence.

In contrast, the longer probe length of the genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the  
20 genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the  
25 microarrays of the present invention than can be achieved for *in situ* synthesis microarrays.

A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed  
30 on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the  
35 melting temperature of probes hybridized to their

complementary target sequence, and thus causes large percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the  
5 microarrays of the present invention create lower percentage differences in melting temperature across the range of arrayed probes.

A further significant advantage of the microarrays of the present invention over *in situ*  
10 synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe basis for the *in situ* synthesized microarrays presently being used.

15 The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari *et al.*, *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

20 Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* - that is, only about 4 - 5% - have standard, spliceosomal, introns, Lopez *et al.*, *Nucl. Acids Res.* 28:85-86 (2000); Spingola *et al.*, *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome  
25 has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

30 Thus, a significant aspect of the present invention is the ability to identify and to confirm expression of predicted coding regions in genomic sequence drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as  
35 *Saccharomyces cerevisiae*, particularly in genomic sequence

drawn from eukaryotes in which at least about 10, 20 or 50% of protein-encoding genes have introns. In preferred embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is performed.

In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon microarrays prepared as above- described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

mRNA can be prepared by standard techniques, see Ausubel et al. and Maniatis et al., or purchased commercially. The mRNA is then typically reverse-transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of



nucleotides labeled with a first label, typically a fluorophore (fluorochrome; fluor; fluorescent dye); the reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically  
5 fluorometrically-distinguishable from the first label. As further described in Example 2, *infra*, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to  
10 standard techniques, typically under a coverslip.

After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage,  
15 to process 500, where the results for each probe are related to the original sequence.

Often, hybridization of target material to the genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it  
20 is often desirable that the user be able readily to obtain sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally  
25 as a solitary solid-phase or solution-phase probe, for further use.

Thus, in another aspect, the present invention provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially  
30 identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well  
35 of a microtiter dish. Although a 96 well microtiter plate

can be used, greater efficiency is obtained using higher density arrays, such as are provided by microtiter plates having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions (wells) are conveniently used, any device that permits addressable withdrawal of reagent from fluidly-noncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genome-derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

In another aspect of the present invention, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing

information, and that can additionally contain annotation information, such as gene expression data. Such recordable media can be packaged with the microarray, with the ordered probe set, or with both.

5           If the microarray is constructed on a substrate that incorporates recordable media, such as is described in international patent application no. WO 98/12559, then separate packaging of the genome-derived single exon microarray and the bioinformatic information is not  
10 required.

The amount of amplifiable probe material should be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

Although the use of high density genome-derived  
15 microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

20           Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

For example, where the function desired to be  
25 identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases,  
30 such as EST databases, SNP ("single nucleotide polymorphism") databases, known cDNA and mRNA sequences, SAGE ("serial analysis of gene expression") databases, and more generalized sequence databases that allow query for expressed sequences. Such query can be done by any  
35 sequence query algorithm, such as BLAST ("basic local

alignment search tool"). The results of such query – including information on identical sequences and information on nonidentical sequences that have diffuse or focal regions of sequence homology to the query sequence –  
5 can then be passed directly to process 500, or used to inform analyses subsequently undertaken in process 200, process 300, or process 400.

Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process  
10 500 where it is usefully related to the sequence data itself, a process colloquially termed "annotation". Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the  
15 record itself, by linking records in a hierarchical or relational database, by linking to external databases, or by a combination thereof. Such database techniques are well within the skill in the art.

The annotated sequence data can be stored  
20 locally, uploaded to genomic sequence database 100, and/or displayed 800.

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at  
25 which sequence now accumulates, the rapid pace of sequence annotation produces a need for methods of displaying the information in meaningful ways.

FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present  
30 invention. Because of its nominal resemblance to artistic works of Piet Mondrian, visual display 80 is alternatively described herein as a "Mondrian".

Each of the visual elements of display 80 is aligned with respect to the genomic sequence being  
35 annotated (hereinafter, the "annotated sequence"). Given

the number of nucleotides typically represented in an annotated sequence, representation of individual nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically – for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other pointer over rectangle 89 – or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed. Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or fulcrum point about which a chosen range of sequence is anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity

or identity to an input query sequence. When visual display 80 is used as a graphical user interface to computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein.

For example, rectangles 83a can represent the results from GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the results from DICTION.

5           Optionally, and preferably, rectangles 83 collectively representing predictions of a single method and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

10           Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction.

15           Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be

20           made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by pointer (e.g., mouse)-activated link.

          As earlier described, increased predictive reliability can be achieved by requiring consensus among

25           methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

          Although FIG. 3 shows three series of

30           horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

35           Furthermore, field 81 can be used to show

predictions of a plurality of different functions.

However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select a single function for display. When display 80 is used as  
5 a graphical user interface for computer query and analysis, such function can usefully be indicated and user-selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including  
10 interposed rectangle 84. Rectangle 84 represents the portion of annotated sequence for which predicted functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right  
15 borders of rectangle 84. Rectangle 85, with optional inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of  
20 annotated genomic sequence. It is expected that an increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing  
25 an increased density of sequence annotation.

Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using  
30 genome-derived single exon microarrays, rectangle 84 identifies the sequence included within the probe immobilized on the support surface of the microarray. As noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during  
35 amplification and designed to permit reamplification of the



probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity

has a user-selectable lower threshold). Alternatively, as many different levels of discrimination can be indicated as can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links directly to the sequences identified by the query of expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be resident on the computer presenting such display, which often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical assay of the sequence delimited by its left and right borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to depict expression less than control, corresponding to the spectra of the Cy3 and Cy5 dyes conventionally used for respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to

indicate expression intensity. As discussed *infra*, such relative expression (expression ratios) and absolute expression (signal intensity) can be expressed using normalized values.

5               Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized  
10 mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*.  
15 BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by  
20 DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates  
25 unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of  
30 such individual Mondrians, as shown in FIGS. 9 and 10.

#### Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present  
35 invention rapidly produce functional information from

genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode  
5 protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in  
10 one or more tissues or cell types.

It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

15 Using the methods and genome-derived single-exon microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray  
20 hybridization analysis, the expression of 13,109 of these ORFs in adult liver.

As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in adult liver is currently  
25 available for use in measuring the level of its ORF's expression in adult liver.

Diseases of the liver are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition,  
30 onset, and/or aggressiveness of most, if not all, of these diseases; although causative mutations in single genes have been identified for some, these disorders are believed for the most part to have polygenic etiologies.

For example, cirrhosis is a major public health  
35 problem. In the industrialized world, it is among the top

ten causes of death; among patients aged 45 to 65, it is the third leading cause of death. The high prevalence is largely the result of alcohol abuse, but other major contributors include chronic hepatitis, biliary disease and iron overload. Approximately 10-15% are cryptogenic.

Cirrhosis is a broad description encompassing the common end stage of many forms of liver injury. Many patients with cirrhosis will remain asymptomatic for years, while others show generalized weakness, anorexia, malaise, and weight loss or, occasionally, more severe symptoms.

The progression from fibrosis, an early consequence of liver disease, to cirrhosis, and the specific histologic morphology that characterizes cirrhosis depend on the extent of injury, the presence of continuing damage, and the response of the liver to damage. The liver may be injured acutely and severely (e.g. necrosis with hepatitis), moderately over months or years (e.g. biliary tract obstruction and chronic active hepatitis), or modestly but continuously (e.g. alcohol abuse).

During the repair process, new vessels connecting the hepatic artery and portal vein to the hepatic venules form within the fibrous sheath that surrounds the surviving nodules of liver cells. These vessels restore the intrahepatic circulatory pathway, but provide relatively low-volume, high-pressure drainage that is less efficient than normal and results in increased portal vein pressure (portal hypertension). Thus, cirrhosis is not static and its features depend on the disease activity and stage.

As cirrhosis is the end stage of many forms of liver disease, many genes have been identified that can contribute to the development of cirrhosis. These include, e.g., the genes responsible for Wilson disease (Online Mendelian Inheritance of Man ("OMIM") 277900), type IV glycogen storage disease (OMIM 232500), galactosemia (OMIM

230400), and a deficiency of alpha-1-antitrypsin (OMIM 107400). There is substantial evidence, however, for as yet uncharacterized loci which cause cirrhosis.

For example, Iber and Maddrey, *Prog. Liver Dis.* 2: 290-302 (1965), reviewed 13 previously reported families and 8 new to this study, each with 2 or more affected members. They pointed out that, with a single exception, the multiple cases were in the same generation. Within a given family, the age of onset, clinical course, and biopsy findings were very similar, but there were wide differences between families.

Kalra et al., *Hum. Hered.* 32:170-175 (1982) studied the families of 220 cases of Indian childhood cirrhosis and 70 families of age-matched controls. The hypotheses of autosomal recessive, partial sex-linkage, and doubly recessive inheritance were found untenable and the authors concluded that multifactorial inheritance was most plausible. Lefkowitz et al., *New Eng. J. Med.* 307:271-277 (1982) described 4 white American sibs who died between ages 4.5 and 6 years of cirrhosis that closely resembled that of the childhood cirrhosis of Asiatic Indians.

Another example of uncharacterized loci which cause cirrhosis are those related to the risk of alcoholism.

Cloninger, *Science* 236:410-416 (1987), defined two separate types of alcoholism. According to these definitions, type 1 alcohol abuse has its usual onset after the age of 25 years and is characterized by severe psychological dependence and guilt. Type 1 occurs in both men and women and requires both genetic and environmental factors to become manifest. By contrast, type 2 alcohol abuse has its onset before the age of 25; persons with this type of alcoholism are characterized by their inability to abstain from alcohol and by frequent aggressive and antisocial behavior. Type 2 alcoholism is rarely found in

women and is much more heritable.

Despite considerable effort to identify genes related to the risk of alcoholism, relatively few genes have been identified. Some of this work has suggested a  
5 relationship between the metabolism of dopamine and alcoholism. Blum et al., J.A.M.A. 263:2055-2060 (1990) and Bolos et al., J.A.M.A. 264:3156-3160 (1990) investigated the relationship of the dopamine D2 receptor (DRD2; OMIM 126450) to alcoholism, but the sample size was small and  
10 their results were inconclusive. However, Tiihonen et al., Molec. Psychiat. 4, 286-289 (1999), found a markedly higher frequency in a population of type 1 alcoholics of the low activity allele of the enzyme catechol-O-methyltransferase (COMT, OMIM 116790), which has a crucial role in the  
15 metabolism of dopamine, suggesting a role for dopamine metabolism in increased risk of alcoholism. For a brief review of recent progress toward the identification of genes related to risk for alcoholism see Buck, Genome 9:927-928 (1998).

20 As another example, multiple genes have been shown to predispose to hyperlipoproteinemia or hyperlipidemia. Much attention has been focused on these disorders because there is a strong association of hyperlipidemia, especially hypercholesterolemia, with  
25 development of coronary artery disease. Coronary artery disease accounts for at least 25% of all deaths in the United States. Coronary artery disease results when the arteries supplying the heart muscle become occluded by plaques composed of lipids like cholesterol, blood clotting  
30 components and blood cells.

The major plasma lipids circulate bound to proteins as macromolecular complexes called lipoproteins. Although closely interrelated, the major lipoprotein classes - chylomicron, very-low-density lipoprotein (VLDL),  
35 low-density lipoprotein (LDL), and high-density lipoprotein

(HDL) - are usually classified in terms of physicochemical properties (e.g., density after centrifugation).

Chylomicrons, the largest lipoproteins, carry exogenous triglyceride from the intestine via the thoracic duct to the venous system and into peripheral sites. VLDL carries endogenous triglyceride primarily from the liver to the same peripheral sites for storage or use. Lipases quickly degrade the triglyceride in VLDL to produce intermediate density lipoproteins (IDL) and within 2 to 6 h, IDL is degraded further to generate LDL, which has a plasma half-life of 2 to 3 days. While the overall fate of LDL is unclear, the liver is responsible for removing approximately 70% and active receptor sites have been found on the surfaces of hepatocytes.

Several monogenic conditions that lead to elevated levels of one or more serum lipoproteins have been defined and the responsible gene identified, including, e.g., hyperlipoproteinemia type I (OMIM 238600), familial hypercholesterolemia (OMIM 143890), and familial defective apolipoprotein B (OMIM 107730). However, in many cases the etiology is unknown and there is strong evidence for additional uncharacterized loci.

For example, Zuliani et al., *Arterioscler. Thromb. Vasc. Biol.* 19:802-809 (1999) identified a Sardinian family with a recessive form of hypercholesterolemia with the clinical features of familial hypercholesterolemia (OMIM 603813), and found that previously identified genes were not responsible for this disorder. They proposed that in this new lipid disorder, a recessive defect causes a selective impairment of the LDL receptor function in the liver. Ciccarese et al., *Am. J. Hum. Genet.* 66:453-460 (2000) recently mapped this novel disease locus.

Another example is designated familial combined hyperlipidemia (OMIM 144250) which affects approximately 1-



2% of the population in the Western world. This disorder can have its basis in mutation in several novel genes, two of which have been mapped to chromosome 1 (Pajukanta et al., Nature Genet. 18:369-373 (1998)) and chromosome 11 (Aouizerat et al., Am. J. Hum. Genet. 65, 397-412 (1999)). The high frequency of this disorder suggests that most, if not all, hyperlipidemias are of multifactorial genetic etiology.

As yet a further example, primary schlerosing cholangitis (PSC) is a disorder characterized by a patchy obliterative inflammatory fibrosis of the large bile ducts. Chronic inflammation leads to extensive bile duct strictures, cholestasis, and gradual progression to biliary cirrhosis. PSC occurs most often in young men and is commonly associated with inflammatory bowel disease, especially ulcerative colitis. The onset is usually insidious, with gradual, progressive fatigue, pruritus, and jaundice. There is no specific therapy for sclerosing cholangitis, and liver transplantation is the only apparent cure.

The etiology of PSC is not known, but both genetic and immunologic abnormalities have been implicated. However, the frequency of HLA-B8 and HLA-DT2, which are associated with a number of autoimmune diseases, is higher in PSC than normal individuals. Prochazka et al., New Eng. J. Med. 322:1842-1844 (1990) found that 100% of 29 patients with primary sclerosing cholangitis carried the HLA-DRw52a antigen, which is normally present in 35% of the population.

As a still further example, sarcoidosis is a disease of unknown cause characterized by non-caseating granulomas in one or more organ systems. These granulomas may resolve completely or proceed to fibrosis. The disorder is systemic, but the liver is affected in approximately 75% of cases. Sarcoidosis occurs mainly in persons aged 20 to

40 yr and is most common in Northern Europeans and American blacks. The lifetime risk of developing sarcoidosis is particularly high among Swedish men (1.15%), Swedish women (1.6%), and African Americans (2.4%).

5           The much greater frequency in African Americans relative to the United States population overall suggests a genetic contribution to etiology. Early research studying familial aggregation indicated that the disease may have a nongenetic basis because the family pattern did not conform  
10 to a simple Mendelian mode of inheritance (Allison, Sth. Med. J. 57: 27-32 (1964)). However, Headings et al., Ann. N.Y. Acad. Sci. 278:377-385 (1976) favored multifactorial genetic inheritance of susceptibility. Nowack et al., Arch. Intern. Med. 147:481-483 (1987), found an unusually  
15 high frequency of HLA-DR5 in a study of 440 patients with sarcoidosis in Marburg, Germany. They also concluded that the role of an environmental or infectious agent triggering sarcoidosis cannot be envisaged without considering genetically linked cofactors.

20           Other significant diseases of liver are also believed to have a genetic, typically polygenic, etiologic component. These diseases include, e.g., primary biliary cirrhosis, Zellweger syndrome, cholestasis-lymphedema syndrome, Alstrom syndrome, primary pulmonary  
25 hypertension; Berardinelli-Seip congenital lipodystrophy, iron overload in Africa, neonatal cholestatic hepatitis, autosomal recessive KID syndrome, familial hypotransferrinemia, type I congenital dyserythropoietic anemia, porphyria variegata, Finnish lactic acidosis with  
30 hepatic hemosiderosis, Rotor syndrome, essential hypertension, ARC syndrome, type II conjugated hyperbilirubinemia, Lambert syndrome, ichthyosis congenita with biliary atresia, Kabuki make-up syndrome, Meckel syndrome, cerebral aneurysm-cirrhosis syndrome, glycogen  
35 storage diseases, polycystic kidney and hepatic disease,

isolated Caroli disease, trisomy 18-like syndrome, Osler-Rendu-Weber syndrome 3, fatal intrahepatic cholestasis, Coach syndrome, type C Niemann-Pick disease, and hepatocellular cancer.

5           Altered responses to a variety of infectious agents that target the liver, especially acute viral hepatitis, have also been shown or are suspected to have genetic bases or contributions. In addition to differential susceptibility to primary infectious agents, 10 these altered responses include predisposition to complicating conditions following contact with particular infectious agents. These include, e.g., development of hepatocellular carcinoma 2 correlated with Hepatitis B infection, and severe hepatic fibrosis following 15 *Schistosoma mansoni* infection.

          The central role of the liver in drug metabolism results in exposure of this organ to a large variety of potentially toxic chemical agents and metabolites. These include naturally occurring plant alkaloids and mycotoxins, 20 industrial chemicals, and, additionally, pharmacologic agents used in treating disease. The range of manifestations of toxin- and drug-induced liver disease are virtually as broad as the range of acute and chronic disorders and have also been shown or suspected to have 25 genetic bases or contributions.

          Such interactions between drugs and genotype have been shown in the response, e.g., to the anticonvulsant phenytoin, which can cause severe hepatitis-like disease in individuals who are impaired in the ability to detoxify a 30 metabolite of phenytoin in the liver, and in the response to the drug sodium valproate, which can produce severe hepatotoxicity in certain individuals. The abnormal responses to both of these drugs are believed to be influenced by underlying genetic factors.

35           The human genome-derived single exon nucleic acid

probes and microarrays of the present invention are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of human liver, particularly those diseases with polygenic etiology. With each of the single  
5 exon probes described herein shown to be expressed at detectable levels in human liver, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

10           For example, diagnosis (including differential diagnosis among clinically indistinguishable disorders, such as cirrhosis), staging, and/or grading of a disease can be based upon the quantitative relatedness of a patient gene expression profile to one or more reference expression  
15 profiles known to be characteristic of a given liver disease, or to specific grades or stages thereof.

          In one embodiment, the patient gene expression profile is generated by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the  
20 patient's liver to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly, using nucleic acids obtained directly or indirectly from transcripts expressed by liver of individuals with known liver disease. Methods for  
25 quantitatively relating gene expression profiles, without regard to the function of the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

          In another approach, the genome-derived single  
30 exon probes and microarrays of the present invention can be used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits predisposition to and/or prognosis of liver disease to be assessed through the massively parallel determination of  
35 altered copy number, deletion, or mutation in the patient's

genome of exons known to be expressed in human liver. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

5           The utility is specific to the probe; at sufficiently high hybridization stringency, which stringencies are well known in the art — see Ausubel et al. and Maniatis et al. — each probe reports the level of expression of message specifically containing that ORF.

10           It should be appreciated, however, that the probes of the present invention, for which expression in the adult liver has been demonstrated are useful for both measurement in the adult liver and for survey of expression in other tissues.

15           Significant among such advantages is the presence of probes for novel genes.

          As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be  
20 identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were  
25 represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence  
30 databases.

          Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes  
35 that are currently available for achieving these utilities.

The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and  
5 for surveying gene expression in the human.

Gene expression analysis using microarrays – conventionally using microarrays having probes derived from expressed message – is well-established as useful in the biological research arts (see Lockhart et al. *Nature* 405,  
10 827-836).

Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct  
15 Programs Regulating Lung Inflammation and Fibrosis," *Proc. Natl. Acad. Sci. USA* 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for  
20 example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of  
25 Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999); Voehringer et al., "Gene Microarray Identification of Redox and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA* 97(6):2680-5 (2000)).

30 Microarrays have also been used to determine abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl. Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al.,  
35

"Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers, *Proc. Natl. Acad. Sci. USA* 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell Carcinoma Using Combination of cDNA Subtraction and Microarray Analysis," *Oncogene* 19(12):1519-28 (2000); Whitney et al., "Analysis of Gene Expression in Multiple Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.* 46(3):425-8 (1999)), in drug discovery screens (see, for example, Scherf et al., "A Gene Expression Database for the Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44 (2000)) and in diagnosis to determine appropriate treatment strategies (see, for example, Sgroi et al., "In vivo Gene Expression Profile Analysis of Human Breast Cancer Progression," *Cancer Res.* 59(22):5656-61 (1999)).

In microarray-based gene expression screens of pharmacological drug candidates upon cells, each probe provides specific useful data. In particular, it should be appreciated that even those probes that show no change in expression are as informative as those that do change, serving, in essence, as negative controls.

For example, where gene expression analysis is used to assess toxicity of chemical agents on cells, the failure of the agent to change a gene's expression level is evidence that the drug likely does not affect the pathway of which the gene's expressed protein is a part.

Analogously, where gene expression analysis is used to assess side effects of pharmacological agents — whether in lead compound discovery or in subsequent screening of lead compound derivatives — the inability of the agent to alter a gene's expression level is evidence that the drug does not affect the pathway of which the gene's expressed protein is a part.

WO 99/58720 provides methods for quantifying the relatedness of a first and second gene expression profile

and for ordering the relatedness of a plurality of gene expression profiles. The methods so described permit useful information to be extracted from a greater percentage of the individual gene expression measurements from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold et al., *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999); Schena et al.

10           The invention particularly provides genome-derived single-exon probes known to be expressed in adult liver.           The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity  
15           sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA complementary to the message, single-stranded RNA  
20           complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained. For example, probes  
25           can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

Usefully, however, such probes are provided in a  
30           form and quantity suitable for amplification, where the amplified product is thereafter to be used in the hybridization reactions that probe gene expression. Typically, such probes are provided in a form and quantity suitable for amplification by PCR or by other well known  
35           amplification technique. One such technique additional to



PCR is rolling circle amplification, as is described, *inter alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and WO 00/15779. As is well understood, where the probes are  
5 to be provided in a form suitable for amplification, the range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

Where the probe is to be provided in form  
10 suitable for amplification, the quantity need not be sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or 100 pg or more.

Each discrete amplifiable probe can also be  
15 packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged therefrom. As earlier mentioned, the ORF-specific  
20 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this embodiment, the use of a single set of 5' and 3'  
25 primers to amplify any one of the probes. The probe composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present  
30 invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived  
35 single exon microarray of the present invention, the

genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however – that is, for use in a  
5 hybridization reaction in which the probe is not first bound to a support substrate (although the target may indeed be so bound) – length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

10 In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable  
15 of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message – a subset of target sequence that is much reduced in complexity as compared to genomic sequence – even fewer nucleotides are required for specificity.

20 Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 13,110 – 25,995, respectively, for probe SEQ ID NOS. 1 – 13,109. The minimum amount of ORF required to be  
25 included in the probe of the present invention in order to provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 13,110 – 25,995 individually by routine experimentation using standard high stringency  
30 conditions.

Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl  
35 poly(dA), 0.2 µg/µl human c<sub>ot</sub>1 DNA, and 0.5 % SDS, in a

humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high stringency conditions can usefully be aqueous hybridization at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in temperature for hybridization and washing to room temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art to determine such complementary sequence. It will further be understood that double stranded probes can be used in

both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have  
5 sequence complementary to those described herein above and below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or  
10 both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution  
15 hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as  $^3\text{H}$ ,  $^{32}\text{P}$ ,  $^{33}\text{P}$ ,  $^{35}\text{S}$ ,  $^{125}\text{I}$ ,  $^{131}\text{I}$ ; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR<sup>®</sup>

20 Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates thereof; labels suitable for chemiluminescent and/or  
25 enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

The probes, either in quantity sufficient for  
30 hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

35 When provided as a collection of plural

individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is  
5 obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second,  
10 different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen  
15 for the common attribute of expression in the human adult liver.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell  
20 type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF  
25 by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to  
30 provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional section of this description, *supra*.

The invention particularly provides genome-  
35 derived single-exon nucleic acid microarrays comprising a

plurality of probes known to be expressed in human adult liver. In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group  
5 consisting of SEQ ID NOS.: 1 - 13,109.

When used for gene expression analysis, the genome-derived single exon microarrays provide greater physical informational density than do the genome-derived single exon microarrays that have lower percentages of  
10 probes known to be expressed commonly in the tested tissue. At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the  
15 same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with  
20 a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to  
25 their utility as probes of gene expression, particularly as probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 13,109 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 13,110 - 25,995, that encodes  
30 a protein domain. Thus, each of SEQ ID NOS. 1 - 13,109 can be used, or that portion thereof in SEQ ID NOS. 13,110 - 25,995 used, to express a protein domain by standard *in vitro* recombinant techniques. See Ausubel et al. and Maniatis et al.

35 Additionally, kits are available commercially

that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT<sup>™</sup> Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA; 5 Adeno-X<sup>™</sup> Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL<sup>™</sup>) System, New England Biolabs, Beverley, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, *inter alia*, in Chan et al. (eds.), Fmoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis 15 (Oxford Chemistry Primers, No 7) , Oxford Univ. Press (August 1992) (ISBN: 0198556683); and Bodanszky, Principles of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

It is, therefore, another aspect of the invention 20 to provide peptides comprising an amino acid sequence translated from SEQ ID NOS.: 13,110 - 25,995. Such amino acid sequences are set out in SEQ ID NOS: 25,996 - 38,578. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, 25 can be conjugated to a carrier protein and used to generate antibody that recognizes the peptide. Thus, it is a further aspect of the invention to provide peptides that have at least 8, preferably at least 15, consecutive amino acids.

30

The following examples are offered by way of illustration and not by way of limitation.

#### EXAMPLE 1

35 Preparation of Single Exon Microarrays from ORFs Predicted

in Human Genomic Sequence

### Bioinformatics Results

5 All human BAC sequences in fewer than 10 pieces  
that had been accessioned in a five month period  
immediately preceding this study were downloaded from  
GenBank. This corresponds to ~2200 clones, totaling ~350  
MB of sequence, or approximately 10% of the human genome.

10 After masking repetitive elements using the  
program CROSS\_MATCH, the sequence was analyzed for open  
reading frames using three separate gene finding programs.  
The three programs predict genes using independent  
algorithmic methods developed on independent training sets:  
GRAIL uses a neural network, GENEFINDER uses a hidden  
15 Markoff model, and DICTION, a program proprietary to  
Genetics Institute, operates according to a different  
heuristic. The results of all three programs were used to  
create a prediction matrix across the segment of genomic  
DNA.

20 The three gene finding programs yielded a range  
of results. GRAIL identified the greatest percentage of  
genomic sequence as putative coding region, 2% of the data  
analyzed. GENEFINDER was second, calling 1%, and DICTION  
yielded the least putative coding region, with 0.8% of  
25 genomic sequence called as coding region.

The consensus data were as follows. GRAIL and  
GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and  
DICTION agreed on 0.5% of genomic sequence, and the three  
programs together agreed on 0.25% of the data analyzed.  
30 That is, 0.25% of the genomic sequence was identified by  
all three of the programs as containing putative coding  
region.

ORFs predicted by any two of the three programs  
("consensus ORFs") were assorted into "gene bins" using two  
35 criteria: (1) any 7 consecutive exons within a 25 kb window



were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single gene if fewer than 7 exons were found within the 25 kb window.

#### PCR

The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

Previously, we had determined that DNA fragments fewer than 250 bp in length do not bind well to the amino-modified glass surface of the slides used as support substrate for construction of microarrays; therefore, amplicons were designed in the present experiments to approximate 500 bp in length.

Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>). A first additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was commonly added to each ORF-unique 3' primer, to permit subsequent reamplification of the amplicon using a single set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant further study.

The ORFs were then PCR amplified from genomic DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon

to be spotted in the microarray.

Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard techniques using human genomic DNA (Clontech, Palo Alto, CA) as template. Each PCR product was verified by SYBR<sup>®</sup> green (Molecular Probes, Inc., Eugene, OR) staining of agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR amplification was classified as successful if a single band appeared.

The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon) length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median size of 150 bp (n=9498). With an average amplicon size of 475 ± 25 bp, approximately 50% of the average PCR amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene finding algorithms.

Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular

Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

Some genomic clones (BACs) yielded very poor PCR and sequencing results. The reasons for this are unclear, but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some submitted sequence data.

Although the intronic and intergenic material flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent empirical results demonstrated that differential expression ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was similarly found not to affect differential expression ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the above-described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using commercially available instrumentation (MicroArray GenII Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("E") values less than  $1 \text{ e}^{-100}$ ) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe sequences showed some homology to a known EST or mRNA (BLAST E values from  $1 \text{ e}^{-5}$  to  $1 \text{ e}^{-99}$ ). The remaining 45% of

the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

All of the probe sequences (as amplified) were then analyzed for protein similarities with the SwissProt database using BLASTX, Gish *et al.*, *Nature Genet.* 3:266 (1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

10

Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis			
Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal
45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

EXAMPLE 2Gene Expression Measurements From Genome-Derived Single  
5 Exon Microarrays

The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series  
10 of simultaneous two-color fluorescence experiments to (1) Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells, and (2) Cy5-labeled cDNA prepared from message  
15 pooled from all ten tissues and cell types, as a control in each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

Briefly, mRNA samples were bought from commercial  
20 sources (Clontech, Palo Alto, CA and Amersham Pharmacia Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg of polyA<sup>+</sup> mRNA performed using 1 µg oligo(dT)12-18 primer and 2 µg random 9mer primers as follows. After heating to  
25 70°C, the RNA:primer mixture was snap cooled on ice. After snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT, 100µM dATP, 100 µM dGTP, 100 µM dTTP, 50 µM dCTP, 50 µM Cy3-dCTP or Cy5-dCTP 50 µM, and 200 U Superscript II  
30 enzyme. The reaction was incubated for 2 hours at 42°C. After 2 hours, the first strand cDNA was isolated by adding 1 U Ribonuclease H, and incubating for 30 minutes at 37°C. The reaction was then purified using a Qiagen PCR cleanup column, increasing the number of ethanol washes to 5.  
35 Probe was eluted using 10 mM Tris pH 8.5.

Using a spectrophotometer, probes were measured for dye incorporation. Volumes of both Cy3 and Cy5 cDNA corresponding to 50 pmoles of each dye were then dried in a Speedvac, resuspended in 30  $\mu$ l hybridization solution containing 50% formamide, 5X SSC, 0.2  $\mu$ g/ $\mu$ l poly(dA), 0.2  $\mu$ g/ $\mu$ l human c<sub>ot</sub>1 DNA, and 0.5 % SDS.

Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C overnight. Before scanning, slides were washed in 1X SSC, 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

Slides were scanned using a Molecular Dynamics Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

Although the use of pooled cDNA as a reference permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of at least 10% in the control channel. Because of this fact, both signal and expression ratios (the latter hereinafter, "expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

Data were accepted for further analysis only when signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is presented in FIG. 6.

FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant signal - where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) - 39% (991) were expressed in all 10 tissues. The next most common class (15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data - that is, presents the results returned by query of EST, NR and SwissProt databases using the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-

05 to  $1e-99$ ; black: E values  $> 1e-05$ ).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective  
5 tissue. In brain, 200 uniquely expressed genes were identified; in heart, 150. The remaining tissues gave the following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; HeLa, 50; HBL, 100; and BT474, 50.

10 It was further observed that there were many more "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose expression was measurable in only a single of the tested  
15 tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, fully 45% were present in existing expressed sequence  
20 databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

#### 25 Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those genes not found in the GenBank human EST database. The  
30 data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than  $1e-30$  (designated "unknown") upon query of existing EST, NR and SwissProt databases, and  
35 shows in blue the normalized Cy3 signal intensity for all



sequence-verified products with a BLAST Expect value of less than  $1e-30$  ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 0.2.

5           As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

10           However, a significant point is that a large number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes  
15 will not have been detected in an end-sequenced cDNA library.

          The significant point is that presence of the gene in an EST database is not a prerequisite for incorporation into a genome-derived microarray, and  
20 further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

#### Verification of Gene Expression

          To ascertain the validity of the approach  
25 described above to identify genes from raw genomic sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

          Two microarray probes were selected on the basis  
30 of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene  
35 expression panel 24 human cDNAs) (OriGene Technologies,

Inc., Rockville, MD).

Sequence AL079300\_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734\_1 was shown by microarray experiment to be present in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology – which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays – to identify novel genes from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain				
Microarray Sequence Name	Normal ized Signal	Expressi on Ratio	Homology to EST present in GenBank	Gene Function as described by GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca <sup>2+</sup> binding protein expressed in central nervous system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system
AC007245-5	1.5		High	Similar to amphiphysin, a synaptic vesicle-associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding protein found in nonmuscle filamin

AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/ Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen
AC004689-3	1.0		High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be  
5 important in the central nervous system or brain. The exon

giving the highest signal (AP00217-1) was found to be the gene encoding an S100B  $\text{Ca}^{2+}$  binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097  
5 (1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3  
10 were both found to be phosphatases present in neurons (Millward *et al.*, *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed  
15 down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless  
20 of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to  
25 tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2 were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L, AC006064-K; AC035604-3; AC006064-L). These genes are often  
30 used as controls or housekeeping genes in microarray experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in the literature to be found in brain and liver (Joshi *et al.*, *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result  
35

duplicated with the array. Other highly expressed chip  
 sequences included a translation elongation factor 1 $\alpha$   
 (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-  
 chromosome RNA-binding motif (Chai et al., *Genomics*  
 5 49(2):283-89 (1998)) (AC007320-3). A low homology analog  
 (AP00123-1/2) to a gene, DSCR1, thought to be involved in  
 trisomy 21 (Down's syndrome), showed high expression in  
 both brain and heart, in agreement with the literature  
 (Fuentes et al., *Mol. Genet.* 4(10):1935-44 (1995)).

10 As a further validation of the approach, we  
 selected the BAC AC006064 to be included on the array.  
 This BAC was known to contain the GAPDH gene, and thus  
 could be used as a control for the ORF selection process.  
 The gene finding and exon selection algorithms resulted in  
 15 choosing 25 exons from BAC AC006064 for spotting onto the  
 array, of which four were drawn from the GAPDH gene. Table  
 3 shows the comparison of the average expression ratio for  
 the 4 exons from BAC006064 compared with the average  
 expression ratio for 5 different dilutions of a  
 20 commercially available GAPDH cDNA (Clontech).

Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH		
	AC006064 (n = 4)	Control (n = 5)
Bone Marrow	-1.81 $\pm$ 0.11	-1.85 $\pm$ 0.08
Brain	-1.41 $\pm$ 0.11	-1.17 $\pm$ 0.05
BT474	1.85 $\pm$ 0.09	1.66 $\pm$ 0.12
Fetal Liver	-1.62 $\pm$ 0.07	-1.41 $\pm$ 0.05
HBL100	1.32 $\pm$ 0.05	2.64 $\pm$ 0.12
Heart	1.16 $\pm$ 0.09	1.56 $\pm$ 0.10
HeLa	1.11 $\pm$ 0.06	1.30 $\pm$ 0.15
Liver	-1.62 $\pm$ 0.22	-2.07 $\pm$

Lung	-4.95 $\pm$ 0.93	-3.75 $\pm$ 0.21
Placenta	-3.56 $\pm$ 0.25	-3.52 $\pm$ 0.43

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

### EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

15

For each genomic clone processed for microarray as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding programs, EST information associated with the probe sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the information.

Accordingly, we devised a new tool for visual display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known

exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION  
5 identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be from the same gene, the carbamyl phosphate synthetase gene  
10 (AF154830.1).

The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show identical expression patterns, elegantly demonstrating the  
15 reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease  
20 inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb,  
25 upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom):  
30 red = kallistatin protease inhibitor (P29622);  
purple = plasma serine protease inhibitor (P05154);  
turquoise =  $\alpha$ 1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

35



EXAMPLE 4Genome-Derived Single Exon Probes Useful For Measuring  
Human Gene Expression

5

The protocols set forth in Examples 1 and 2, *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique exons in the human genome that could be shown to be  
10 expressed at significant levels in liver tissue.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon microarray; sequencing confirms the exact chemical  
15 structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the single exon probes were first obtained by PCR amplification  
20 from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 13,109 single exon probes, each fragment corresponding to an extension product from one of the two amplification primers.)

25 The structures of the 13,109 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 13,109. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not included in the sequence listing. The sequences of the  
30 exons present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 13,110 - 25,995, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than one amplicon.

35 As detailed in Example 2, expression was

demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant expression is based on a statistical confidence that the signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give a total of 64 spots.

10           For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the population median.

15           Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

          The median of the signal from the remaining control spots is calculated and all subsequent calculations are done with normalised signals.

20           Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations) are eliminated. Spots with such high signals are considered to be "outliers".

          The mean and standard deviation of the modified control spot populations are calculated.

          The mean + 3x the standard deviation (mean + (3\*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

          This means that, assuming that the data is distributed normally, there is a 99% confidence that any signal exceeding the threshold is significant.

35           The probes and their expression data are

presented in Table 4, set forth respectively in Example 5. Example 5 presents the subset of probes that is significantly expressed in the human adult liver and thus presents the subset of probes that was recognized to be  
5 useful for measuring expression of their cognate genes in human adult liver tissue.

The sequence of each of the exon probes identified by SEQ ID NOS.: 13,110 - 25,995 was individually used as a BLAST (or, for SWISSPROT, BLASTX) query to  
10 identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because the query sequences are themselves derived from genomic sequence in GenBank, only nongenic hits from NR were scored.

15 The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted in descending order based on this measure, reported as  
20 "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were found to have no similar sequences.

As sorted, Table 4 thus lists its respective probes (by "AMPLICON SEQ ID NO.:" and additionally by the  
25 SEQ ID NO.: of the exon contained within the probe:"EXON SEQ ID NO.:" from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be expressed (i.e., lowest BLAST E value), at the bottom of  
30 the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the name of the database in which the database sequence is  
35 found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS.

corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide sequences. These are set out as PEPTIDE SEQ ID NOS.:. The  
5 peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs are first determined in a uniform way according to each  
10 prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the exon, initial ORFs are merged into one or more final ORFs  
15 in an exhaustive process based on the following criteria:  
1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all of the data presented in Table 4, further includes, for  
20 each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

Table 4 further lists, for each probe, a portion of the descriptor for the top hit ("Top Hit Descriptor") as  
25 provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about  $1e-05$  and  $1e-100$ ), the descriptor reveals the likely function of the protein encoded by the probe's ORF.

30 Using BLAST E value cutoffs of  $1e-05$  (i.e.,  $1 \times 10^{-5}$ ) and  $1e-100$  (i.e.,  $1 \times 10^{-100}$ ) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, *supra*, a BLAST E value of  $1e-30$  was used as the boundary when only two classes were to be defined for  
35 analysis (unknown,  $>1e-30$ ; known  $<1e-30$ ) (see also FIG. 8).

Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about  $1e-100$  – which is probative evidence that the query sequence has previously been shown to be expressed – the top hit is highly unlikely  
5 exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even the ORF itself is unlikely in such cases to be present  
10 identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent a proper subset of the data present within the attached  
15 sequence listing. For each amplicon probe (SEQ ID NOs.: 1 – 13,109) and probe exon (SEQ ID NOs.: 13,110 – 25,995, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

(a) the accession number of the BAC from which  
20 the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;

(b) the most similar sequence provided by BLAST query of the EST database, with accession number and BLAST  
25 E value for the "hit";

(c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

(d) the most similar sequence provided by BLASTX  
30 query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

#### EXAMPLE 5

35 Genome-Derived Single Exon Probes Useful For Measuring

## Expression of Genes in Human Adult liver

Table 4 (545 pages) presents expression, homology, and functional information for the genome-derived single exon  
5 probes that are expressed significantly in human adult liver.

Page 1 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
472	13543	26465	4.79				
914	13966	26913	10.74				
1071	14115		2.15				
1328	14392	27310	10.84				
1519	14550	27511	1.03				
1519	14550	27512	1.03				
1937	14697	27630	1.56				
1662	14692	27652	3.77				
1755	14782	27752	1.72				
1781	14807	27778	7.27				
1909	14930	27907	1.05				
1994	15012	28002	2.13				
2179	15190	28196	2.41				
2298	15309	28312	2.27				
2608	15606	28599	1.49				
2608	15606	28600	1.49				
3229	16277	29178	2.44				
3510	16548	29448	1.58				
3575	16812	29515	8.4				
3620	16936		0.8				
3725	16757	29645	1.21				
4025	17052		0.99				
4293	17307	30178	1.88				
4361	17375	30238	11.97				
4449	17457		1.55				
4500	17510	30376	0.65				
4850	17949	30807	1.16				
4896	17985		0.72				
5174	18166	31011	5.51				
5188	18180	31025	1.15				
5438	18520	31245	2.5				
5438	18520	31246	2.5				
5607	18683		3.94				
5791	18863		8.49				

Page 2 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Database Source	Top Hit Descriptor
5876	18683		3.56			
5937	19004	32123	1.15			
5943	19010	32129	3.4			
6255	25645	32471	1.64			
6284	19335	32501	1.77			
6683	19719		1.31			
6829	19862	33074	1.26			
6829	19862	33075	1.26			
7485	20425	33705	1.39			
7485	20425	33705	1.39			
7811	20740	34043	1.28			
7811	20740	34044	1.28			
8330	21235		0.47			
8639	21570	34909	1.51			
9055	21694	35339	1.14			
9419	22347	35711	0.84			
9419	22347	35712	0.84			
10063	22979	36370	5.03			
10266	23176	36588	0.58			
10394	23283	36703	1.42			
10526	23412	36825	1.15			
10601	23687	37116	0.74			
10801	23687	37117	0.74			
10911	23796	37224	0.57			
10911	23796	37225	0.57			
11126	24056		3.49			
11467	24380		1.49			
11532	24442	37902	1.43			
11798	24720	38213	2.14			
11934	24778		2.59			
6287	19338	32605	15.42	9.9E+00 AJ239028.1	NT	Homo sapiens LSS gene, partial, exons 15, 16, 17 and 18
8585	21516	34860	1.8	9.8E+00 U32716.1	NT	Haemophilus influenzae Rd section 31 of 163 of the complete genome
10263	23153	36562	0.51	9.8E+00 Y18930.1	NT	Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2
10263	23153	36563	0.51	9.8E+00 Y18930.1	NT	Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2



Page 3 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7342	20338	33604	0.88	9.6E+00	AF05630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
7342	20338	33605	0.88	9.6E+00	AF05630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
10904	23789	37217	1.06	9.6E+00	AF242432.1	NT	Mus musculus Nalip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Nalip1) and general transcription factor IIH polypeptide 2 (Gif2h2) genes, complete cds
10904	23789	37218	1.06	9.6E+00	AF242432.1	NT	Mus musculus Nalip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Nalip1) and general transcription factor IIH polypeptide 2 (Gif2h2) genes, complete cds
2715	15709	28704	1	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2715	15709	28705	1	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2966	19018	28915	4	9.4E+00	AB043785.1	NT	Mus musculus A13 gene for antithrombin, complete cds
6580	19621	32808	0.51	9.4E+00	P75130	SWISSPROT	HYPOTHETICAL PROTEIN MG447 HOMOLOG
8677	21608	34950	1.22	9.3E+00	AF130690.1	NT	Homo sapiens ectodysplasin-A receptor protein (EDAR) gene, exons 2, 3, and 4
9555	22482	35842	3.44	9.3E+00	P11210	SWISSPROT	IMMEDIATE-EARLY PROTEIN 1 (IE1) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP89)
7874	20801	34104	0.44	9.2E+00	Q61767	SWISSPROT	3 BETA-HYDROXYSTEROID DEHYDROGENASE TYPE IV (3BETA-HSD IV) (3-BETA-HYDROXY-DELTA(5)-STEROID DEHYDROGENASE) (3-BETA-HYDROXY-5-ENE STEROID DEHYDROGENASE) (PROGESTERONE REDUCTASE)
5479	18560	31403	2.54	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5479	18560	31404	2.54	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
9964	22899		1.21	9.0E+00	P09241	SWISSPROT	RF-ODOPIN
6269	19320	32484	5.18	8.9E+00	BE971806.1	EST_HUMAN	601651038R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934592 3'
6641	19680	32870	2.11	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds
6641	19680	32871	2.11	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds
463	13535	26455	1.63	8.4E+00	5031804	NT	Homo sapiens insulin receptor substrate 1 (IRS1) mRNA
9987	21345	34880	4.11	8.1E+00	AJ131719.1	NT	Zea mays mRNA for legumain-like protease (see2a)
11611	24519		1.73	8.0E+00	P41820	SWISSPROT	BREFELDIN A RESISTANCE PROTEIN
8730	21690		1.07	7.6E+00	Z21489.1	NT	African swine fever virus NP1450L gene encoding RNA polymerase largest subunit
7733	20665		1.9	7.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
8933	21863	36219	1.68	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
8933	21863	36220	1.58	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
6011	19074	32200	3.41	7.4E+00	BF700517.1	EST_HUMAN	602128876F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285508 5'
9313	22241	35602	3.81	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR

Page 4 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9313	22241	35603	3.81	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3018	18070	28871	3.82	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
3018	16070	28972	3.82	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
7380	20374	33943	0.52	7.2E+00	BE179090.1	EST_HUMAN	RCO-HT0613-200300-031-a07 HT0613 Homo sapiens cDNA
7509	20448	33731	1.3	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
7509	20448	33732	1.3	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
10125	23016		10.55	7.1E+00	AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
11823	24743	38234	2.63	7.1E+00	P05850	SWISSPROT	HYPOTHETICAL 17.3 KDA PROTEIN IN MRDA-PHPB INTERGENIC REGION
10489	23376	36791	2.64	7.0E+00	P48910	SWISSPROT	ARGININE KINASE (AK)
11695	24598	38076	1.82	7.0E+00	Q22469	SWISSPROT	WD-40 REPEAT PROTEIN MS13
8860	21790	35141	2.11	6.9E+00	P35979	SWISSPROT	60S RIBOSOMAL PROTEIN L4 (L2)
10838	23724	37147	1.37	6.8E+00	P44834	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10856	23742	37165	0.54	6.9E+00	P34226	SWISSPROT	SKT5 PROTEIN
8487	21418	34754	1.8	6.8E+00	W03412.1	EST_HUMAN	z07c11.1 Soares melanocyte 2NBM Homo sapiens cDNA clone IMAGE:281860 5'
8487	21418	34755	1.6	6.8E+00	W03412.1	EST_HUMAN	z07c11.1 Soares melanocyte 2NBM Homo sapiens cDNA clone IMAGE:281860 5'
9677	22603		1.5	6.8E+00	P36307	SWISSPROT	OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) [CONTAINS: OUTER CAPSID PROTEINS VP5 AND VP8]
10705	23591	37018	3.32	6.8E+00	Q03570	SWISSPROT	HYPOTHETICAL 157.0 KDA PROTEIN C38C10.5 IN CHROMOSOME III
5469	18547		0.78	6.6E+00	Q89028	SWISSPROT	CATECHOL-O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)
6824	19857	33099	0.71	6.6E+00	BF672121.1	EST_HUMAN	602162573F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293427 5'
9585	25991		0.57	6.6E+00	P51825	SWISSPROT	AF-4 PROTEIN (FEL PROTEIN)
10576	23462	36884	2.64	6.6E+00	Q9ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
10576	23462	36885	2.64	6.6E+00	Q9ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
11569	24477		1.92	6.6E+00	Q10309	SWISSPROT	PROBABLE CATION-TRANSPORTING ATPASE C6C3.05C
9723	22848	36030	8.05	6.5E+00	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]
10794	23690	37110	0.55	6.5E+00	BE86000.1	EST_HUMAN	601678435F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3960689 5'
10282	23152	36561	1.31	6.2E+00	AY010901.1	NT	Schizaphyllum commune unknown mRNA
7387	20380	33649	1.35	6.0E+00	BE780163.1	EST_HUMAN	601468031F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871303 5'
10993	23877	37306	0.65	6.0E+00	AE001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
10993	23877	37307	0.65	6.0E+00	AE001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
							[Mus musculus mixed lineage kinase 3 (Mik3) and two pore domain K+ channel subunit (Kcnk8) genes, complete cds
6799	19832	33043	6.98	5.9E+00	AF155142.1	NT	
12060	24801		1.4	5.9E+00	BE958630.1	EST_HUMAN	601645278F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930461 5'
3585	16822		0.92	5.8E+00	7661557	NT	Homo sapiens DESCI1 protein (DESC1), mRNA

Page 5 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7523	20462	33749	0.79	5.7E+00	AF302046.1	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds
7523	20462	33750	0.79	5.7E+00	AF302046.1	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds
8002	20920		1.3	5.6E+00	P75080	SWISSPROT	DNA POLYMERASE III, ALPHA CHAIN POLC-TYPE (POLIII)
11906	24008	37450	2.46	5.6E+00	Q55279	SWISSPROT	LYOPENE BETA CYCLASE
6800	19544	32720	0.81	5.5E+00	P47447	SWISSPROT	HEAT-INDUCIBLE TRANSCRIPTION REPRESSOR HRCa
11218	24144		1.51	5.5E+00	AF175425.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 30, 31, and 32
11906	24006	37447	5.09	5.5E+00	P11990	SWISSPROT	PNEUMOLYSIN (THIOL-ACTIVATED CYTOLYSIN)
12163	24992		1.53	5.5E+00	AL161571.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 87
7259	20169	33407	1.2	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
7259	20168	33408	1.2	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
7715	20647		0.82	5.4E+00	Q99435	SWISSPROT	NEL PROTEIN PRECURSOR (NEL-RELATED PROTEIN 2)
8373	21277	34809	0.48	5.4E+00	P50391	SWISSPROT	NEUROPEPTIDE Y RECEPTOR TYPE 4 (NPY4R) (PANCREATIC POLYPEPTIDE RECEPTOR 1) (PP1)
8451	21383		1.58	5.4E+00	Q91062	SWISSPROT	VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELLIN LV-1N; LIPOVITELLIN LV-1C;
9357	22265	35947	1	5.4E+00	P40379	SWISSPROT	LIPOVITELLIN LV-2J
9357	22265	35948	1	5.4E+00	P40379	SWISSPROT	REP1 PROTEIN
10539	23425	36842	1.43	5.4E+00	Q17094	SWISSPROT	REP1 PROTEIN
10539	23425	36843	1.43	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
4897	17896	30761	1.38	5.3E+00	L43126.1	NT	Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds
6763	19797		0.55	5.3E+00	P41779	SWISSPROT	HOMEOBOX PROTEIN CEH-20
8657	21588		3.77	5.3E+00	P54098	SWISSPROT	DNA POLYMERASE GAMMA (MITOCHONDRIAL DNA POLYMERASE CATALYTIC SUBUNIT)
9535	22462		0.6	5.3E+00	A5034990.1	NT	Homo sapiens HERPUD1 gene for stress protein Herp, complete cds
12054	24805	38309	3.68	5.3E+00	Q27805	SWISSPROT	PROBABLE ANTIBACTERIAL PEPTIDE POLYPROTEIN PRECURSOR
5650	19724		1.18	5.2E+00	BE184840.1	EST_HUMAN	QV4-HT0691-270400-186-09 HT0691 Homo sapiens cDNA
10860	23746		0.89	5.2E+00	AF248070.1	NT	Drosophila orientacea R1B reticulospore element reverse transcriptase gene, partial cds
11640	24546		2.11	5.2E+00	Q10136	SWISSPROT	HYPOTHETICAL 61.1 KD PROTEIN C23E2.03C IN CHROMOSOME 1
9515	22442	35806	0.81	5.1E+00	O16005	SWISSPROT	RHODOPSIN
10340	23229	36846	1.56	5.1E+00	P09182	SWISSPROT	COLICIN N IMMUNITY PROTEIN (MICROGICIN N IMMUNITY PROTEIN)
8539	19582	32766	0.82	5.0E+00	BF310443.1	EST_HUMAN	601894910F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124114 5'
9597	22523	35887	0.52	5.0E+00	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10691	23577		0.81	5.0E+00	BF309591.1	EST_HUMAN	601890420F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131509 5'
10912	23797	37226	3.92	5.0E+00	AF182445.2	NT	Canis familiaris skeletal muscle chloride channel ClC-1 (CLCN1) mRNA, complete cds
11735	24637	38119	8.47	5.0E+00	Z83860.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 103/162

Page 6 of 545  
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Single Exon Probes Expressed in Adult Liver

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10727	23813		0.78	4.0E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
4147	17168		13.45	4.8E+00	AF185255.1	NT	Enlase australis histone H3 (H3) gene, partial cds
9105	22033		5.51	4.8E+00	AW730067.1	EST_HUMAN	PMD-BT0547-310100-002-504 BT0547 Homo sapiens cDNA
309	13402	26319	3.7	4.7E+00	BF240552.1	EST_HUMAN	601873654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4089716 5'
310	13402	26319	3.33	4.7E+00	BF240552.1	EST_HUMAN	601873654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4089716 5'
3318	16365	29265	1	4.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
8257	21162	34495	0.58	4.6E+00	U87569.1	NT	Methanococcus jannaschii section 111 of 150 of the complete genome
9738	22662	36048	1.04	4.6E+00	BE649437.1	EST_HUMAN	7886g10.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3292098 3' similar to TR:075140 O75140 KIAA0845 PROTEIN, contains element PTR5 repetitive element;
9738	22662	36047	1.04	4.6E+00	BE649437.1	EST_HUMAN	7886g10.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3292098 3' similar to TR:075140 O75140 KIAA0845 PROTEIN, contains element PTR5 repetitive element;
10877	23763		0.73	4.6E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
8239	21144		0.54	4.5E+00	AF126177.1	NT	Isaichenkia orientalis inositolphosphoryltransferase (IPC1) gene, complete cds
12034	24876	38381	2.37	4.5E+00	AE001044.1	NT	Archaeoglobus fulgidus section 63 of 172 of the complete genome
12175	25011	38515	1.86	4.5E+00	BF668841.1	EST_HUMAN	602123238F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4280216 5'
13107	25777		4.27	4.5E+00	BE069317.1	EST_HUMAN	QV3-BT0381-170100-060-c12 BT0381 Homo sapiens cDNA
3087	16138	28035	1.02	4.4E+00	BF630893.1	EST_HUMAN	602072585F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215284 5'
3087	16138	29038	1.02	4.4E+00	BF530893.1	EST_HUMAN	602072585F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215284 5'
6443	19489		1.76	4.4E+00	X13414.1	NT	Murine I gene for MHC class II (Ia) associated invariant chain
6515	19559	32741	0.61	4.4E+00	AF155606.1	NT	Nicotiana tabacum inorganic phosphate transporter (PT1) mRNA, complete cds
6357	19408		0.7	4.3E+00	AF059678.1	NT	Homo sapiens neutrophil collagenase (CLGNA) gene, promoter region and 5'UTR
7842	20769	34072	2.49	4.3E+00	Y13402.1	NT	Plasmodium falciparum R28R+var1 gene, exon 1
8060	20873	34289	0.8	4.3E+00	AE001222.1	NT	Treponema pallidum section 38 of 87 of the complete genome
11296	24218	37666	5.49	4.3E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
11371	24288		1.59	4.3E+00	11526311	NT	Homo sapiens DGeorge syndrome critical region gene 2 (DGCR2) mRNA
5707	18780		3.07	4.2E+00	P16444	SWISSPROT	MICROSOMAL DIPEPTIDASE PRECURSOR (MDP) (DEHYDROPEPTIDASE-1) (RENAL DIPEPTIDASE) (RDP)
5788	18860	31968	1.09	4.2E+00	P51828	SWISSPROT	LAF-4 PROTEIN (LYMPHOID NUCLEAR PROTEIN)
5968	19035		0.52	4.2E+00	Q27830	SWISSPROT	PUTATIVE ATP-DEPENDENT HELICASE MTH1802
7079	20285	33542	1.63	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)

Page 7 of 545  
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7079	20285	33543	1.63	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
9513	22440	35605	6.13	4.2E+00	A1809013.1	EST_HUMAN	wf97g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:230692 3'
10429	23318	36735	1.42	4.2E+00	P31368	SWISSPROT	NUBBIN PROTEIN (TWAIN PROTEIN) (POU DOMAIN PROTEIN 1) (PDM-1) (DPOU-1) (DOCT1)
6161	26642	32360	0.55	4.1E+00	O09185	SWISSPROT	CELLULAR TUMOR ANTIGEN P53
6161	26642	32361	0.55	4.1E+00	O09185	SWISSPROT	CELLULAR TUMOR ANTIGEN P53
7471	20411	33689	0.74	4.1E+00	BE233688.1	EST_HUMAN	601110727F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351534 5'
7579	20515	33803	0.44	4.1E+00	BF247939.1	EST_HUMAN	601859030F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4089758 5'
8111	21023	34349	7.96	4.1E+00	O23810	SWISSPROT	YY1 PROTEIN PRECURSOR
8255	21160		0.58	4.1E+00	AB041523.1	NT	Pallopecten yessoensis mRNA for calcineurin A, complete cds
8258	21163	34496	4.78	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN
8258	21163	34497	4.78	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN
8495	21426	34767	1.14	4.1E+00	U57503.1	NT	Pan troglodytes novel repetitive solo LTR element in the RNU2 locus
10069	22985	36378	0.53	4.1E+00	P11253	SWISSPROT	SOS RIBOSOMAL PROTEIN L4
10197	23088	36489	1.6	4.1E+00	BF692425.1	EST_HUMAN	602247938F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333209 5'
10663	23549		0.65	4.1E+00	AJ235273.1	NT	Rickettsia prowazekii strain Madrid E, complete genome; segment 4/4
10798	23682		0.64	4.1E+00	P46414	SWISSPROT	CYCLIN-DEPENDENT KINASE INHIBITOR 1B (CYCLIN-DEPENDENT KINASE INHIBITOR P27) (P27KIP1)
11322	24241		3.68	4.1E+00	P09716	SWISSPROT	HYPOTHETICAL PROTEIN HVLf1
11409	24325		14.72	4.1E+00	BE885880.1	EST_HUMAN	601507510F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908051 5'
3604	18641		0.72	4.0E+00	P38229	SWISSPROT	GLC7-INTERACTING PROTEIN 1
5644	20176	33417	0.96	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE ; ISOMALTASE]
5644	20176	33418	0.96	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE ; ISOMALTASE]
7267	20176	33417	0.88	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE ; ISOMALTASE]
7267	20176	33418	0.88	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE ; ISOMALTASE]
7553	20490	33779	1.15	4.0E+00	O33010	SWISSPROT	CELL DIVISION PROTEIN FTSY HOMOLOG
9431	22359	35722	0.61	4.0E+00	Q14157	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0144
10452	23341	36768	0.54	4.0E+00	O61309	SWISSPROT	NITRIC-OXIDE SYNTHASE (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS)
10661	23547	36981	0.67	4.0E+00	AE002132.1	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
11905	24005	37446	1.77	4.0E+00	P14546	SWISSPROT	CYTOCHROME C OXIDASE POLYPEPTIDE III
11981	24824	38319	2.61	4.0E+00	P07564	SWISSPROT	GENOME POLYPEPTIDE [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]

Page 8 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11981	24824	38320	2.61	4.0E+00	P07564	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
3560	16597	28501	5.4	3.9E+00	X64518.1	NT	N. labacum chitinase gene 30 for class I chitinase C
4427	17438		0.79	3.9E+00	AF055466.1	NT	Mus musculus seminal vesicle secretory protein 99 (MSVSP99) gene, promoter region
5856	18926	32042	2.69	3.9E+00	BE814337.1	EST_HUMAN	MR0-BN0070-300500-028+05 BN0070 Homo sapiens cDNA
5855	18926	32043	2.69	3.9E+00	BE814337.1	EST_HUMAN	MR0-BN0070-300500-028+05 BN0070 Homo sapiens cDNA
6926	18955	33175	0.71	3.9E+00	AF288209.1	NT	Diclyostelium discoideum non-LTR retrotransposon TRES-B, polyprotein (gag) and group-specific antigen (pol) genes, complete cds
6987	20014	33245	0.92	3.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
7109	20169	33445	3.78	3.9E+00	P39299	SWISSPROT	HYPOTHEtical TRANSCRIPTIONAL REGULATOR IN AIDB-RPSF INTERGENIC REGION
7754	20684	33983	4.35	3.9E+00	M23907.1	NT	Human MHC class II lymphocyte antigen (DPw4-beta-1) gene, exon 2
8892	21822	35174	2.85	3.9E+00	X65865.1	NT	X. laevis mRNA for M4 muscarinic receptor
11829	23684	37399	4.12	3.9E+00	Y18000.1	NT	Homo sapiens NF2 gene
2676	19672		1.55	3.8E+00	AE001582.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
6654	19693	32887	0.83	3.8E+00	Q57830	SWISSPROT	HYPOTHEtical PROTEIN M10385
7078	20284	33541	0.52	3.8E+00	A1493949.1	EST_HUMAN	q251f07.x1 NCI CGAP_K1211 Homo sapiens cDNA clone IMAGE:2030437 3'
9001	21930	35286	1.16	3.8E+00	D44725.1	EST_HUMAN	HUMSUPY135 Human brain cDNA Homo sapiens cDNA clone 148
10311	23200		0.69	3.8E+00	AJ390961.1	NT	Streptococcus oralis partial xpt gene for xanthine phosphoribosyltransferase, strain NCTC7864
4106	17180	30004	11.53	3.7E+00	AL161599.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
7529	20468		0.91	3.7E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
9720	22845	38027	0.68	3.7E+00	U43541.1	NT	Mus musculus lamihin beta 2 gene, exons 17-33, and complete cds
11863	24753	38247	2.33	3.7E+00	BF669279.1	EST_HUMAN	602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
11863	24753	38248	2.33	3.7E+00	BF669279.1	EST_HUMAN	602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
12339	25134		1.81	3.7E+00	AB013746.3	NT	Gallus gallus mRNA for hypoxia-inducible factor-1 alpha, complete cds
614	13679	28581	1.95	3.6E+00	AV761055.1	EST_HUMAN	AV761055 MDS Homo sapiens cDNA clone MDSBUE10 5'
6436	18518	31243	0.58	3.6E+00	BF316316.1	EST_HUMAN	601901866F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4131016 5'
9205	22133	35489	4.38	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
9205	22133	35490	4.38	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
10188	23079	36480	0.53	3.6E+00	U72775.1	NT	Olonia episcopus cytochrome b gene, mitochondrial gene encoding mitochondrial protein, partial cds

Page 9 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

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10188	23079	36481	0.53	3.6E+00	U72775.1	NT	Ciconia episcopus cytochrome b gene, mitochondrial gene encoding mitochondrial protein, partial cds
11288	24209						Escherichia coli glycerophosphate dehydrogenase (gld) gene, partial cds; and the translation start site has been verified (gldE), the translation start site has been verified (gldE), and repressor protein (gldR) genes, complete cds
3292	16339	29241	3.15	3.6E+00	M86795.1	NT	Cryptosporidium felis heat shock protein 70 (HSP70) gene, partial cds
6232	19286		1.3	3.5E+00	AF221538.1	NT	Borrelia burgdorferi (strain 25015) outer surface protein (ospC) gene, partial cds
6456	19501	32676	0.83	3.5E+00	L42898.1	NT	Y940c08.f1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:34940 5'
			1.12	3.5E+00	R19745.1	EST_HUMAN	cd3710.a1 Soares testis, NHT Homo sapiens cDNA clone IMAGE:1618987 3' similar to gb-J04213
8301	21205	34540	0.52	3.5E+00	AA992102.1	EST_HUMAN	CELLULAR RETINALDEHYDE-BINDING PROTEIN (HUMAN);
8343	21248	34583	0.51	3.5E+00	4505284	NT	Homo sapiens macrophage stimulating 1 receptor (c-met-related tyrosine kinase) (MST1R) mRNA
9054	21983		0.7	3.5E+00	P24557	SWISSPROT	THROMBOXANE-A SYNTHASE (TXA SYNTHASE) (TXS)
9583	22510	35872	0.97	3.5E+00	AA190998.1	EST_HUMAN	zp86b04.s1 Siratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element ;
9583	22510	35873	0.97	3.5E+00	AA190998.1	EST_HUMAN	zp86b04.s1 Siratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element ;
10026	22926	36315	1.2	3.5E+00	AL181553.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 53
11000	23884	37316	0.55	3.5E+00	AJ133723.1	NT	Bos taurus mRNA for Ran-binding protein 2, partial
1533	14563	27523	3.15	3.4E+00	AF284577.1	NT	Brassica napus RPB5d mRNA, complete cds
2614	15612	28607	0.95	3.4E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7033	20059	33292	0.42	3.4E+00	U77817.1	NT	Chloranth-Aster yellow phytoplasmic acetate kinase gene, complete cds
7753	20683	33982	2.63	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
8157	21064	34394	0.8	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
							Human alternatively spliced potassium channels ROM-K1, ROM-K2, ROM-K3, ROM-K4, ROM-K5, and ROM-K6 (KCNU1) gene, complete cds
9235	22163		0.79	3.4E+00	U65408.1	NT	ROM-K6 (KCNU1) gene, complete cds
9656	22592	35953	0.59	3.4E+00	AJ250567.1	NT	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 6
10757	23643	37076	2.96	3.4E+00	AF013167.1	NT	Saccharomyces cerevisiae MSS1 gene, complete cds
11963	24806	39304	1.98	3.4E+00	L77570.1	NT	Homo sapiens Digeorge syndrome critical region, centromeric end
6303	19354	32524	0.84	3.3E+00	Q09669	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
6303	19354	32525	0.84	3.3E+00	Q09669	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
8473	21404	34742	1.06	3.3E+00	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
10942	23827	37253	1.39	3.3E+00	AP001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
			1.39	3.3E+00	AP001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
523	13593	25605	1.50	3.2E+00	X96422.1	NT	D. rerio zp-50 POU gene

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4110	13593	26505	0.84	3.2E+00	X96422.1	NT	D. rerio zp-50 POU gene
4841	17842	30711	1.49	3.2E+00		NT	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1), mRNA
5760	18833	31934	1.43	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5760	18833	31935	1.43	3.2E+00	P4924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5760	18833	31936	2.58	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5766	18868	31977	2.58	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
6561	19602	32787	1.89	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
6561	19602	32788	1.89	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
8049	20662	34278	0.73	3.2E+00	P04276	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
8245	21150	34484	2.35	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
8245	21150	34485	2.35	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
9581	22508	36368	6.46	3.2E+00	P13061	SWISSPROT	PERIPLASMIC [NIFE] HYDROGENASE SMALL SUBUNIT [NIFE HYDROGENLYASE SMALL CHAIN]
10060	22976	36961	1.21	3.2E+00	M56363.1	NT	S. cerevisiae threonine deaminase (LV1) gene, complete cds
10640	23526	36961	2.39	3.2E+00	AB016081.2	NT	Oryzias latipes OIGC6 gene for guanylyl cyclase C, complete cds
12303	25111	32287	4.71	3.2E+00	L33836.1	NT	Sus scrofa choline acetyltransferase gene, promoter region
6090	19151	32287	1.91	3.1E+00	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME 1
7785	20714	34016	0.88	3.1E+00	P52178	SWISSPROT	TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, NON-GREEN PLAS TID PRECURSOR (CTPT)
8160	21097		1.09	3.1E+00	AF303225.1	NT	Bacillus alcalophilus peactate lyase [pelE] gene, complete cds
8666	21597	34937	0.58	3.1E+00	P40985	SWISSPROT	PROBABLE UBIQUITIN-PROTEIN LIGASE HUL4
9164	22092	35449	5.22	3.1E+00	P49894	SWISSPROT	TYPE 1 IODOTHYRONINE DEIODINASE (TYPE-1 5DEIODINASE) (DIO) (TYPE 1 DI) (5DI)
9164	22092	35450	5.22	3.1E+00	P49894	SWISSPROT	TYPE 1 IODOTHYRONINE DEIODINASE (TYPE-1 5DEIODINASE) (DIO) (TYPE 1 DI) (5DI)
9801	22765		4.47	3.1E+00	Q14957	SWISSPROT	GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
9865	22780	36169	0.54	3.1E+00	Q01149	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
10408	23297	36717	0.68	3.1E+00	7624759	NT	Chlorella vulgaris chloroplast, complete genome
10494	23382		0.62	3.1E+00	Q10125	SWISSPROT	HYPOTHETICAL 56.3 KD PROTEIN F52C9.5 IN CHROMOSOME III
10824	23710	37137	5.35	3.1E+00	P49365	SWISSPROT	DEOXYHYPSINE SYNTHASE (DHS)
11895	23995		2.49	3.1E+00	P33515	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4B AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
11913	24760		4.16	3.1E+00	S56660.1	NT	retrodo acid nuclear receptor isoform beta 2 [mice, embryonal carcinoma cell line, PCC7-MZ1, mRNA, 2971 nt]
5522	18601	31450	1.42	3.0E+00	X53098.1	NT	S. aureus genes encoding Sau961 DNA methyltransferase and Sau961 restriction endonuclease



Page 11 of 545  
Table 4

Single Exon Probes Expressed in Adult Liver

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6837	19869	33083	0.68	3.0E+00	X56037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
6837	19869	33084	0.68	3.0E+00	X56037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
7517	20468		10.11	3.0E+00	P18406	SWISSPROT	CYR61 PROTEIN PRECURSOR (3CH61)
7560	20497		0.75	3.0E+00	Q13201	SWISSPROT	ENDOTHELIAL CELL MULTIMERIN PRECURSOR
9464	22392		1.65	3.0E+00	X67838.1	NT	B. napus DNA for myrosinase
10783	23669	37098	0.66	3.0E+00	Q58605	SWISSPROT	S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE)
11092	24023	37465	1.39	3.0E+00	Q16181	SWISSPROT	CDC10 PROTEIN HOMOLOG
11447	24363	37811	5.92	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
11447	24363	37812	5.92	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
12016	24858	38358	1.56	3.0E+00	P34194	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
2024	15042	28036	2.11	2.9E+00	AEO02225.2	NT	Chlamydomonas reinhardtii AR39, section 53 of 84 of the complete genome
6309	19359		0.56	2.9E+00	A8028033.1	NT	Bonapartia pedaliata mitochondrial DNA for 16S ribosomal RNA
7237	20146	33386	10.73	2.9E+00	Z36878.1	NT	F. pingii gdcSPa gene for P-protein of the glycine cleavage system
7577	20513	33799	4.82	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7577	20513	33800	4.82	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7660	20787	34090	5.2	2.9E+00	P46589	SWISSPROT	ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN)
8449	21381	34722	0.61	2.9E+00	P05844	SWISSPROT	STRUCTURAL POLYPEPTIDE (CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3)
8449	21381	34723	0.61	2.9E+00	P05844	SWISSPROT	STRUCTURAL POLYPEPTIDE (CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3)
8678	21607	34949	0.88	2.9E+00	BF344171.1	EST_HUMAN	602017413F1 NCL_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4153089 5'
9779	22703		0.66	2.9E+00	AJ002153.2	NT	Sagittaria arifolia mature K (matK) gene, partial cds; chloroplast gene for chloroplast product
1478	14507	27468	3.83	2.8E+00	AF186398.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
1657	14687		2.32	2.8E+00	AL161552.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
7681	20623	33923	5.61	2.8E+00	8393724	NT	Mus musculus endomucin (LOC53423), mRNA
10140	23031		0.71	2.8E+00	BE505182.1	EST_HUMAN	601342759F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3684807 5'
11131	20623	33923	1.57	2.8E+00	8393724	NT	Mus musculus endomucin (LOC53423), mRNA
248	13347	26259	9.41	2.7E+00	6878306	NT	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA
249	13347	26260	9.41	2.7E+00	6878306	NT	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA

Page 12 of 545  
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## Single Exon Probes Expressed in Adult Liver

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5743	18816	31912	1.43	2.7E+00	L14005.1	NT	Homo sapiens apoA polymorphism Kringle IV gene, exons 1 and 2
8724	21654		0.7	2.7E+00	U15947.1	NT	Ipomoea purpurea chalcone synthase (CHSB) gene including complete 5'UTR and complete cds
9520	22447		2.43	2.7E+00	AL116459.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9966	21324	34657	0.64	2.7E+00	AW088191.1	EST_HUMAN	xc88e12.x1 NCL_COAP_Bm35 Homo sapiens cDNA clone IMAGE:2591374 3' similar to gb:M17733
10978	23862		1.7	2.7E+00	BE063527.1	EST_HUMAN	THYMOSIN BETA-4 (HUMAN).
4766	17791	30558	5.9	2.6E+00	AF068749.1	NT	CM0-BT0281-031199-087-h04 BT0281 Homo sapiens cDNA
5739	18812	31907	1.75	2.6E+00	6755601	NT	Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds
5739	18812	31908	1.75	2.6E+00	6755601	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
6038	19100		1.55	2.6E+00	Y17082.1	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
7986	25984		0.79	2.6E+00	AJ224639.1	NT	Mycobacterium fortuitum furA II gene
8156	21063		8.96	2.6E+00	AF235502.1	NT	Homo sapiens Surf-5 and Surf-6 genes
8637	21668	34905	1.33	2.6E+00	AJ132180.1	NT	Mus musculus SH2-containing inositol 5-phosphatase (Ship) gene, exons 16 through 27, and complete cds
8637	21668	34906	1.33	2.6E+00	AJ132180.1	NT	faba bean necrotic yellow virus C2-Eg gene, isolate Egyptian EV1-93
10162	23073	36473	2.87	2.6E+00	AL161540.2	NT	faba bean necrotic yellow virus C2-Eg gene, isolate Egyptian EV1-93
10841	23727		1.97	2.6E+00	9055193	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
11488	24381	37828	1.48	2.6E+00	AF143675.1	NT	Mus musculus cleavage and polyadenylation specificity factor 3 (Cpsf3), mRNA
12889	25859		2.17	2.6E+00	11419220	NT	Hemavirus Z10 segment M G1/G2 glycoprotein (Z10) gene, complete cds
1483	14514	27474	2.58	2.5E+00	AJ271844.1	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), mRNA
1483	14514	27475	2.58	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
6024	19086	32210	1.99	2.5E+00	P13485	SWISSPROT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
6024	19086	32211	1.99	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6730	19086	32210	1.54	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6730	19086	32211	1.54	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
7032	20059	33291	0.88	2.5E+00	D30052.1	NT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
8227	21132	34462	1.06	2.5E+00	AW949158.1	EST_HUMAN	Vibrio cholerae cbaA gene and cbaB gene for cholera toxin, complete cds
8302	21206	34541	0.49	2.5E+00	4502902	NT	QV4-FT0005-110500-205-g07 FT0005 Homo sapiens cDNA
9648	22574	35945	1.64	2.5E+00	D50307.1	NT	Homo sapiens clathrin, heavy polypeptide-like 1 (CLTCL1) mRNA
10366	23255	36675	0.85	2.5E+00	BE297758.1	EST_HUMAN	Rice DNA for aldolase C-1, complete cds
11871	24814		2.02	2.5E+00	P40170	EST_HUMAN	601175779F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531090 5'
12300	25109		2.91	2.5E+00	AF289665.1	SWISSPROT	DNAJ PROTEIN
3057	16109	28015	1.1	2.4E+00	M24282.1	NT	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
5015	18013	30872	5.08	2.4E+00	4503352	NT	Chicken alpha-3 collagen type VI mRNA, 3' and
							Homo sapiens double C2-like domains, alpha (DOC2A) mRNA

Page 13 of 545  
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Single Exon Probes Expressed in Adult Liver

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6243	19297	32455	4.27	2.4E+00	P02843	SWISSPROT	VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1)
7773	20703	34002	0.63	2.4E+00	BF667502.1	EST_HUMAN	602120856F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278012 5'
7773	20703	34003	0.63	2.4E+00	BF667502.1	EST_HUMAN	602120856F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278012 5'
7789	20718	34021	0.43	2.4E+00	P20126	SWISSPROT	RNA REPLICASE POLYPROTEIN
7789	20718	34022	0.43	2.4E+00	P20126	SWISSPROT	RNA REPLICASE POLYPROTEIN
8718	21649	34994	2.25	2.4E+00	P26842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8718	21649	34995	2.25	2.4E+00	P26842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8780	21720		3.32	2.4E+00	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
9210	22138		1.82	2.4E+00	AW875126.1	EST_HUMAN	RC2-PT0004-031298-011-d05 PT0004 Homo sapiens cDNA
9387	22315	35577	8.12	2.4E+00	P24091	SWISSPROT	ENDOCHITINASE B PRECURSOR (CHN-B)
10541	23427	36846	2.58	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10541	23427	36847	2.58	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10608	23494	36924	2.52	2.4E+00	X62511.1	NT	H sapiens CTGF gene and promoter region
10737	23623		7.42	2.4E+00	P06099	SWISSPROT	XYLOSE KINASE (XYLOKINASE)
10811	23697	37123	1.98	2.4E+00	BE326702.1	EST_HUMAN	hr63108.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
10811	23697	37124	1.96	2.4E+00	BE326702.1	EST_HUMAN	hr63108.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
11063	23947	37385	1.4	2.4E+00	Q51481	SWISSPROT	DENITRIFICATION REGULATORY PROTEIN NIRQ
11797	24719	38212	2.5	2.4E+00	AF158652.2	NT	Fragaria x ananassa cytosolic ascorbate peroxidase (ApxSC) gene, ApxSC-c allele, complete cds
1281	14314	27263	9.93	2.3E+00	Z46724.1	NT	G.domesticus artificial single chain antibody gene (L3)
4217	17233		1.68	2.3E+00	AJ401081.1	NT	Bos taurus partial cytb gene for cytochrome b
6048	18110		0.91	2.3E+00	N86245.1	EST_HUMAN	J7340F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7340 5' similar to PROLYLCARBOXYPEPTIDASE
7858	20785	34038	2.43	2.3E+00	Q07076	NT	Rattus norvegicus ATPase, Ca++ transporting, ubiquitous (Atp2a3), mRNA
8038	25995		3.15	2.3E+00	P07189	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
8253	21158	34491	1.5	2.3E+00	X60265.1	NT	M.mazai dnaK and dnaJ genes homologues coding for DnaK and DnaJ
9654	22590	35952	0.59	2.3E+00	5535317	NT	Polymerus ornithinylis mitochondrion, complete genome
9712	22637	36018	1.73	2.3E+00	Q11127	SWISSPROT	ALPHA-(1-3)-FUCOSYLTRANSFERASE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE)
11241	24167	37613	3.36	2.3E+00	Q07076	SWISSPROT	(FUCOSYLTRANSFERASE 4) (FUCT-IV)
11714	24616	38092	1.58	2.3E+00	P28059	SWISSPROT	ANNEXIN VII (SYNEXIN)
12190	25025	38526	2.66	2.3E+00	BF541987.1	EST_HUMAN	ENDOCHITINASE 3 PRECURSOR
12190	25025	38527	2.66	2.3E+00	BF541987.1	EST_HUMAN	602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
12499	26238	31862	5.44	2.3E+00	BE895237.1	EST_HUMAN	602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
							601433673F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918643 5'

Page 14 of 545  
Table 4

## Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4103	17128	30003	0.91	2.2E+00	AF020528.1	NT	Magnaporthe grisea Class IV chitin synthase (chs4) gene, complete cds
4418	17429	30291	5.4	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
4418	17429	30292	5.4	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
							SORTLIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND- BINDING REPEATS) (LR11)(>
5526	18605	31453	11.77	2.2E+00	O88307	SWISSPROT	SORTLIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND- BINDING REPEATS) (LR11)(>
5526	18605	31454	11.77	2.2E+00	O88307	SWISSPROT	RC3-CT0254-300800-022-e06 CT0254 Homo sapiens cDNA
6067	19128	32259	1.04	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022-e06 CT0254 Homo sapiens cDNA
6067	19128	32260	1.04	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022-e06 CT0254 Homo sapiens cDNA
6297	19348	32516	7.46	2.2E+00	BE260383.1	EST_HUMAN	80094340T11 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2959777 3'
6612	19653	32837	3.09	2.2E+00	Q00335	SWISSPROT	MINOR VIRION STRUCTURAL PROTEIN MU-2
6882	19912	33128	2.79	2.2E+00	P51459	SWISSPROT	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
7293	18462		3.6	2.2E+00	AA694574.1	EST_HUMAN	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
7701	20653	33930	0.87	2.2E+00	AA137027.1	EST_HUMAN	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
8051	20864	34280	20.17	2.2E+00	AA449012.1	EST_HUMAN	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
8142	21051	34383	0.55	2.2E+00	P54918	SWISSPROT	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
8414	21316	34648	0.41	2.2E+00	O67099	SWISSPROT	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
8681	21612	34953	0.71	2.2E+00	BE301560.1	EST_HUMAN	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
8681	21612	34954	0.71	2.2E+00	BE301560.1	EST_HUMAN	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
9880	22765		13.66	2.2E+00	BE741678.1	EST_HUMAN	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
10097	24691		2.64	2.2E+00	Q04706	SWISSPROT	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
10556	23442	36862	1.93	2.2E+00	A1290373.1	EST_HUMAN	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
10556	23442	36863	1.93	2.2E+00	A1290373.1	EST_HUMAN	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
10598	23464	36913	2.2	2.2E+00	BE246782.1	EST_HUMAN	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
10935	23820	37247	2.49	2.2E+00	AF183416.1	NT	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11039	23923	37366	0.51	2.2E+00	P22909	SWISSPROT	ALPHA-2A ADRENERGIC RECEPTOR (ALPHA-2A ADRENERGIC RECEPTOR) (ALPHA-2AAR) (CA2-47)
11874	23974	37411	3.47	2.2E+00	P07911	SWISSPROT	(ALPHA-2D ADRENERGIC RECEPTOR)
12041	24883	38989	5.96	2.2E+00	P10407	SWISSPROT	URMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP)
591	15878	28982	6.8	2.1E+00	AF132612.2	NT	EARLY E1A 28 KD PROTEIN
3649	16655		0.85	2.1E+00	AW449366.1	EST_HUMAN	Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region
6372	19421		0.92	2.1E+00	P75357	SWISSPROT	U1-H-F13-ek-e-08-0-UJ.s1 NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734550 3'
7119	20323	33587	3.56	2.1E+00	O70159	SWISSPROT	HYPOTHETICAL PROTEIN MG302 HOMOLOG
7376	20369	33638	0.67	2.1E+00	4503430	NT	ALPHA-2HS-GLYCOPROTEIN PRECURSOR (FETUIN-A) Homo sapiens dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive) (DYSF) mRNA, and translated products
7397	20996	33330	5.66	2.1E+00	N28575.1	EST_HUMAN	W08a10.s1 Scores melanocyte 2Nb-HM Homo sapiens cDNA clone IMAGE:270618 3' similar to gb.M55654
9064	21993		2.3	2.1E+00	AU123630.1	EST_HUMAN	TRANSCRIPTION INITIATION FACTOR TFIIID (HUMAN); AU123630 NT2RM2 Homo sapiens cDNA clone NT2RM200671 5'
1224	14261	27203	1.1	2.0E+00	AF180527.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1224	14261	27204	1.1	2.0E+00	AF180527.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1363	14394	27349	1.08	2.0E+00	AF204927.1	NT	Oryzodagus cuticulus Na <sup>+</sup> /K <sup>+</sup> -ATPase beta 1 subunit mRNA, complete cds
1597	14628		3.72	2.0E+00	P25582	SWISSPROT	POTATIVE RNA METHYLTRANSFERASE SPB1
2163	15175	28180	2.97	2.0E+00	Z78278.1	NT	R. norvegicus mRNA for collagen alpha1 type I
2163	15175	28181	2.67	2.0E+00	Z78279.1	NT	R. norvegicus mRNA for collagen alpha1 type I
4191	17211	30077	1.63	2.0E+00	AW664498.1	EST_HUMAN	h13c05.x1 NCL CGAP GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb.X01677
4191	17211	30078	1.63	2.0E+00	AW664498.1	EST_HUMAN	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN); h13c05.x1 NCL CGAP GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb.X01677
7981	20902		0.84	2.0E+00	P07566	SWISSPROT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN); STRUCTURAL POLYPROTEIN [CONTAINS: NUCLEOCAPSID PROTEIN C; MEMBRANE GLYCOPROTEINS E1 AND E2]
8602	21533	34874	4.37	2.0E+00	AB008676.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
8602	21533	34875	4.37	2.0E+00	AB008676.1	NT	Escherichia coli 0167 DNA, map position at 46 min., complete cds
8602	21533	34876	4.37	2.0E+00	AB008676.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
9478	22406	35766	3.1	2.0E+00	F31500.1	EST_HUMAN	HSPD22703 HM3 Homo sapiens cDNA clone s4000117B08
12808	25823	31483	6.51	2.0E+00	5834843	NT	Gallus gallus mitochondrion, complete genome
5792	18664	31971	4.67	1.9E+00	6754399	NT	Mus musculus inositol 1,4,5-triphosphate receptor 1 (lpr1), mRNA
5792	18664	31972	4.67	1.9E+00	6754399	NT	Mus musculus inositol 1,4,5-triphosphate receptor 1 (lpr1), mRNA
6337	19387	32556	1.21	1.9E+00	BE969695.1	EST_HUMAN	901579636F1 NIH_MGC_78 Homo sapiens cDNA clone IMAGE:3949881 5'
6947	19976		0.87	1.9E+00	AW845889.1	EST_HUMAN	MRO-CT0063-071099-002-g02 CT0063 Homo sapiens cDNA

Page 16 of 545  
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Single Exon Probes Expressed in Adult Liver

Single Exon Probes Expressed in Adult Liver							
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
							CTD-BINDING SR-LIKE PROTEIN RA4
7053	20079		1.89	1.9E+00	Q63627	SWISSPROT	
							COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
9027	21956	35314	2.43	1.9E+00	P02467	SWISSPROT	
							COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
9027	21956	35315	2.43	1.9E+00	P02467	SWISSPROT	
							CM3-MT0114-010900-323-h12 MT0114 Homo sapiens cDNA
9217	22145		2.97	1.9E+00	BF300206.1	EST_HUMAN	
							ARGININE DEIMINASE (ADI) (ARGININE DIHYDROLASE) (AD)
9451	22379		2.45	1.9E+00	O51781	SWISSPROT	
							ab9404.s1 Stratiagene lung (#937210) Homo sapiens cDNA clone IMAGE:854574 3' similar to contains Alu
							repetitive element; contains element L1 L1 repetitive element;
10156	23047	36446	0.7	1.9E+00	AA669125.1	EST_HUMAN	
							Homo sapiens gag-p10-pol precursor protein gene, partial cds
11038	23922	37365	0.84	1.9E+00	AF248269.1	NT	
							PROTEIN B8 PRECURSOR
3141	16191	29084	2.04	1.8E+00	P21004	SWISSPROT	
							Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit
3165	16215	29104	1.09	1.8E+00	U04356.1	NT	
							(atpE) genes, complete cds
							Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit
3165	16215	29105	1.09	1.8E+00	U04356.1	NT	
							(atpE) genes, complete cds
6082	19143		1.69	1.8E+00	P18502	SWISSPROT	
							HEDGEHOG RECEPTOR (PATCHED PROTEIN)
6342	19392	32661	1.89	1.8E+00	BF311999.1	EST_HUMAN	
							601897854F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127384 5'
6663	19701		3.59	1.8E+00	BF683327.1	EST_HUMAN	
							602139470F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4298272 5'
7044	20070	33304	1.26	1.8E+00	BF305652.1	EST_HUMAN	
							6018931489F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139038 5'
7412	20111	33345	0.93	1.8E+00	P21249	SWISSPROT	
							MAJOR ANTIGEN
							LIPOPOLYSACCHARIDE 1,6-GALACTOSYLTRANSFERASE (UDP-D-GALACTOSE--
							(GLUCOSYL)LIPOPOLYSACCHARIDE-ALPHA-1,3-D-GALACTOSYLTRANSFERASE)
7635	20570		0.74	1.8E+00	P27127	SWISSPROT	
							RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
							ENDONUCLEASE]
8694	21625	34968	0.95	1.8E+00	P11369	SWISSPROT	
							RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
							ENDONUCLEASE]
8694	21625	34969	0.95	1.8E+00	P11369	SWISSPROT	
							ENDONUCLEASE]
9038	21967	35326	0.55	1.8E+00	P48634	SWISSPROT	
							LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
9038	21967	35327	0.55	1.8E+00	P48634	SWISSPROT	
							LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
9038	21967	35328	0.55	1.8E+00	P48634	SWISSPROT	
							LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
9413	22341	35706	2.66	1.8E+00	O43281	SWISSPROT	
							EMBRYONAL FYN-ASSOCIATED SUBSTRATE (HEFS)
9717	22642	36023	0.81	1.8E+00	R31042.1	EST_HUMAN	
							ynt7c08.11 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:135278 5'
9804	22710	36092	1.06	1.8E+00	AW880004.1	EST_HUMAN	
							QV0-OT0030-070300-148-a03 OT0030 Homo sapiens cDNA
10363	23252	36672	0.77	1.8E+00	P27050	SWISSPROT	
							CHITINASE D PRECURSOR
10775	23661		3.37	1.8E+00	AF111849.1	NT	
							Homo sapiens PRO0530 mRNA, complete cds
11031	23915		0.92	1.8E+00	P44325	SWISSPROT	
							CYTIDINE DEAMINASE (CYTIDINE AMINOHYDROLASE) (CDA)

Page 17 of 545  
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Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12616	25797		8.13	1.8E+00	AF314254.1	NT	Chlamydomonas reinhardtii alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein
12692	25349		4.6	1.8E+00	9506404	NT	Rattus norvegicus Actin-related protein complex 1b (Arpc1b), mRNA
1135	14177	27114	2.24	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
2290	15298	28305	4.2	1.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21Co80
2396	15401	28405	2.03	1.7E+00	A1141067.1	EST_HUMAN	oz43h05.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1678137 3'
4570	17578	30440	1.92	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
5807	18879	31985	1.95	1.7E+00	BE063546.1	EST_HUMAN	CMO-BT0282-171289-127-e05 BT0282 Homo sapiens cDNA
5807	18879	31986	1.95	1.7E+00	BE063546.1	EST_HUMAN	CMO-BT0282-171289-127-e05 BT0282 Homo sapiens cDNA
6069	19130	32263	0.49	1.7E+00	R58748.1	EST_HUMAN	G4846 Fetal heart Homo sapiens cDNA clone G4846 5' end
6230	19303	32464	3.4	1.7E+00	Q9TTR8	SWISSPROT	COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TF I)
6832	19884	33078	0.53	1.7E+00	P35816	SWISSPROT	[PYRUVATE DEHYDROGENASE (LIPOAMIDE)]-PHOSPHATASE, MITOCHONDRIAL PRECURSOR (PDP) (PYRUVATE DEHYDROGENASE PHOSPHATASE, CATALYTIC SUBUNIT) (PDPC)
7587	20523	33811	1.19	1.7E+00	Q03703	SWISSPROT	HYPOHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
7587	20523	33812	1.19	1.7E+00	Q03703	SWISSPROT	HYPOHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
8318	21223		0.44	1.7E+00	P06180	SWISSPROT	HISTONE-BINDING PROTEIN N1/N2
8437	21369	34710	1.19	1.7E+00	AF021335.1	NT	Mus musculus T cell receptor gamma locus, TOR gamma 2 and gamma 4 gene clusters
8611	21542	34884	1.3	1.7E+00	6755715	NT	Mus musculus T-cell acute lymphocytic leukemia 1 (Talt1), mRNA
8640	21571	34910	0.64	1.7E+00	BF530630.1	EST_HUMAN	602071817F1 NCI CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4214669 5'
9106	22034	35388	0.56	1.7E+00	AF245513.1	NT	Hippoglossus hippoglossus interferon inducible Mx protein (Mx) mRNA, complete cds
9187	22115		1.5	1.7E+00	BF308000.1	EST_HUMAN	601894255F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4140084 5'
9262	22190	35547	0.65	1.7E+00	X69083.1	NT	M.musculus Ank-1 mRNA for erythroid ankyrin
9262	22190	35548	0.65	1.7E+00	X69083.1	NT	M.musculus Ank-1 mRNA for erythroid ankyrin
9373	22301	35662	0.52	1.7E+00	U19832.1	NT	Rattus norvegicus SA gene, partial cds
9682	25690	35993	1.76	1.7E+00	O60479	SWISSPROT	HOMEBOX PROTEIN DLX-3
9692	25690	35994	1.76	1.7E+00	O60479	SWISSPROT	HOMEBOX PROTEIN DLX-3
10133	23024		1.26	1.7E+00	AF161380.1	NT	Homo sapiens HSPC282 mRNA, partial cds
10668	23554		0.63	1.7E+00	AW953691.1	EST_HUMAN	EST365751 IMAGE sequences, MAGC Homo sapiens cDNA
12026	24888	38370	1.83	1.7E+00	W22424.1	EST_HUMAN	6787 Human retina cDNA Tsp509-cleaved sublibrary Homo sapiens cDNA not directional
2047	15064	28065	10.72	1.6E+00	AF199339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
2057	15074	28074	3.51	1.6E+00	AF077374.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
2063	15078	28078	1.14	1.6E+00	Y11344.1	NT	Mus musculus ST8GaiNAcII gene, exon 2

Page 18 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2303	16311		1.26	1.6E+00	X98373.1	NT	B. napus gene encoding endo-polygalacturonase
3002	16054	28958	1.25	1.6E+00	W58426.1	EST_HUMAN	z22501.1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341689 5' similar to gb:D29805 N-ACETYLACTOSAMINE SYNTHASE (HUMAN);
3825	16855		1.09	1.6E+00	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4115	17138		6.97	1.6E+00	BF570077.1	EST_HUMAN	60218609571 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310591 3'
4462	17473	30329	0.97	1.6E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
4462	17473	30330	0.97	1.6E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
5207	18198	31041	10.6	1.6E+00	AF127897.1	NT	Salmonella enteritidis olfactory receptor (SBO27) gene, partial cds
5218	18208	31053	3.06	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
5218	18208	31054	3.08	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
6039	19101	32228	2.33	1.6E+00	L04808.1	NT	Brachydanio rerio MHC class II DA-beta-2'01 gene, 3' end
6135	19194	32331	0.86	1.6E+00	AF005631.1	NT	Homo sapiens transglutaminase type I (Tgase1) gene, promoter region
6108	19254	32309	0.48	1.6E+00	BE971873.1	EST_HUMAN	601851111R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934443 3'
6198	19254	32400	0.48	1.6E+00	BE971873.1	EST_HUMAN	601851111R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934443 3'
6743	19777	32990	0.85	1.6E+00	BF380703.1	EST_HUMAN	IL2-UT0073-060900-145-E02 UT0073 Homo sapiens cDNA
7007	20034	33267	1.16	1.6E+00	AW294881.1	EST_HUMAN	U1H-B12-ahr-b-04-O-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727511 3'
7615	20550	33842	2.24	1.6E+00	BE697267.1	EST_HUMAN	RC0-CT0415-200700-032-c10 CT0415 Homo sapiens cDNA
8608	21539		1.82	1.6E+00	Q46378	SWISSPROT	VIRULENCE FACTOR M/VIN HOMOLOG
8950	21880	36240	3.13	1.6E+00	AJ297131.1	NT	Mus musculus SIL, MAP_17, CYP_a, SCL & CYP_b genes
9457	22385	35747	1.05	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
9457	22385	35748	1.05	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
6992	25688	34684	1.44	1.6E+00	X52046.1	NT	M. musculus COL3A1 gene for collagen alpha-1
9992	25688	34685	1.44	1.6E+00	X52046.1	NT	M. musculus COL3A1 gene for collagen alpha-1
10115	23006		0.67	1.6E+00	AF043466.1	NT	Thermotoga maritima ethanolic D-xylase-binding protein (xylF) gene, complete cds
10264	23144	36553	1.6	1.6E+00	T41290.1	EST_HUMAN	ph5b6_19/1TV Outward Au-primed hncDNA library Homo sapiens cDNA clone ph5b6_19/1TV
10645	23531	36963	0.64	1.6E+00	AF121361.1	NT	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase Ial (IAL), and zinc finger protein (DNZ1) genes, complete cds
10682	23568	36997	1.08	1.6E+00	AW835644.1	EST_HUMAN	QV4-LT0016-090200-100-407 LT0016 Homo sapiens cDNA
10682	23568	36998	1.08	1.6E+00	AW835644.1	EST_HUMAN	QV4-LT0016-090200-100-407 LT0016 Homo sapiens cDNA
11209	24135	37584	2.3	1.6E+00	P54817	SWISSPROT	CAPSID PROTEIN P40 (CONTAINS: ASSEMBLIN (PROTEASE); CAPSID ASSEMBLY PROTEIN)
11246	24170	37617	2.47	1.6E+00	P54817	SWISSPROT	CAPSID PROTEIN P40 (CONTAINS: ASSEMBLIN (PROTEASE); CAPSID ASSEMBLY PROTEIN)
11265	24188	37637	1.52	1.6E+00	AA216387.1	EST_HUMAN	nc16b02.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1008267 similar to contains element MER4 repetitive element;



Page 19 of 545  
Table 4  
Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11281	19164	32331	5.56	1.6E+00	AF005693.1	NT	Homo sapiens transglutaminase type I (Tgase1) gene, promoter region
12129	24970	38474	3.45	1.6E+00	AF104313.1	NT	Homo sapiens unknown mRNA
13084	25560		1.66	1.6E+00	AV764043.1	EST_HUMAN	AV764043 MDS Homo sapiens cDNA clone MDSDAH08 5'
34	13150	26039	4.94	1.5E+00	U53449.1	NT	Rattus norvegicus jun dimethylization protein 2 (jdp-2) mRNA, complete cds
250	13348	26261	1.62	1.5E+00	AE002201.2	NT	Chlamydia pneumoniae AR39, section 32 of 94 of the complete genome
844	13705		1.65	1.5E+00	6752981	NT	Mus musculus a disintegrin and metalloproteinase domain (ADAM) 15 (metagridin) (Adam15), mRNA
2434	15438	28438	2.19	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
2541	15541	28540	2.39	1.5E+00	6678350	NT	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA
3183	15438	28438	1.89	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
3433	16474	29381	0.75	1.5E+00	AE001945.1	NT	Delnoccocus radiolurans R1 section 82 of 229 of the complete chromosome 1
5930	18997	32116	1.1	1.5E+00	AI655301.1	EST_HUMAN	h12f10.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:O00237 O00237 HKF-1.1
5930	18997	32117	1.1	1.5E+00	AI655301.1	EST_HUMAN	h12f10.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:O00237 O00237 HKF-1.1
6577	19618	32903	0.99	1.5E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21G002
6671	19708	32903	2.34	1.5E+00	R17879.1	EST_HUMAN	Y910602.r1 Soares infant brain T1N1B Homo sapiens cDNA clone IMAGE:31693 5'
7190	20190	33434	0.54	1.5E+00	BE907771.1	EST_HUMAN	601502041F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3903659 5'
7488	20428	33747	1.4	1.5E+00	BE785356.1	EST_HUMAN	601478745F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3881555 5'
7522	20461	33748	20.78	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7731	20663	33961	0.67	1.5E+00	AA89259.1	EST_HUMAN	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
8035	20950	34285	0.62	1.5E+00	AI003254.1	EST_HUMAN	ak28710.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1684893 3' similar to gb:S96936 SEROTRANSFERRIN PRECURSOR (HUMAN);
8375	21279	34975	0.66	1.5E+00	AB039887.1	NT	an07b11.s1 Sitalagene schizo brain S11 Homo sapiens cDNA clone IMAGE:3911181 5'
8699	21630	35025	1.03	1.5E+00	BE887446.1	EST_HUMAN	Homo sapiens WDR4 gene for WD repeat protein, complete cds
8762	21892	35025	0.54	1.5E+00	AB040887.1	NT	601509566F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911181 5'
9204	22132	35488	1.11	1.5E+00	K02138.1	NT	Homo sapiens mRNA for KIAA1454 protein, partial cde
10016	22916	36305	0.63	1.5E+00	R81928.1	EST_HUMAN	Mouse germline IgM chain gene, mu-delta region
10161	23062	36453	1.33	1.5E+00	AW376697.1	EST_HUMAN	Y133h01.r1 Soares placenta NB22-IP Homo sapiens cDNA clone IMAGE:147697 5'
10374	23263	36685	7.79	1.5E+00	BF376754.1	EST_HUMAN	QV3-CT0192-261009-008-408 CT0192 Homo sapiens cDNA
10555	23441	37007	1.41	1.5E+00	AF337944.1	EST_HUMAN	RC0-TN0078-160900-034-g08 TN0078 Homo sapiens cDNA
10692	23578	37007	4.46	1.5E+00	AA017688.1	EST_HUMAN	G02035771F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183865 5'
10692	23578	37008	4.46	1.5E+00	AA017688.1	EST_HUMAN	ze38g06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'
10692	23578	37008	4.46	1.5E+00	AA017688.1	EST_HUMAN	ze38g06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'

Page 20 of 545  
Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11226	24152	37603	1.63	1.5E+00	U79186.1	NT	Coprinus cinereus sec17-like protein (Isa17) and hyphal tip 1 (hyt1) genes, complete cds
11836	24687	38176	4.39	1.5E+00	AL134197.1	EST_HUMAN	DKFZp547P243_s1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547P243 3'
11973	24816		4.68	1.5E+00	X07380.1	NT	Maize mitochondrial rRNA-Ser gene and rRNA-PIIe pseudogene
12055	24898	38400	1.43	1.5E+00	AI400798.1	EST_HUMAN	ig94409.x1 NCL CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116433 3'
12055	24898	38401	1.43	1.5E+00	AI400798.1	EST_HUMAN	ig94409.x1 NCL CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116433 3'
12427	25189		2	1.5E+00	6753287	NT	Mus musculus caspase 8 associated protein 2 (Casp8ap2), mRNA
12776	25405		4.8	1.5E+00	AL445086.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
31	13147	28035	1.89	1.4E+00	7691685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
31	13147	28036	1.69	1.4E+00	7691685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
2296	15304		1.03	1.4E+00	AF053357.1	NT	Helicobacter pylori glutamine synthetase (gluA) gene, complete cds
2356	15363		10.15	1.4E+00	U57922.1	NT	Ovis aries prion protein gene, complete cds
2718	15711	28709	1.85	1.4E+00	X74463.1	NT	Human papillomavirus type 7 genomic DNA
2823	15812	28808	2.74	1.4E+00	AF084584.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
2823	15812	28809	2.74	1.4E+00	AF084584.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
4354	17368	30231	1.54	1.4E+00	AW900455.1	EST_HUMAN	CM0-NN1005-140300-286-h06 NN1005 Homo sapiens cDNA
4354	17368	30232	1.54	1.4E+00	AW900455.1	EST_HUMAN	CM0-NN1005-140300-286-h06 NN1005 Homo sapiens cDNA
4699	17704		2.33	1.4E+00	BF681547.1	EST_HUMAN	602166687F1 NIH MGC 83 Homo sapiens cDNA clone IMAGE:4297556 5'
5557	18635	31515	1.04	1.4E+00	AW054976.1	EST_HUMAN	wf45g07.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510460 3'
5718	18791		4.98	1.4E+00	AB032983.1	NT	Homo sapiens mRNA for KIAA1157 protein, partial cds
6531	19575	32757	2.62	1.4E+00	Q13472	SWISSPROT	DNA TOPOISOMERASE III ALP4A
6548	25978		3.91	1.4E+00	AB020712.1	NT	Homo sapiens mRNA for KIAA0905 protein, complete cds
6679	19716	32913	2.89	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
6679	19716	32914	2.89	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
6726	19762	32869	0.51	1.4E+00	11096333	NT	Mus musculus WW domain binding protein 11 (Wbp11-pending), mRNA
6916	19946	33165	0.51	1.4E+00	BE007870.1	EST_HUMAN	QV0-BN0148-050500-215-b11 BN0148 Homo sapiens cDNA
6916	19946	33166	0.51	1.4E+00	BE007870.1	EST_HUMAN	QV0-BN0148-050500-215-b11 BN0148 Homo sapiens cDNA
7135	20243	33494	0.81	1.4E+00	AW893057.1	EST_HUMAN	CM3-NN0006-300300-132-b12 NN0006 Homo sapiens cDNA
7665	20599	33898	2.38	1.4E+00	AJ133269.1	NT	Homo sapiens caveolin-1/-2 locus, Contig1, DTS822, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
7683	20617	33917	1.19	1.4E+00	AW467760.1	EST_HUMAN	he23705.x1 NCL CGAP_CML1 Homo sapiens cDNA clone IMAGE:2919873 3' similar to contains Alu repetitive element
7749	20680	33979	0.85	1.4E+00	P65268	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)

Page 21 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7749	20680	33980	0.65	1.4E+00	P55288	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)
7778	20707	34010	0.59	1.4E+00	Q80605	SWISSPROT	MINOR CAPSID PROTEIN L2
8910	21840		0.91	1.4E+00	P07683	SWISSPROT	GLUCOAMYLASE PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
9352	22280		5.77	1.4E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 12
9639	22865	35934	1.63	1.4E+00	R20459.1	EST_HUMAN	yg33f12.1 Soares Infant brain T1NB Homo sapiens cDNA clone IMAGE:34345 5'
9739	22663	36048	3.08	1.4E+00	BE064667.1	EST_HUMAN	RC1-BT0313-301299-012-05 BT0313 Homo sapiens cDNA
9773	22697	36083	0.7	1.4E+00	AF134944.1	NT	Sceloporus undulatus ornithine transcarbamylase (OTC) mRNA, complete cds
10704	23590	37017	1.05	1.4E+00	BF575545.1	EST_HUMAN	602133135F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288137 5'
10746	23631	37063	0.91	1.4E+00	BE145374.1	EST_HUMAN	IL5-HT0198-291099-008-C04 HT0198 Homo sapiens cDNA
10745	23631	37064	0.91	1.4E+00	BE145374.1	EST_HUMAN	IL5-HT0198-291099-008-C04 HT0198 Homo sapiens cDNA
11005	23889	37323	0.81	1.4E+00	D63441.1	NT	Pandorina colemaniae chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
11005	23889	37324	0.81	1.4E+00	D63441.1	NT	Pandorina colemaniae chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
11508	24418	37870	1.47	1.4E+00	AA195528.1	EST_HUMAN	zr36e09.1 Soares NIH-MP_u_S1 Homo sapiens cDNA clone IMAGE:665512 5' similar to contains element
11674	24578	38054	6.73	1.4E+00	AB00592.1	NT	MER22 repetitive element;
11842	24693	38182	5.4	1.4E+00	BE962107.2	EST_HUMAN	Homo sapiens APECED mRNA for AIRE-1, complete cds
11842	24693	38183	5.4	1.4E+00	BE962107.2	EST_HUMAN	601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
11842	24693	38183	5.4	1.4E+00	BE962107.2	EST_HUMAN	601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
11869	24749	38241	2.89	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
11859	24749	38242	2.89	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
12426	25815		2.1	1.4E+00	AL161500.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12
12787	25969		1.92	1.4E+00	11546896	NT	Homo sapiens cutaneous T-cell lymphoma tumor antigen sa70-2 (SE70-2), mRNA
592	13659		1.99	1.3E+00	Z73640.1	NT	M.mucedo gene encoding 4-Dihydroxymethyl-trispartate dehydrogenase
927	13979	26925	2.66	1.3E+00	AJ271192.1	NT	Cantharellus sp. partial 28S rRNA gene, isolate Tibet
1166	14197		13.38	1.3E+00	Y19213.1	NT	Homo sapiens putative psih-HaA pseudogene for hair keratin, exons 2 to 7
1323	14357	27304	11.53	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1323	14357	27305	11.53	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1384	14416		1.18	1.3E+00	U61730.2	NT	Coix laevaria-jobi dihydrodipicolinate synthase (dapA) gene, complete cds
1633	14663		2.30	1.3E+00	AE002338.2	NT	Citramydia muridarum, section 66 of 85 of the complete genome
2258	15288		1.02	1.3E+00	AB030447.1	NT	Cyprinus carpio MRPs and MASPs genes for mannose-binding lectin-associated serine protease (MASP) end MASP-related protein, complete cds
2429	15433	28433	0.92	1.3E+00	P25391	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)

Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2582	15581		3.91	1.3E+00	BE966735.2	EST_HUMAN	601661233R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915945 3'
2981	16032	28933	0.94	1.3E+00	6755621	NT	Mus musculus alpha-spectrin 1, erythroid (Spna1), mRNA
3659	16894	28590	0.68	1.3E+00	AF016494.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synapto vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c>
5336	18320	31168	1.36	1.3E+00	AF080222.1	NT	Homo sapiens thrombin-activable fibrinolysis inhibitor gene, 5'-flanking region
5336	18320	31169	1.36	1.3E+00	AF080222.1	NT	Homo sapiens thrombin-activable fibrinolysis inhibitor gene, 5'-flanking region
5704	18777	31706	0.95	1.3E+00	P19732	SWISSPROT	PHENOL HYDROXYLASE P3 PROTEIN (PHENOL 2-MONOOXYGENASE P3 COMPONENT)
5908	18977	32094	0.42	1.3E+00	M27138.1	NT	Human estradiol 17 beta-dehydrogenase gene, complete cds
6178	19235	32381	0.55	1.3E+00	BF663825.1	EST_HUMAN	602145284F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4309095 5'
6251	19304	32465	8.52	1.3E+00	AW362834.1	EST_HUMAN	PfMO-CT0289-291199-004-108 CT0289 Homo sapiens cDNA
6251	19304	32466	8.52	1.3E+00	AW362834.1	EST_HUMAN	PfMO-CT0289-291199-004-108 CT0289 Homo sapiens cDNA
6684	19720	32920	1.58	1.3E+00	M33496.1	NT	D.melanogaster no-on-transient A gene product, complete cds
7055	20081		0.8	1.3E+00	Q00156	SWISSPROT	HYPOTHETICAL GENE 64 PROTEIN
7097	20303		0.5	1.3E+00	P49940	SWISSPROT	SPORE GERMINATION PROTEIN KB
7153	20281	33515	1	1.3E+00	M13918.2	NT	Homo sapiens fibronectin receptor alpha-subunit precursor (ITGA5) mRNA, partial cds
7268	25664	33419	0.42	1.3E+00	AW821580.1	EST_HUMAN	IL2-ST0311-020200-040-G12 S T0311 Homo sapiens cDNA
7285	20238	33488	0.89	1.3E+00	BE538819.1	EST_HUMAN	601061420F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447965 5'
7459	20399	33672	0.96	1.3E+00	BE243571.1	EST_HUMAN	TCBAP1D0959 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HQSC project-TCBA Homo sapiens cDNA clone TCBAP0959
7862	20789	34092	0.67	1.3E+00	P24540	SWISSPROT	ACYLPHOSPHATASE, ORGAN-COMMON TYPE ISOZYMES A AND B (ACYLPHOSPHATE PHOSPHOHYDROLASE)
8873	21803	35157	1.69	1.3E+00	AJ009912.1	NT	Sus scrofa plp gene
8015	21944	35300	2.16	1.3E+00	BE963379.2	EST_HUMAN	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866195 3'
9124	22052	35412	0.95	1.3E+00	BE974280.1	EST_HUMAN	601680250R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950532 3'
9268	22196		2.25	1.3E+00	8910247	NT	Homo sapiens GL004 protein (GL004), mRNA
9348	22276	35638	0.99	1.3E+00	AJ927629.1	EST_HUMAN	wo88a07.x1 NCL CGAP Kid11 Homo sapiens cDNA clone IMAGE:2462100 3'
9689	22615	35988	0.65	1.3E+00	H42881.1	EST_HUMAN	yo38c03.s1 Soares breast 3NbhBst Homo sapiens cDNA clone IMAGE:183076 3'
9689	22615	35989	0.65	1.3E+00	H42881.1	EST_HUMAN	yo38c03.s1 Soares breast 3NbhBst Homo sapiens cDNA clone IMAGE:183076 3'
10046	22962		5.24	1.3E+00	AF042084.1	NT	Homo sapiens topanan glucosaminyl N-deacetylase/N-sulfotransferase-2 gene, complete cds
10054	22970	30358	2.7	1.3E+00	X72019.1	NT	S. alba phi-1 mRNA for photolyase
10054	22970	30359	2.7	1.3E+00	X72019.1	NT	S. alba phi-1 mRNA for photolyase
10150	23041	36440	1.16	1.3E+00	AF059250.1	NT	Homo sapiens lipoxigenase (ALOX12B) mRNA, complete cds

Page 23 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10195	23096	36487	1.87	1.3E+00	000754	SWISSPROT	LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID
10271	23161	36571	1.53	1.3E+00	A1927629.1	EST_HUMAN	ALPHA-MANNOSIDASE (LAMANA)
10341	23230	36647	0.89	1.3E+00	AJ223962.1	NT	wc85a07.xt NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462100 3'
10341	23230	36648	0.89	1.3E+00	AJ223962.1	NT	Lactococcus lactis cremoris NCDO-invt chromosomal inversion junction DNA
10379	23268	36690	3.8	1.3E+00	BE983378.2	EST_HUMAN	Lactococcus lactis cremoris NCDO-invt chromosomal inversion junction DNA
10709	23596	37023	1.37	1.3E+00	AE004392.1	NT	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866195 3'
10725	23611	37040	1.93	1.3E+00	IM29953.1	NT	Vibrio cholerae chromosome II, section 49 of 93 of the complete chromosome
11066	23940		1.04	1.3E+00	AL163302.2	NT	Campylobacter jejuni kanamycin phosphotransferase (aphA-7) gene, complete cds
11135	24064		4.55	1.3E+00	Q14117	SWISSPROT	Homo sapiens chromosome 21 segment HS21C102
11344	24263	37703	2.47	1.3E+00	P25289	SWISSPROT	DIHYDROPYRIMIDINASE (DHPASE) (HYDANTOINASE) (DHP)
11366	24294	37728	2.01	1.3E+00	Z18892.2	NT	MRNA 3'-END PROCESSING PROTEIN RNA15
11970	24813	38308	3.49	1.3E+00	D42042.1	NT	Mus musculus desmin gene
12049	24890	38394	5.06	1.3E+00	Z98682.1	NT	Human mRNA for KIAA0085 gene, partial cds
12224	25058		1.39	1.3E+00	AF174585.1	NT	Bacillus subtilis genomic DNA 23.9kb fragment
12556	25270		3.14	1.3E+00	AF187873.1	NT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds
12722	25369	31800	3.77	1.3E+00	BF348043.1	EST_HUMAN	Cavia porcellus inwardly-rectifying potassium channel Kir2.2 (KCNJ12) gene, complete cds
12732	25724		1.49	1.3E+00	P33464	SWISSPROT	602023185F1 NOI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4158452 5'
12814	25436		1.8	1.3E+00	AF187035.1	NT	E1 GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN)
13098	25614		1.54	1.3E+00	U38978.1	NT	Stumira lillum cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
673	13735	26647	7.6	1.2E+00	AA678246.1	EST_HUMAN	Naphthalenesulfonate-degrading bacterium BN6 2,3-dihydroxybiphenyl dioxygenase (bphCII) gene, complete cds
848	13903	26843	1.31	1.2E+00	P05228	SWISSPROT	Z12203.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431535 3'
848	13903	26844	1.31	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
848	13903	26845	1.31	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
903	13955		1.84	1.2E+00	8924234	NT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
1188	14227	27168	3.19	1.2E+00	AF080245.2	NT	Homo sapiens hypothetical protein PRO3077 (PRO3077), mRNA
1233	14269	27212	1.25	1.2E+00	AJ252242.1	NT	Eleis oleifera sesquiterpene synthase mRNA, complete cds
1233	14269	27213	1.25	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
2023	15041	28035	1.06	1.2E+00	AF140631.1	NT	pea seed-borne mosaic virus complete genome
2400	15405	28408	0.99	1.2E+00	AF156495.1	NT	Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds
3156	16208	28096	1.73	1.2E+00	AB020681.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
3207	16255	29152	8.26	1.2E+00	AL161563.2	NT	Homo sapiens mRNA for KIAA0874 protein, partial cds
3207	16255	29153	8.26	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3207	16255	29153	8.26	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63

Page 24 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3330	16376		4.2	1.2E+00	P54910	SWISSPROT	CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR
3408	16448	29356	0.67	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
3407	16449		1.23	1.2E+00	M81779.1	NT	G.gallus T-cadherin mRNA, complete cds
3775	16808	29693	10.11	1.2E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LFC (PC7) gene, exons 1 to 9, partial cds
4072	17098	29681	2.44	1.2E+00	BF373570.1	EST_HUMAN	MR0-FT0175-050900-203-q08_1 FT0175 Homo sapiens cDNA
4401	16448	29356	0.97	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
4583	17591		2.21	1.2E+00	M87080.1	NT	Rattus rattus cardiac AE3 gene, exons 1-23
4676	17681	30549	1.86	1.2E+00	AF156495.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
4702	17707		7.25	1.2E+00	Y09200.1	NT	T.pinnatum chloroplast rbcL gene, partial
4795	16449		0.8	1.2E+00	M81779.1	NT	G.gallus T-cadherin mRNA, complete cds
5145	18140	30983	1.25	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
5145	18140	30984	1.25	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
5146	18140	30986	1.25	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
5623	18659	31597	1.33	1.2E+00	U20760.1	NT	Human extracellular calcium-sensing receptor mRNA, complete cds
5746	18819	31916	2.05	1.2E+00	AW813278.1	EST_HUMAN	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
6007	19071		0.51	1.2E+00	X81879.1	NT	Calicivirus cDNA for orf1, orf2 and orf3
6089	19150	32286	0.92	1.2E+00	AF016052.1	NT	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds
6392	19441	32608	2.21	1.2E+00	X74885.1	NT	D.hydrel ay1 repeat cluster DNA, fragment D
6457	19502	32677	4.18	1.2E+00	BE003113.1	EST_HUMAN	QYA-BN0090-270400-190-a03 BN0090 Homo sapiens cDNA
6544	19587	32773	1.57	1.2E+00	X89084.1	NT	G.glutamicum pta gene and eckA gene
6544	19587	32774	1.57	1.2E+00	X89084.1	NT	G.glutamicum pta gene and eckA gene
6590	19631	32813	31.21	1.2E+00	AA759254.1	EST_HUMAN	afn84g12.s1 Soares, testis, NHT Homo sapiens cDNA clone 1322374.3'
6704	19740	32941	0.73	1.2E+00	N33295.1	EST_HUMAN	y93b12.s1 Soares melanocyte 2NkHM Homo sapiens cDNA clone 1322374.3'
6778	19812	33023	0.74	1.2E+00	P17671	SWISSPROT	g9jM87936jHUMALU472 Human carcinoma cell-derived Alu RNA transcript, (rRNA), gb:J04970
6782	19815	33027	2.02	1.2E+00	AW813276.1	EST_HUMAN	CARBOXYPEPTIDASE M PRECURSOR (HUMAN);
7243	201E2	33391	1.02	1.2E+00	AB029010.1	NT	ECDYSONE-INDUCIBLE PROTEIN E75-A
7257	20166	33405	2.63	1.2E+00	AJ002141.1	NT	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
7386	20379	33648	0.57	1.2E+00	AA107810.1	EST_HUMAN	Homo sapiens mRNA for KIAA1087 protein, partial cds
7624	20559		0.75	1.2E+00	AJ271735.1	NT	Mus musculus DSSP gene
7777	25676	34009	2.59	1.2E+00	AV734585.1	EST_HUMAN	z38f05.r1 Strategene hNT neuron (#837253) Homo sapiens cDNA clone IMAGE:632001 5' similar to
8059	21011	34337	2.59	1.2E+00	X74207.1	NT	gb:U0522 Human mRNA for 80K-L protein, complete cds, (HUMAN);
							Homo sapiens Xq pseudautosomal region, segment 1/2
							AV734585 cdA Homo sapiens cDNA clone cDAAFH03 5'
							L.lactis pyrD and pyrF genes

Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8162	21069	34398	0.44	1.2E+00	J05218.1	NT	Chicken muscarinic acetylcholine receptor (m4 mAChR) gene, complete cds
8340	21245	34579	0.47	1.2E+00	BE787646.1	EST_HUMAN	601481761F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884270 5'
8345	21250	34585	0.48	1.2E+00	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds. Sacm21 gene, partial>
9132	22060	35420	4.63	1.2E+00	AB033030.1	NT	Homo sapiens mRNA for KIAA1204 protein, partial cds
9221	22149	35502	0.86	1.2E+00	P38427	SWISSPROT	ALPHA-ALPHA-TREHALOSE-PHOSPHATE SYNTHASE (UDP-FORMING) 123 KD SUBUNIT (TREHALOSE-6-PHOSPHATE SYNTHASE) (UDP-GLUCOSE-GLUCOSEPHOSPHATE GLUCOSYLTRANSFERASE)
9434	22362		0.82	1.2E+00	7706271	NT	Homo sapiens CGI-30 protein (LOC51611), mRNA
9576	22503	35867	2.33	1.2E+00	AW377210.1	EST_HUMAN	NR2-CT0222-201099-001-e07 CT0222 Homo sapiens cDNA
9781	22705	36089	0.56	1.2E+00	H48599.1	EST_HUMAN	Yd80a06.r1 Soares fetal liver spleen TNF1S Homo sapiens cDNA clone IMAGE:202069 5'
9834	22839	36227	3.1	1.2E+00	Z32850.1	NT	R. communis gene for pyrophosphate-dependent phosphofructokinase beta subunit
10132	23023	36419	1.9	1.2E+00	D11745.1	EST_HUMAN	HUM-HM01A01 Liver HepG2 cell line. Homo sapiens cDNA clone hmo01a01
10441	23330	36748	3.55	1.2E+00	X66832.1	NT	H. sapiens ENO3 gene for muscle specific enolase
10815	23701		0.86	1.2E+00	AB009666.1	NT	Homo sapiens Klotho gene, exon 1
11786	24708	38200	1.74	1.2E+00	AW817817.1	EST_HUMAN	PM0-ST0264-161195-001-001 ST0264 Homo sapiens cDNA
11822	24742		12.4	1.2E+00	BE160761.1	EST_HUMAN	PM1-HT0422-160200-007-g10 HT0422 Homo sapiens cDNA
11890	23950	37429	5.19	1.2E+00	U50147.1	NT	Rattus norvegicus synapse-associated protein 102 mRNA, complete cds
12523	25750	31577	36.12	1.2E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
12543	25262		2.45	1.2E+00	AP001515.1	NT	Beddlii halodurans genomic DNA, section 9/14
486	13557	26473	1.31	1.1E+00	D86980.1	NT	Human mRNA for KIAA0227 gene, partial cds
1787	14813	27782	1.2	1.1E+00	AW995393.1	EST_HUMAN	QY0-BN0042-170300-163-g12 BN0042 Homo sapiens cDNA
1917	14938	27915	1.21	1.1E+00	AW575889.1	EST_HUMAN	UI-HF-BR0p-ajk-f-02-0-UI.61 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3074834 3'
3377	16421	28323	11.07	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3377	16421	28324	11.07	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3545	16583	29488	0.89	1.1E+00	8922641	NT	Homo sapiens chromosome 21 segment HS21C013
3640	16676	29574	1.05	1.1E+00	AI608960.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
3782	16813	29099	1.79	1.1E+00	AE003866.1	NT	SW:P631_HUMAN Q12888 P63-BINDING PROTEIN 53BP1 ;
3782	16813	29700	1.79	1.1E+00	AE003866.1	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
3801	16832	29718	1.96	1.1E+00	5729767	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
3888	16917		0.68	1.1E+00	X65374.1	NT	Homo sapiens calpain 9 (nCL-4) (CAPN9) mRNA
4021	17048	29937	0.67	1.1E+00	8922641	NT	H. parahaemolyticus hphIM(A), hphIM(C), hphIR and menB genes
							Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA

Page 26 of 545  
Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4079	17105	29984	0.72	1.1E+00	AB040053.1	NT	Oryza sativa subsp. japonica rCOP1 mRNA for COP1, complete cds
4311	17325		6.63	1.1E+00	5836331	NT	R.unicornis complete mitochondrial genome
4794	17768		0.77	1.1E+00	U34692.1	NT	Carcharias plumbeus Ig lambda light chain gene, complete cds
5113	18110	30955	5.02	1.1E+00	U18466.1	NT	African swine fever virus, complete genome
5114	18111	30956	2.46	1.1E+00	AJ271740.1	NT	Drosophila melanogaster D-Titin gene, exons 1-37
5204	18195	31037	1.01	1.1E+00	X78425.1	NT	E. faecalis pbp5 gene
5407	18388		0.72	1.1E+00	AF140522.1	NT	Glossina morsitans morsitans salivary gland growth factor-2 (TSGF-2) mRNA, complete cds
5411	18392		0.98	1.1E+00	BE409837.1	EST_HUMAN	601299534F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3628605 6'
5448	18529	31255	0.45	1.1E+00	P13181	SWISSPROT	GALACTOSE TRANSPORTER (GALACTOSE PERMEASE)
5490	18670	31416	1.51	1.1E+00	6978530	NT	Rattus norvegicus Aquaporin 4 (Aqp4), mRNA
5808	18860	31987	40.8	1.1E+00	BE680184.1	EST_HUMAN	601552776R1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3825635 3'
5828	18859	32013	14.89	1.1E+00	AJ138582.1	EST_HUMAN	q88c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736260 3'
6329	19379	32546	1.24	1.1E+00	11419739	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter), member 14 (SLC6A14), mRNA
6526	19570	32753	0.65	1.1E+00	AF197861.1	NT	Macgregoria pulchra cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
6672	19709	32904	0.68	1.1E+00	R08037.1	EST_HUMAN	ye99e03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124924 5'
7015	20042	33276	0.71	1.1E+00	AJ404004.1	NT	Mus musculus mRNA for ER protein 58 (EP58 gene)
7163	20270	33526	0.45	1.1E+00	AF267747.1	NT	Mus musculus p47-phox gene, complete cds
7627	20562		0.66	1.1E+00	AF101091.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exons 25 through 28
7676	20610	33909	0.68	1.1E+00	X55981.1	NT	Maize mRNA for endolase (2-phospho-D-glycerate hydrolase)
7881	20807	34112	0.61	1.1E+00	BF683714.1	EST_HUMAN	602139579F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301322 5'
7911	20835	34137	2.14	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7911	20835	34138	2.14	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7934	20856	34164	8.75	1.1E+00	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
8016	26682	34250	0.94	1.1E+00	11987960	NT	Mus musculus silent mating type information regulation 2, (S. cerevisiae, homolog)-like (Sir2), mRNA
8709	21640	34987	3.73	1.1E+00	BF693996.1	EST_HUMAN	602082582F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246628 5'
8789	21729	35078	0.86	1.1E+00	AJ478339.1	EST_HUMAN	tm30h11.x1 NCI_OGAP_Kid11 Homo sapiens cDNA clone IMAGE:2160549 3'
9296	22224	35583	1.08	1.1E+00	AB003088.1	NT	Acetabularia caliculus mitochondrial COXI-like gene
9374	22302	35663	0.93	1.1E+00	S80750.1	NT	VH=anti-cytomegalovirus glycoprotein B antibody 4D4 heavy chain variable region [human, mRNA Partial, 375 nt]
9871	21329		0.58	1.1E+00	BE384876.1	EST_HUMAN	601276278F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617418 5'
10154	23045	38444	0.7	1.1E+00	AJ245772.1	NT	Mus musculus mRNA for stretch responsive muscle (X-chromosome) protein (Srmx gene)



Page 27 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10206	23097		0.83	1.1E+00	Y12227.1	NT	Arabidopsis thaliana DNA, 24 kb surrounding PFL locus
10291	23181	36593	0.56	1.1E+00	L76301.1	NT	Yersinia pseudotuberculosis psaE, psaF, adhesin (psaA), chaperone (psaB), and usher (psaC) genes, complete cds
10348	23237	36885	2.17	1.1E+00	AB023151.1	NT	Homo sapiens mRNA for KIAA0834 protein, partial cds
10446	23335	36753	5.97	1.1E+00	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
10503	23391	36802	20.33	1.1E+00	6754021	NT	Mus musculus guanine nucleotide binding protein (G protein), gamma 3 subunit (Gng3), mRNA
10979	23863	37290	1.18	1.1E+00	P73769	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
11095	24026	37469	2.49	1.1E+00	11097364	NT	Homo sapiens KIAA0828 gene product (KIAA0828), mRNA
11150	24079		3.12	1.1E+00	AF068942.1	NT	Klebsoridium fluitans cytochrome c oxidase subunit 2 (cox2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11526	24436	37894	1.68	1.1E+00	11439586	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 11 (KCNJ11), mRNA
11543	18425		4.92	1.1E+00	8922973	NT	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA
11547	24456	37918	4.06	1.1E+00	AF012862.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
11547	24456	37919	4.06	1.1E+00	AF012862.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
11794	24716	38208	4.19	1.1E+00	AI809699.1	EST_HUMAN	wf76e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361548 3'
12002	24844	38340	1.5	1.1E+00	D89501.1	NT	Human PBI gene, complete cds
12002	24844	38341	1.5	1.1E+00	D89501.1	NT	Human PBI gene, complete cds
12496	25236		1.95	1.1E+00	P07866	SWISSPROT	LOW TEMPERATURE ESSENTIAL PROTEIN
12591	25288	31842	2.59	1.1E+00	AF216886.1	NT	Tecnia solum immunogenic protein Ts76 mRNA, partial cds
12714	25787		2.93	1.1E+00	AF234169.1	NT	Dictyostellium discoideum isopentenyl pyrophosphate isomerase (Dip) mRNA, complete cds
102	13215		2.91	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
117	13225		2.72	1.0E+00	D88425.1	NT	Cavia cobaya mRNA for serine/threonine kinase, complete cds
441	13512		1.72	1.0E+00	AB021884.1	NT	Marchantia polymorpha genes for 26S rRNA, 18S rRNA, 5S rRNA, 5.8S rRNA and 26S rRNA
598	13665	26567	1.38	1.0E+00	AJ251660.1	NT	Girardinia tigrina mRNA for homeodomain transcription factor (so gene)
700	13759	26676	8.98	1.0E+00	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
702	13761		0.89	1.0E+00	AF125984.1	NT	Aedes aegypti mucin-like protein MUC1 mRNA, complete cds
1413	15900		1.41	1.0E+00	X80416.1	NT	V. carteri Algal-CAM mRNA
2308	15309	26511	1.57	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2308	15309	26512	1.57	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2589	15587		0.95	1.0E+00	AA628453.1	EST_HUMAN	af26g08.s1 Soares, total, fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032830 3' similar to WP:C42D8.3 CE04204, contains element MER22 repetitive element ;

Page 28 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2919	15972	28869	4.6	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2919	15972	28870	4.6	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
3008	16060		0.95	1.0E+00	O14226	SWISSPROT	HYPOPHOSPHATE 67.9 KD PROTEIN C6F12.08C IN CHROMOSOME 1
3242	16250	29193	1.18	1.0E+00	AA628453.1	EST_HUMAN	af20608.s1 Scores: total_fetus_Nb22-IF8_9w Homo sapiens cDNA clone IMAGE:1032830 3' similar to WPC42D8.3 CE04204 ;contains element MER22 MER22 repetitive element;
3431	16472		0.65	1.0E+00	AF222781.1	NT	Rattus norvegicus neuromedin U precursor (NmU) gene, exons 5 and 6
3661	13215		0.98	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
3748	16780	29569	1.93	1.0E+00	AJ223816.1	NT	Agaricus bisporus mRNA for tyrosinase
4157	17178	30050	1	1.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CAVNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5166	18158	31006	0.79	1.0E+00	AF092505.1	NT	Mus musculus dipeptidyl aminopeptidase-like protein 6 (Dpp6) gene, partial cds; and proximal Rump white inversion breakpoint
5394	18376	31218	0.98	1.0E+00	BE142914.1	EST_HUMAN	MRQ-HT0157-310300-010-g11 HT0157 Homo sapiens cDNA
5464	18545	31385	2.83	1.0E+00	Z97022.1	NT	Hordeum vulgare gene encoding cysteine proteinase
6063	19125	32253	4.77	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6063	19125	32254	4.77	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6182	19239	32386	1.23	1.0E+00	Z97341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA1 FCA contig fragment No. 6
6353	19402	32569	5.15	1.0E+00	P04501	SWISSPROT	FIBER PROTEIN
6360	19409	32574	1.92	1.0E+00	AW482782.1	EST_HUMAN	U1-H-B13-alk-d-09-0-U1s1 NOI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068969 3'
6765	19799	33011	2.14	1.0E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
6920	19853	33066	0.74	1.0E+00	AF104669.1	NT	Homo sapiens cell cycle protein (PA2G4) gene, exons 2 through 5
6921	19951		0.9	1.0E+00	P48506	SWISSPROT	SRB-11 PROTEIN
6950	19979	33202	0.48	1.0E+00	BE797716.1	EST_HUMAN	601681891F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936382 5'
6950	19979	33203	0.48	1.0E+00	BE797716.1	EST_HUMAN	601681891F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936382 5'
7084	20290	33549	1	1.0E+00	Y11204.1	NT	V. carteri gene encoding volvoxopsin
7174	18446	31315	0.56	1.0E+00	U63721.1	NT	Human elastin (ELN) gene, partial cds, and LIM-kinase (LIMK1) gene, complete cds
7498	20438	33719	1.36	1.0E+00	S52770.1	NT	insulin-like growth factor-binding protein 4 [cattle, pulmonary artery endothelial cells, mRNA, 2028 nt]
7898	20824		9.02	1.0E+00	P20273	SWISSPROT	B-CELL RECEPTOR CD22 PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM)

Page 29 of 545  
Table 4 -  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8171	21078	34408	1.51	1.0E+00	AF192531.1	NT	Homo sapiens endothelin-converting enzyme 2 (ECE2) mRNA, complete cds
8188	21095	34426	9.27	1.0E+00	AA775191.1	EST_HUMAN	ac79b08.s1 Stragena lung (#637210) Homo sapiens cDNA clone IMAGE:868791 3'
8407	21310		0.61	1.0E+00	BF079213.1	EST_HUMAN	602163792F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294727 5'
8539	21470	34810	1.18	1.0E+00	BE868267.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5'
8539	21470	34811	1.18	1.0E+00	BE868267.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5'
8720	18431		1.66	1.0E+00	D10952.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
8924	21854	35209	2.66	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE]
8924	21854	35210	2.66	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE]
9047	21976		0.66	1.0E+00	P51784	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (UBIQUITIN THIOLESTERASE 11) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 11) (DEUBIQUITINATING ENZYME 11)
9102	25689		2.23	1.0E+00	BE147331.1	EST_HUMAN	RC1-HT0229-181099-011-e08 HT0229 Homo sapiens cDNA
9140	22068	35429	1.46	1.0E+00	U42720.2	NT	Simian immunodeficiency virus Gag protein (gag) gene, complete cds; Pol protein (pol) gene, partial cds; and Vif protein (vif), Vpr protein (vpr), Tat protein (tat), Rev protein (rev), Vpu protein (vpu), Env protein (env), and Nef protein (nef) genes; >
9283	22211	35569	1.71	1.0E+00	M38427.1	NT	Human immunodeficiency virus type 1 (HIV-1), isolate SF33.
9811	22717	36099	1.83	1.0E+00	BE907592.1	EST_HUMAN	601497581F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899421 5'
9903	22891	36275	0.58	1.0E+00	AF257519.1	NT	Danio rerio eukaryotic translation initiation factor eIF4E-1 mRNA, complete cds
9903	22891	36276	0.58	1.0E+00	AF257519.1	NT	Danio rerio eukaryotic translation initiation factor eIF4E-1 mRNA, complete cds
10014	22914	36303	1.43	1.0E+00	6753428	NT	Mus musculus chloride channel activated 1 (Clca1), mRNA
10014	22914	36304	1.43	1.0E+00	6753429	NT	Mus musculus chloride channel activated 1 (Clca1), mRNA
10137	23028	36425	1.87	1.0E+00	AV689554.1	EST_HUMAN	AV689554 GK Homo sapiens cDNA clone GKCGYA11 5'
10142	23033	36430	1.33	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (xlZPC) mRNA, complete cds
10142	23033	36431	1.33	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (xlZPC) mRNA, complete cds
10367	23256	36676	0.51	1.0E+00	X15498.1	NT	Human Coronavirus gene for membrane protein
10367	23256	36677	0.51	1.0E+00	X15498.1	NT	Human Coronavirus gene for membrane protein
10613	23499	36931	0.83	1.0E+00	5174502	NT	Homo sapiens MHC binding factor, beta (MHCBBF) mRNA
10613	23499	36932	0.83	1.0E+00	5174502	NT	Homo sapiens MHC binding factor, beta (MHCBBF) mRNA
10700	23566	37015	1.13	1.0E+00	A1077920.1	EST_HUMAN	oy15d07.s1 Soares_senscent_fibroblasts_NHHSF Homo sapiens cDNA clone IMAGE:1605501 3'
10816	23702	37129	2.99	1.0E+00	AV758825.1	EST_HUMAN	AV758825 BM Homo sapiens cDNA clone BMFAW04 5'
10955	23839	37266	21.78	1.0E+00	AA004982.1	EST_HUMAN	2f94e02.r1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:428806 5'

Page 30 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10955	23839	37267	21.78	1.0E+00	AA004982.1	EST_HUMAN	zh94e02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'
10988	23872	37300	1.11	1.0E+00	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
11528	24438	37896	1.59	1.0E+00	AA701494.1	EST_HUMAN	z63b1.1.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:435453 3' similar to contains Alu repetitive element; contains element MER38 repetitive element;
12162	18545	31385	1.57	1.0E+00	Z97022.1	NT	Hordeum vulgare gene encoding cysteine proteinase
12399	25172		3.26	1.0E+00	P15306	SWISSPROT	T-THROMBOMODULIN PRECURSOR (PETOMODULIN) (TM)
12703	25358		2.04	1.0E+00	AW979184.1	EST_HUMAN	EST388293 MAGE sequences, MAGN Homo sapiens cDNA
2684	15678	28877	1.27	9.9E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
3667	16701		0.95	9.9E-01	AF174985.1	NT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds
5630	19901	32016	11.74	9.9E-01	P49657	SWISSPROT	SERINE/THREONINE PROTEIN KINASE MINIBRAIN
6084	19145	32280	0.92	9.9E-01	Q09632	SWISSPROT	PROBABLE OXIDOREDUCTASE ZK1290.5 IN CHROMOSOME II
6803	22709		1.76	9.9E-01	U65667.1	NT	Lycopodium esculentum putative Mit copy 1 nematode resistance gene
10084	22977		2.07	9.9E-01	Q28842	SWISSPROT	B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR)
11157	24089	37533	2.45	9.9E-01	AJ005029.1	NT	Danio rerio mRNA for Eph-like receptor tyrosine kinase rtk8
546	13615	28523	1.13	9.8E-01	P22867	SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS) (NAGS)
2316	15324		1.1	9.8E-01	AJ003108.1	NT	Callitrix jacchus UBE1 gene derived retroposon on the Y chromosome
7564	20501	33789	4.61	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
7564	20501	33790	4.61	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
8094	21006	34330	1.23	9.8E-01	BF034016.1	EST_HUMAN	601456337F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:3860049 5'
8094	21006	34331	1.23	9.8E-01	BF034016.1	EST_HUMAN	601456337F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:3860049 5'
9278	22206	35563	0.98	9.8E-01	P38862	SWISSPROT	PHOSPHOGLUCOMUTASE (GLUCOSE PHOSPHOMUTASE) (PGM)
10978	23803		0.71	9.8E-01	AA825565.1	EST_HUMAN	cd55d04.st NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371847 3'
11432	24348	37793	2.02	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350760 5'
11432	24348	37794	2.02	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350760 5'
12698	25204		1.64	9.8E-01	U62111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
7520	20459	33745	2.22	9.7E-01	U26716.1	NT	Drosophila melanogaster sodium channel protein (para) gene, exons 9,10,11,12 and optional segments b, c, d and e, partial cds
9070	21999	35363	1.89	9.7E-01	AF149112.1	NT	Triticum aestivum stripe rust resistance protein Yr10 (Yr10) gene, complete cds
9076	22005	35359	1.49	9.7E-01	M90544.1	NT	Salmonella typhimurium adenine-methyltransferase (moe) and restriction endonuclease (res)
9397	22325	35688	0.92	9.7E-01	BE799822.1	EST_HUMAN	601592165F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945804 5'

Single Exon Probes Expressed in Adult Liver

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11612	24520		5.75	9.7E-01	BF911209.1	EST_HUMAN	U1-H-B14-aol-e-07-0-U1.s1 NCL CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085140 3'
13105	25620		5.01	9.7E-01	AL114281.1	NT	Bovine chinease strain T4 cDNA library under conditions of nitrogen deprivation
4344	17553	30413	0.71	9.6E-01	AF197925.1	NT	Bromus thermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4544	17553	30414	0.71	9.6E-01	AF197925.1	NT	Bromus thermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4669	17577	30439	1.72	9.6E-01	AW799574.1	EST_HUMAN	PM2-UM0053-240300-003-112 UM0053 Homo sapiens cDNA
5560	19027	32147	3.54	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2994
5560	19027	32148	3.54	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2994
7051	20077	33310	0.55	9.6E-01	Z97341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA1 FCA contig fragment No. 6
7747	20678	33976	0.5	9.6E-01	AF197981.1	NT	Helix lucorum presenilin (PS) mRNA, complete cds
8963	21893		1.74	9.6E-01	X98275.1	NT	P. falciparum complete gene map of plastid-like DNA (IR-A)
9410	22338	35702	0.85	9.6E-01	L81138.1	NT	Rattus norvegicus (strain R21) Rps2r gene, complete cds
11530	24440	37869	1.44	9.6E-01	AF041427.1	NT	Homo sapiens ribosomal protein s4 Y isoform gene, complete cds
11951	24795	38284	4.1	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPDBAG06 5'
11951	24795	38285	4.1	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPDBAG06 5'
12308	25115		2.73	9.6E-01	11421722	NT	Homo sapiens centromeric protein 2 (CEP2), mRNA
12887	25856	31473	1.88	9.6E-01	U91423.1	NT	Sphyrna tiburo NADH dehydrogenase subunit 2 (NADH2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
2498	15500	28501	1.34	9.5E-01	7705591	NT	Homo sapiens CGI-125 protein (LOC51003), mRNA
3847	16876	29759	2.53	9.5E-01	BE902340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3858473 5'
3847	16876	29760	2.53	9.5E-01	BE902340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3858473 5'
9553	22480	35839	0.83	9.5E-01	AI190162.1	EST_HUMAN	qds7d07 x1 Soares, testis NHT Homo sapiens cDNA clone IMAGE:1733581 3'
9553	22480	35840	0.83	9.5E-01	AI190162.1	EST_HUMAN	qds7d07 x1 Soares, testis NHT Homo sapiens cDNA clone IMAGE:1733581 3'
9650	22578	36047	1.2	9.5E-01	AW861102.1	EST_HUMAN	RC1-CT0295-241199-011-b02 CT0295 Homo sapiens cDNA
9650	22578	36047	1.2	9.5E-01	AW861102.1	EST_HUMAN	RC1-CT0295-241199-011-b02 CT0295 Homo sapiens cDNA clone IMAGE:4109830 5'
11690	24592	38070	1.89	9.5E-01	BF218771.1	EST_HUMAN	U1-H-B12-ahp-f-03-0-U1.s1 NCL CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727677 3'
11885	23935	37423	1.63	9.5E-01	AW293799.1	EST_HUMAN	U1-H-B12-ahp-f-03-0-U1.s1 NCL CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727677 3'
12186	26031	38532	2.32	9.5E-01	T87204.1	EST_HUMAN	ya53d04 s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:66631 3'
3245	16233		4.67	9.4E-01	AF165990.1	NT	Bartonella clarridgeiae RNA polymerase beta subunit (rpoB) gene, partial cds
3284	16312		2.72	9.4E-01	AF080595.1	NT	Pimpinella brachycarpa zinc finger protein (ZFP1) mRNA, complete cds
9423	22351	35717	0.78	9.4E-01	M90724.1	NT	Human Fc-gamma-receptor (FCGR2A) gene, exon 4
12547	25285		1.59	9.4E-01	BE781251.1	EST_HUMAN	601466703F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:3869929 5'
12547	25285		1.59	9.4E-01	BE781251.1	EST_HUMAN	601466703F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:3869929 5'
12886	25782		1.45	9.4E-01	11418837	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR), mRNA
1762	14788		7.14	9.3E-01	AF242382.1	NT	Homo sapiens phytanoyl-CoA hydroxylase (PHYH) gene, exon 5
2860	15675	28674	1.35	9.3E-01	BE071172.1	EST_HUMAN	RC5-BT0503-271199-011-B01 BT0503 Homo sapiens cDNA
4119	17142	30014	1.43	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome

Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4119	17142	30015	1.43	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
5786	18853	31966	1.67	9.3E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
5875	18943	32081	3.99	9.3E-01	L36189.1	NT	Spodoptera frugiperda methyltetrahydrofolate dehydrogenase mRNA, complete cds
7717	20649		0.84	9.3E-01	AF270648.1	NT	Plasmodium falciparum mature parasite-infected erythrocyte surface antigen (MESA) gene, complete cds
8644	21575	34912	2.15	9.3E-01	AA847040.1	EST_HUMAN	0609b03.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1385357
9372	22300		0.89	9.3E-01	AF081981.1	NT	Xenopus laevis CCHC zinc finger protein C3H-2 (C3H-2) mRNA, complete cds
9493	22421	35784	0.89	9.3E-01	AL161534.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 34
12991	25547	31753	1.62	9.3E-01	11440298	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 2 (ITPR2), mRNA
12998	25551		2.01	9.3E-01	AF271207.1	NT	Aedes triseriatus putative large subunit ribosomal protein rpl34 mRNA, complete cds
3285	16332	29238	5.18	9.2E-01	BE622702.1	EST_HUMAN	601441338T1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916184 3'
5919	18086		1.47	9.2E-01	7106410	NT	Mus musculus solute carrier family 30 (zinc transporter), member 4 (Slc30a4), mRNA
6218	19273	32427	4.94	9.2E-01	BF037666.1	EST_HUMAN	601461153F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3864681 5'
6924	19953	33173	0.5	9.2E-01	M64703.1	NT	N. crassa vglX-tRNA synthetase (cyl-20/un-3) gene
10184	23075	36476	0.87	9.2E-01	AL161555.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
10288	23159	36559	0.9	9.2E-01	6671677	NT	Mus musculus carbonic anhydrase 4 (Car4), mRNA
10768	23644	37077	4.12	9.2E-01	11430963	NT	Homo sapiens lysosomal pyruvate kinase-like protein 1 (LALP1), mRNA
10899	23794	37210	1.63	9.2E-01	BF593251.1	EST_HUMAN	7058d06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3578219 3' similar to SW:NU5M_TRYBB
11091	24022	37484	1.94	9.2E-01	BE563811.1	EST_HUMAN	P04540 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 ;
12144	24994	38494	1.72	9.2E-01	BF132402.1	EST_HUMAN	601334943F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688714 5'
							601820312F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052018 5'
1648	14679	27642	1.15	9.1E-01	T96675.1	EST_HUMAN	ye5201.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121369 3' similar to contains
2138	15151		0.96	9.1E-01	8923056	NT	Alu repetitive element;
							Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
3249	16297	29200	0.98	9.1E-01	T26418.1	EST_HUMAN	AB200G8R Infant brain, LNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'
3249	16297	29201	0.98	9.1E-01	T26418.1	EST_HUMAN	AB200G8R Infant brain, LNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'
4547	17556		1.71	9.1E-01	D17428.1	NT	Corynebacterium glutamicum secA gene for SecA protein, complete cds
6408	19456	32630	1.43	9.1E-01	L36039.1	NT	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
6783	19816	33028	3.41	9.1E-01	Q61704	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3)
8010	20927	34244	17.06	9.1E-01	AA806623.1	EST_HUMAN	0b71g08.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1336862 3'
8202	21108	34438	2.17	9.1E-01	U72995.1	NT	Rattus norvegicus Rab3 GDP/GTP exchange protein mRNA, complete cds

Page 33 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10672	23598	36990	0.71	9.1E-01	P38432	SWISSPROT	P80-COLLIN
12632	25849		28.85	9.1E-01	AF050113.1	NT	Homo sapiens uncoupling protein-3 (UGP3) gene, complete cds
3251	19299	29204	1.05	9.0E-01	7661625	NT	Homo sapiens DKFZP564M2423 protein (DKFZP564M2423), mRNA
4486	17487	30387	1.31	9.0E-01	AF098810.1	NT	Homo sapiens neuroxin III-alpha gene, partial cds
5139	18134	30977	0.83	9.0E-01	AF017729.1	NT	Oryzias latipes cuniculus Rad51 (RAD51) mRNA, complete cds
7790	20719	34023	0.71	9.0E-01	L42547.1	NT	Danio rerio LIM class homeodomain protein (lim5) mRNA, complete cds
7822	20761		1.33	9.0E-01	D38921.1	NT	Xenopus laevis gene for aldolase, complete cds
9887	22802	35189	0.52	9.0E-01	AF088761.1	NT	Danio rerio semaphorin 71a mRNA, complete cds
10345	23234	36652	0.52	9.0E-01	U39702.1	NT	Mycoplasma genitalium section 24 of 51 of the complete genome
5895	18864	32081	2.54	8.9E-01	AF026198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds, and calcium channel alpha-1 subunit>
6497	19541		1.29	8.9E-01	X60386.1	NT	Rabbit MHC fragment RLA-DF DNA
6734	28653	32977	0.57	8.9E-01	BF217939.1	EST_HUMAN	601882708F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095216 5'
6734	28653	32978	0.57	8.9E-01	BF217939.1	EST_HUMAN	601882708F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095216 5'
7587	20503		0.52	8.9E-01	AB042297.1	NT	Homo sapiens PTS gene for 6-pyruvoyl-tetrahydropterin synthase, complete cds
7638	20571	33866	0.46	8.9E-01	AA194201.1	EST_HUMAN	z38c05.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:666674 5'
7638	20571	33867	0.46	8.9E-01	AA194201.1	EST_HUMAN	z38c08.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:665674 5'
8789	21719		0.51	8.9E-01	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
8996	21925	35280	0.87	8.9E-01	AF259667.1	NT	Oryzias nana cytochrome-c oxidase subunit 1 (cox1) gene, partial cds; mitochondrial gene for mitochondrial product
12193	25028	38529	2.36	8.9E-01	AE003944.1	NT	Xylella fastidiosa, section 90 of 229 of the complete genome
12481	25225		3.78	8.9E-01	AE002186.2	NT	Chlamydia pneumoniae AR39, section 21 of 84 of the complete genome
4658	17663	30531	2.44	8.8E-01	O26350	SWISSPROT	PUTATIVE F420-DEPENDENT NADP REDUCTASE
5347	18330	31179	0.96	8.8E-01	L41654.1	NT	Trypanosoma brucei microtubule-associated protein (MAP15) mRNA, 3' end of cds
5558	18636	31516	0.8	8.8E-01	AF310617.1	NT	Pseudorabies virus Ea glycoprotein M gene, complete cds
7957	20879	34160	0.47	8.8E-01	M81182.1	NT	Homo sapiens peroxisomal 70 kD membrane protein mRNA, complete cds
10726	23612	37041	0.67	8.8E-01	7656978	NT	Homo sapiens cell death-inducing DFFA-like effector B (CIDEb), mRNA
11520	24430	37898	2.9	8.8E-01	Z28937.1	NT	M. aeruginosa (HUB 5-2-4) DNA from plasmid PMA1
12323	25928		4.13	8.8E-01	D9091.1	NT	Synochocystis sp. PCC6803 complete genome, 13/27, 1576553-1719643
487	13558	25474	1.49	8.7E-01	AF106953.2	NT	Homo sapiens SOS1 (SOS1) gene, partial cds
2424	15428	28429	0.91	8.7E-01	5901893	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
2918	18971	28868	5.93	8.7E-01	AA559893.1	EST_HUMAN	m05f11.s1 NCL CGAP_P4.1 Homo sapiens cDNA clone IMAGE:1076877

Page 34 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5129	18125		3.52	8.7E-01	AF121970.1	NT	Pseudomonas aeruginosa topoisomerase (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-halobenzoate 1,2-dioxygenase beta-ISP protein OhbA (ohbA), OhbC (ohbC), ortho-halobenzoate 1,2-dioxygenase alpha-ISP protein OhbB (ohbB), and put
5330	18314		0.75	8.7E-01	AJ288085.1	NT	Homo sapiens partial LGALS9 gene for galectin-9, exon 3
5359	18342	31186	0.73	8.7E-01	BF219306.1	EST_HUMAN	601883175F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095378 5'
8617	21548	34889	0.65	8.7E-01	AW897335.1	EST_HUMAN	RC4-NN0057-120500-013-c07 NN0057 Homo sapiens cDNA
9485	22413	35774	0.74	8.7E-01	AI239456.1	EST_HUMAN	q136e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846786 3'
9485	22413	35775	0.74	8.7E-01	AI239456.1	EST_HUMAN	q136e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846786 3'
10258	23148	36556	1.77	8.7E-01	AE004963.1	NT	Pseudomonas aeruginosa PA01, section 624 of 629 of the complete genome
10793	23679	37108	0.59	8.7E-01	BF570169.1	EST_HUMAN	60218554T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309906 3'
10793	23679	37109	0.59	8.7E-01	BF570169.1	EST_HUMAN	60218554T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309906 3'
11271	24163	37644	6.02	8.7E-01	BF363970.1	EST_HUMAN	QV0-NN1021-100800-337-c03 NN1021 Homo sapiens cDNA
12157	24996	38496	4.03	8.7E-01	BF107694.1	EST_HUMAN	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
12157	24996	38497	4.03	8.7E-01	BF107694.1	EST_HUMAN	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
12679	25755		2.12	8.7E-01	AV661898.1	EST_HUMAN	AV661898 GLC Homo sapiens cDNA clone GLCYG07 3'
497	13567		1.55	8.6E-01	X17012.1	NT	Rat GFII gene for insulin-like growth factor II
883	13936	28884	4.44	8.6E-01	W69089.1	EST_HUMAN	z444e03.r1 Soares_fetal_heart_NBHF19W Homo sapiens cDNA clone IMAGE:343516 5'
2289	15297	28304	1.17	8.6E-01	4503210	NT	Homo sapiens cytochrome P450, subfamily XXV1A (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
3686	16719	29611	0.9	8.6E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
3865	16894	29778	1.54	8.6E-01	U49724.1	NT	Drosophila melanogaster methyl (Dmterlin) mRNA, complete cds
5413	18394		1.8	8.6E-01	AB014075.1	NT	Clostridium histolyticum genes for hypoxanthine-guanine phosphoribosyl-transferase (HGPRTase), GTPase and 12 ORFs, complete and partial cds
6116	19175	32309	8.31	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
6116	19175	32310	8.31	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
6639	25651	32868	0.51	8.6E-01	S76772.1	NT	polyprotein [Coxsackie B4 virus CB4, host-mimic, E2, originally derived from Edwards CB4 human strain, Genomic RNA Complete, 7397 nt]
7006	20033	33285	1.98	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
7006	20033	33266	1.98	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
7951	20873		0.03	8.6E-01	AE000591.1	NT	Helicobacter pylori 26695 section 60 of 134 of the complete genome
8506	21437		1.45	8.6E-01	AF001518.1	NT	Bacillus halodurans genomic DNA, section 12/14
8620	21551	34892	0.78	8.6E-01	AF077837.1	NT	Drosophila melanogaster collapsin response mediator protein (CRMP) mRNA, complete cds
7027	20053	33285	1.25	8.5E-01	AF165214.1	NT	Bacteriophage D3, complete genome
7949	20871	34182	2.64	8.5E-01	BE542612.1	EST_HUMAN	601067107F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453505 5'



Table 4

## Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8570	21501	34844	0.53	8.5E-01	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 98
8089	21918	35273	0.76	8.5E-01	P06601	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8089	21918	35274	0.76	8.5E-01	P06601	SWISSPROT	SEGMENTATION PROTEIN PAIRED
9071	22000	35354	1.41	8.5E-01	AJ243213.1	NT	Homo sapiens partial 5-HT <sub>4</sub> receptor gene, exons 2 to 6
10837	23723	37145	2.64	8.5E-01	AB006799.1	NT	Cyanidium caldarium gene for SigC, complete cds
10837	23723	37146	2.64	8.5E-01	AB006799.1	NT	Cyanidium caldarium gene for SigC, complete cds
12617	25852		3.3	8.5E-01	11418543	NT	Homo sapiens human immunodeficiency virus type 1 enhancer-binding protein 1 (HIVEP1), mRNA
12624	25308		7.93	8.6E-01	9507008	NT	Rattus norvegicus protein tyrosine phosphatase, non-receptor type 5 (Ptpn5), mRNA
4299	17313	30180	1.03	8.4E-01	AF143509.1	NT	Mus musculus NK cell receptor 2B4 gene, promoter region and partial cds
5682	26631	31677	2.54	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
5682	26631	31678	2.54	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
8322	21227	34561	0.52	8.4E-01	AF051142.1	NT	Maestra brassicae pheromone binding protein 2 precursor (PBP2) mRNA, complete cds
10464	23352		3.57	8.4E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/8
765	13822	28751	2.8	8.3E-01	M83437.1	NT	Thermus thermophilus cytochrome c-552 (cycA) and CycB (cycB) genes, complete cds
3142	16162	29085	4.33	8.3E-01	AL161506.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
3878	16807	29788	0.81	8.3E-01	AB010879.1	NT	Nicotiana tabacum mRNA for chloroplast ribosomal protein L10, complete cds
4098	17123	30000	3.46	8.3E-01	Y19177.1	NT	Streptomyces antibioticus polyketide biosynthesis gene cluster
5451	18532	31258	2.38	8.3E-01	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
10194	23086		3.67	8.3E-01	A1791952.1	EST_HUMAN	nm011212, y6 NCL CGAP_Cc9 Homo sapiens cDNA clone IMAGE:1076495 5' similar to contains THR.11 THR repetitive element;
10611	23497	36928	1.42	8.3E-01	AF098070.1	NT	Drosophila melanogaster Lis1 homolog mRNA, complete cds
10714	23600	37027	4.01	8.3E-01	AF108133.1	NT	Mus musculus neuro-d4 gene, exons 3 through 12 and partial cds
11118	24048	37494	2.58	8.3E-01	AE000903.1	NT	Methanobacterium thermoautotrophicum from bases 1270510 to 1283409 (section 108 of 148) of the complete genome
11133	24062		1.91	8.3E-01	7212472	NT	Phytophthora infestans mitochondrion, complete genome
11749	24660	38131	1.78	8.3E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHLT) gene, exon 5
2068	15081	28080	1.68	8.2E-01	AB000499.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
2102	15116		1.82	8.2E-01	AF145589.1	NT	Mus musculus trophoblast (Tm) gene, complete cds
2728	16721		1.47	8.2E-01	AW376990.1	EST_HUMAN	IL3-CT0219-161109-031-C08 CT0219 Homo sapiens cDNA
3994	17021	29911	0.99	8.2E-01	AF063417.1	NT	Tarneylum orbiculare elongation factor 1-alpha mRNA, partial cdo
5249	18236	31088	0.98	8.2E-01	AB000499.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
5935	19864	33185	0.59	8.2E-01	X95283.1	NT	G. gallus mRNA for C-Serrate-1 protein
6935	19964	33186	0.59	8.2E-01	X95283.1	NT	G. gallus mRNA for C-Serrate-1 protein

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7081	20287	33546	0.82	8.2E-01	AJ010142.1	NT	Amenita muscaria mRNA for SCII25 protein
7225	20224	33472	3.3	8.2E-01	AW376433.1	EST_HUMAN	CM4-HT0243-081199-037-e01 HT0243 Homo sapiens cDNA
7645	25073	33875	4.19	8.2E-01	Z12128.1	NT	S. cerevisiae MET, LEU4, and POL1 genes encoding MET14 protein, alpha-isopropylmalate (alpha-IPM) synthetase (partial), and DNA polymerase alpha (partial)
9012	21941	35297	0.82	8.2E-01	BE263145.1	EST_HUMAN	601144885F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160412 5'
9492	22420	35782	0.57	8.2E-01	AW614205.1	EST_HUMAN	hg77g11.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2951684 3'
9492	22420	35783	0.57	8.2E-01	AW614205.1	EST_HUMAN	hg77g11.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2951684 3'
10528	23414	36828	0.6	8.2E-01	AB014530.1	NT	Homo sapiens mRNA for KIAA0630 protein, partial cds
10561	23447	36869	2.17	8.2E-01	AF052659.1	NT	Homo sapiens thioredoxin-related protein mRNA, complete cds
10719	23605	37034	0.56	8.2E-01	AF223888.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1
10719	23605	37035	0.56	8.2E-01	AF223888.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1
10873	23759	37185	4.09	8.2E-01	Q8J170	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
10873	23759	37186	4.09	8.2E-01	Q8J170	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
12068	24909	38412	4	8.2E-01	L10127.1	NT	Molluscum contagiosum virus type 1 ORF1 and ORF2 DNA
12181	24990	38490	6.37	8.2E-01	P10383	SWISSPROT	OVARIAN TUMOR LOCUS PROTEIN
12158	24997	38498	6.67	8.2E-01	H87398.1	EST_HUMAN	wt4402.r1 Soares_placenta_8to9weeks_2NbhP8169W Homo sapiens cDNA clone IMAGE:252185 5'
12841	25317	31820	3.05	8.2E-01	AJ001261.1	NT	similar to gb:M38072 60S RIBOSOMAL PROTEIN L7A (HUMAN);
2809	15798		1.26	8.1E-01	AF191839.1	NT	Mus musculus mRNA for NIPSNAP2 protein
3518	16556	29457	3.4	8.1E-01	AF055068.1	NT	Mus musculus TANK binding kinase TBK1 (Tbk1) mRNA, complete cds
3518	16556	29458	3.4	8.1E-01	AF055068.1	NT	Homo sapiens MHC class 1 region
5029	18026		0.67	8.1E-01	AF202634.1	NT	Homo sapiens MHC class 1 region
5906	18975	32093	0.51	8.1E-01	Q01727	SWISSPROT	Drosophila melanogaster NaK-ATPase beta subunit isoform 4 (JYbeta2) mRNA, complete cds
6570	19611	32796	0.8	8.1E-01	U16790.1	NT	MELANOCORTIN-1 RECEPTOR (MC1-R)
6912	19942	33160	2.69	8.1E-01	Q13491	SWISSPROT	Mus musculus putative collagen alpha-2 (X1) chain (COL11A2) gene, partial cds
6912	19942	33161	2.69	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M6-B
7935	20857	34185	0.57	8.1E-01	O47477	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M6-B
							GYTOCHROME B
							Drosophila melanogaster putative inorganic phosphate cotransporter (Pico1) gene, partial cds; putative sodium channel (Nack) and putative amylase-related protein (Amyral) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cd>
8490	21421	34759	1.21	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Pico1) gene, partial cds; putative sodium channel (Nack) and putative amylase-related protein (Amyral) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cd>
8490	21421	34780	1.21	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Pico1) gene, partial cds; putative sodium channel (Nack) and putative amylase-related protein (Amyral) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cd>

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9170	22098	35458	0.99	8.1E-01	AP001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
9170	22098	35459	0.99	8.1E-01	AP001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
9329	22257	35621	1.24	8.1E-01	AW242847.1	EST_HUMAN	xc31h03.x1 NC1_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2692469 3' similar to SW:LYAR_MOUSE
10625	23511	36944	0.56	8.1E-01	P06425	SWISSPROT	Q08288 CELL GROWTH REGULATING NUCLEOLAR PROTEIN, contains MER22.b1 PTR5 repetitive element
10890	23781	37208	0.55	8.1E-01	N84541.1	EST_HUMAN	PROBABLY E4 PROTEIN
11914	24761	38257	3.42	8.1E-01	BE938558.1	EST_HUMAN	KK9872F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK9872 5' similar to EST(CLONE C-0PE11)
11914	24761	38258	3.42	8.1E-01	BE938558.1	EST_HUMAN	RC0-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
12377	25157	31871	1.51	8.1E-01	AE001711.1	NT	RC0-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
187	13286		2.84	8.0E-01	AJ271510.1	NT	Thermotoga maritima section 23 of 136 of the complete genome
308	13401	26318	8.55	8.0E-01	AJ132772.1	NT	Staphylococcus aureus partial pta gene for phosphate acetyltransferase allele 15
2049	15066		1.46	8.0E-01	BF530962.1	EST_HUMAN	Boc tauris tub and rif genes
3126	16177	28072	1.18	8.0E-01	AF127897.1	NT	602072473F1 NC1_CGAP_Bn87 Homo sapiens cDNA clone IMAGE:4215091 5'
3358	16402	29303	0.9	8.0E-01	AB006193.1	NT	Salmir boliviensis olfactory receptor (SBO27) gene, partial cds
3767	16799		0.98	8.0E-01	AL162758.2	NT	Mus musculus gene for olfactory glycoprotein, complete cds
4649	17655	30521	7.44	8.0E-01	X83739.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 717
5103	18100	30948	1.18	8.0E-01	7657352	NT	G.gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit
5345	18328	31177	0.91	8.0E-01	BE277215.1	EST_HUMAN	Mus musculus myosin IXb (Myosin)
8669	21600		1.96	8.0E-01	AW901489.1	EST_HUMAN	601178571F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3051088 5'
9089	22018	35374	1.38	8.0E-01	Y11095.1	NT	RC0-NN1012-270300-021-H06 NN1012 Homo sapiens cDNA
11394	24310	37756	1.54	8.0E-01	Q92793	SWISSPROT	Rice stripe virus RNA 3
476	13547	26467	1.01	7.9E-01	D11476.1	NT	CREB-BINDING PROTEIN
738	13796		0.92	7.9E-01	AE002130.1	NT	Lymnaea dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds
1627	14657		16.76	7.9E-01	AB040885.1	NT	Ureaplasma urealyticum section 31 of 59 of the complete genome
1882	14712		0.97	7.9E-01	U32739.1	NT	Homo sapiens mRNA for KIAA1462 protein, partial cds
2280	15289	28297	6.28	7.9E-01	AB040816.1	NT	Haemophilus influenzae Rd section 54 of 163 of the complete genome
2281	15290	28298	2.4	7.9E-01	AF130459.1	NT	Oryctolagus cuniculus mRNA for mitsugumin29, complete cds
3376	16613	29516	3.17	7.9E-01	AF226864.1	NT	Danio rerio Trp4-associated protein Tap1A (tap1A) mRNA, complete cds
4403	17415		0.67	7.9E-01	BE263612.1	EST_HUMAN	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds
4722	17727	30590	0.82	7.9E-01	6763745	NT	601192033F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535785 5'
4722	17727	30591	0.82	7.9E-01	6763745	NT	Mus musculus embigin (Emb), mRNA
5320	18304		0.68	7.9E-01	AF139718.1	NT	Mus musculus embigin (Emb), mRNA
							Chrysonye bezziana peritrophin-48 precursor, gene, complete cds

Page 38 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8602	19643	32825	0.69	7.9E-01	D38145.1	NT	Human mRNA for prostacyclin synthase, complete cds
8687	21618	34960	5.93	7.9E-01	X90996.1	NT	P. sativum GR gene
10076	22991	36387	4.42	7.9E-01	U01912.1	NT	Giardia lamblia variant-specific surface protein G3M-B (vpG3M-B) mRNA, partial cds
10552	23438	36859	4.89	7.9E-01	P19719	SWISSPROT	SMALL HYDROPHOBIC PROTEIN
10693	23479	36906	0.9	7.9E-01	AV700860.1	EST_HUMAN	AY700860 GK-C Homo sapiens cDNA clone GKCDRE12 3'
10989	23873	37301	0.97	7.9E-01	AB000631.1	NT	Streptococcus mutans DNA for sigma 42 protein, dTDP-4-keto-L-thamnose reductase, complete cds
11445	24361		2.21	7.9E-01	7662471	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
11660	24566	38039	2.63	7.9E-01	P19022	SWISSPROT	NEURAL-CADHERIN PRECURSOR (N-CADHERIN)
901	13953		1.78	7.8E-01	Z43785.1	EST_HUMAN	HSC1KH041 normalized infant brain cDNA Homo sapiens cDNA clone c-1kh04
2294	15302	28308	3.77	7.8E-01	AW959567.1	EST_HUMAN	EST1371637 MAGE resequences, MAGF Homo sapiens cDNA
4613	17621	30484	0.87	7.8E-01	AE000869.1	NT	Methanobacterium thermoautotrophicum from bases 862690 to 876388 (section 75 of 148) of the complete genome
4814	17815	30682	1.15	7.8E-01	U87305.1	NT	Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds
5348	18331		0.72	7.8E-01	Z43785.1	EST_HUMAN	HSC1KH041 normalized infant brain cDNA Homo sapiens cDNA clone c-1kh04
6304	19355	32526	2.03	7.8E-01	AF115856.1	NT	Sphenodon punctatus alpha enolase mRNA, partial cds
8463	19508	32684	1	7.8E-01	P05231	SWISSPROT	INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR)
8735	19769	32979	0.65	7.8E-01	AL445066.1	NT	Thermoplasma acidophilum complete genome; segment 4/5
8160	21067	34397	0.41	7.8E-01	Q09908	SWISSPROT	HYPOTHETICAL 60.7 KD PROTEIN C30D11.08C IN CHROMOSOME 1
9060	21089	36312	1.28	7.8E-01	BF108927.1	EST_HUMAN	7154005.x1 Soares_NSF_F8_9W_OT_PA_P_ST Homo sapiens cDNA clone IMAGE:3528176 3'
9775	22699	36085	1.44	7.8E-01	Y10159.1	NT	D.discoideum recGAP gene
9872	22787	36177	0.53	7.8E-01	4826673	NT	Homo sapiens nucleoporin 214KD (NUP214), mRNA
10624	23510		1.15	7.8E-01	Q25452	SWISSPROT	MUSCLE CALCIUM CHANNEL ALPHA-1 SUBUNIT (MDL-ALPHA1)
12611	25833		1.86	7.8E-01	L29260.1	NT	Arabidopsis thaliana 1-amino-1-cyclopropanecarboxylate synthase (ACS5) gene, complete cds
149	13249	26166	5.28	7.7E-01	AF184345.1	NT	Lycopodium obscurum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
749	13806		1.94	7.7E-01	AF060187.1	NT	Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (Ia alpha) and major histocompatibility protein class II beta chain (Ib beta) genes, complete cds;
2761	15753	28749	1.85	7.7E-01	O33915	SWISSPROT	butyrophilin-like (NC9), butyrophilin-like
3055	16107	29013	11.84	7.7E-01	AB011094.1	NT	CITRATE SYNTHASE
3409	16451		0.79	7.7E-01	8393408	NT	Homo sapiens mRNA for KIAA0522 protein, partial cds
							Homo sapiens UDP-N-acetyl-alpha-D-glactosamine:polypeptide N-acetylglactosaminyltransferase 7 (GalNAc-T7) (GALNAc-T7), mRNA

Page 39 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3662	16696	29592	4.62	7.7E-01	AF118085.1	NT	Homo sapiens PRO1975 mRNA, complete cds
4503	17513	30379	2.52	7.7E-01	AF199488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
4503	17513	30380	2.52	7.7E-01	AF199488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
5752	18825	31923	1.38	7.7E-01	P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
5752	18825	31924	1.38	7.7E-01	P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
6181	19238	32385	0.86	7.7E-01	R08800.1	EST_HUMAN	Y24b02.s1 Soares fetal liver spleen 1NFL3 Homo sapiens cDNA clone IMAGE:127755 3'
10359	23248	36668	0.63	7.7E-01	AB021134.1	NT	Daphnia magna hemoglobin gene cluster (dhb3, dhb1 and dhb2 genes), complete cds
12505	25240		6.05	7.7E-01	11487821	NT	Archaeoglobus fulgidus, complete genome
6336	19386	32554	3.97	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-bidilylated subunit (MCCB) mRNA, complete cds
6336	19386	32555	3.97	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-bidilylated subunit (MCCB) mRNA, complete cds
6793	19829	33039	0.78	7.6E-01	P37938	SWISSPROT	MATING-TYPE PROTEIN A-ALPHA.24
7170	18442	31311	0.97	7.6E-01	AI253399.1	EST_HUMAN	eq14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
7170	18442	31345	0.97	7.6E-01	AI253399.1	EST_HUMAN	eq14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
7404	20103	33338	0.93	7.6E-01	U72487.1	NT	Rattus norvegicus calcium-independent alpha-latrotoxin receptor mRNA, complete cds
8642	21573	34911	1.44	7.6E-01	AF146793.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; (Phlp) (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and H5AR (H5ar) gene, complete cds
8703	21634	34979	2.41	7.6E-01	6857752	NT	Mus musculus advillin (Advil-pending), mRNA
8703	21634	34980	2.41	7.6E-01	6857752	NT	Mus musculus advillin (Advil-pending), mRNA
8900	21830	35183	0.6	7.6E-01	Q01098	SWISSPROT	GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
8900	21830	35184	0.6	7.6E-01	Q01098	SWISSPROT	GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
9519	22446	35810	1.53	7.6E-01	6753577	NT	Mus musculus cytochrome P450, 2b9, phenobarbital inducible, type a (Cyp2b9), mRNA
9819	22725	36108	3.76	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
9819	22725	36109	3.76	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
11796	24718	38210	2.5	7.6E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70
11796	24718	38211	2.5	7.6E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70
12133	24974		3.69	7.6E-01	AL161592.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
12289	25100		5.4	7.6E-01	AB020702.1	NT	Homo sapiens mRNA for KIA0895 protein, partial cds
536	13605		1.29	7.5E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101

Page 40 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
605	13671	26574	1.39	7.5E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, cladenosine triphosphate hydrolase (FHIT) gene, exon 5
3413	16455	26361	1.22	7.5E-01	C14203.1	EST_HUMAN	C14203 Clontech human aorta polyA+ mRNA (#5572) Homo sapiens cDNA clone GEN-037E11 5'
4785	17790		1.71	7.5E-01	U48498.1	NT	Human skeletal muscle ryanodine receptor gene (RYR1), exon 92
5338	18415		1.15	7.5E-01	U48498.1	NT	Human skeletal muscle ryanodine receptor gene (RYR1), exon 92
7945	20867	34179	0.85	7.5E-01	AF052730.1	NT	Drosophila melanogaster tyrosine kinase receptor protein (eph) mRNA, complete cds
12569	25274		4.74	7.5E-01	AF163161.2	NT	Homo sapiens dentin sialoporphoprotein precursor (DSPP) gene, complete cds
13001	25553	31757	1.95	7.5E-01	D90907.1	NT	Synchoocytis sp. PCC0803 complete genome, 9/27, 1058467-1188885
1157	14198	27134	1.1	7.4E-01	AI598148.1	EST_HUMAN	In1409.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167577 3' similar to contains Alu repetitive element; contains element MIR repetitive element;
2366	15372	28375	1.03	7.4E-01	AB011106.1	NT	Homo sapiens mRNA for KIAA0534 protein, partial cds
3790	16821	29708	1.38	7.4E-01	AF112538.1	NT	Maize pusilla actin (Act1) mRNA, complete cds
3973	17001	29888	0.69	7.4E-01	AF133310.1	NT	Vibrio cholerae phage CTXphi Calcutta-rsR-a (rsR-e) and Calcutta-rsR-b (rsR-b) genes, complete cds
4415	17427	30289	4.86	7.4E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8426	21358	34597	1.09	7.4E-01	AL161651.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
8426	21358	34608	1.09	7.4E-01	AL161651.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
9192	22120	35476	0.9	7.4E-01	BF346268.1	EST_HUMAN	602018456F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4154340 5'
9272	22200		0.9	7.4E-01	U67960.1	NT	Rattus norvegicus leukocyte common antigen receptor (LAR) gene, trans-spliced alternative untranslated exon
9642	22568	35939	7.39	7.4E-01	BE747503.1	EST_HUMAN	G01573026F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834174 5'
9699	22624	36002	1.31	7.4E-01	AA187986.1	EST_HUMAN	zp37h01.s1 StrataGene endothelial cell 837223 Homo sapiens cDNA clone IMAGE:525297 3' similar to SW:TCPO_MOUSE_P42932 T-COMPLEX PROTEIN 1, THETA SUBUNIT ;
10887	23772	37198	0.62	7.4E-01	11424933	NT	Homo sapiens NY-REN-45 antigen (LOC51133), mRNA
12090	24931	38436	1.43	7.4E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
12090	24931	38437	1.43	7.4E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
12257	25077		5.27	7.4E-01	6753217	NT	Mus musculus complement component 1 inhibitor (C1inh), mRNA
12363	25150		1.89	7.4E-01	AI472641.1	EST_HUMAN	ta13h01.x1 NCI_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:2043985 3'
4059	17085		0.72	7.3E-01	AF000082.1	NT	Aeropyrum pernix genomic DNA, section 5/7
4729	17734	30596	0.7	7.3E-01	AE001166.1	NT	Borrelia burgdorferi (section 62 of 70) of the complete genome
4813	17814	30681	4.08	7.3E-01	AF226421.1	NT	Homo sapiens HT017 mRNA, complete cds
5238	18225	31074	0.95	7.3E-01	O43103	SWISSPROT	FERRICHRONE SIDEROPHORE PEPTIDE SYNTHETASE
6893	19923	33137	5.62	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
6893	19923	33138	5.62	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene

Page 41 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7463	26670	33684	0.9	7.3E-01	AJ011418.1	NT	Lycopodium esculentum mRNA for ubiquitin activating enzyme
7863	20790	34083	0.45	7.3E-01	Z14133.1	NT	D.melanogaster Cdc mRNA for clathrin heavy chain
7977	20898	34211	8.65	7.3E-01	M26511.1	NT	V.alginolyticus sucrose (scrB) gene, complete cds
7977	20898	34212	8.65	7.3E-01	M26511.1	NT	V.alginolyticus sucrose (scrB) gene, complete cds
8332	21237	34570	0.51	7.3E-01	U34631.1	NT	Mus musculus alpha-4 integrin gene, exon 7
11862	24752	38246	3.93	7.3E-01	AA678019.1	EST_HUMAN	225b08.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431789 3'
11862	24752	38246	3.93	7.3E-01	AA678019.1	EST_HUMAN	225b08.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431799 3'
856	13910	27972	2.41	7.2E-01	L29281.1	NT	Rattus norvegicus initiation factor-2 kinase (aIF-2a) mRNA, complete cds
1971	14989	27972	1.78	7.2E-01	X79140.1	NT	N.labacum Nelf-4A13 mRNA
2485	13487	28488	1.5	7.2E-01	AB009805.1	NT	Gallus gallus gene for melanocortin 2-receptor, complete cds
3115	16166	29060	1.5	7.2E-01	AF198100.1	NT	Fowlpox virus, complete genome
3514	16552	29452	2.37	7.2E-01	AF065606.1	NT	Giardia intestinalis variant-specific surface protein (vop417-6) gene, vop417-6(A-I allele, complete cds
3678	16711	29602	1.43	7.2E-01	AB002307.1	NT	Human mRNA for KIAA0309 gene, partial cds
3940	16968	29851	0.97	7.2E-01	BF338350.1	EST_HUMAN	602035589F1 NCI CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183222 5'
4149	17170		0.78	7.2E-01	AF108083.1	NT	Homo sapiens IA-2 gene, intron 18
4882	17881	30746	2.94	7.2E-01	D90314.1	NT	L.mesenteroides gene for sucrose phosphorylase (EC 2.4.1.7)
5264	18250	31100	1.27	7.2E-01	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a>
5264	18250	31101	1.27	7.2E-01	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a>
5398	18378	31220	1.94	7.2E-01	Z97335.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA I FCA contig fragment (No. 0
7580	20516	33804	1.04	7.2E-01	U66633.1	NT	Solanum tuberosum cold-stress inducible protein (C17) gene, complete cds
8046	20959		0.44	7.2E-01	8625875	NT	Human herpesvirus 3, complete genome
8288	21192	34529	0.48	7.2E-01	A1610765.1	EST_HUMAN	tp38b01.x1 NCI CGAP_U14 Homo sapiens cDNA clone IMAGE:2190028 3' similar to gb:M23115 CALCIUM-TRANSPORTING ATPASE SARCOPLASMIC RETICULUM TYPE, SLOW (HUMAN);
9022	21951	35307	1.44	7.2E-01	AF236061.1	NT	Oryctolagus cuniculus RING-finger binding protein mRNA, partial cds
9516	22443		0.6	7.2E-01	AV743773.1	EST_HUMAN	AV743773 CB Homo sapiens cDNA clone CBMAFD08 5'
10828	23714	37140	2.4	7.2E-01	BF670081.1	EST_HUMAN	602116381F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4275381 5'
11180	24108	37653	3.59	7.2E-01	U82623.1	NT	Rattus norvegicus cytochrome mRNA, complete cds
11698	24600		1.49	7.2E-01	AW450487.1	EST_HUMAN	UHH-B13-akog-01-Q.UJ.s1 NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2735040 3'
12575	18427	31351	1.74	7.2E-01	U02568.1	NT	Dielisocaulis viviparus nematode polypeptide precursor (DvA) mRNA, complete cds

Table 4

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12757	25391		4.27	7.1E-01	AF000063.1	NT	Aeropyrum pernix genomic DNA, section 6/7
716	13774	26694	11.44	7.1E-01	D21070.1	NT	Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform(RyR1), complete cds
3110	16161	29057	20.14	7.1E-01	AJ270777.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 15-16
4304	17318	30186	5.04	7.1E-01	7305360	NT	Mus musculus otogelin (Otog), mRNA
4304	17318	30187	5.04	7.1E-01	7305360	NT	Mus musculus otogelin (Otog), mRNA
6173	19230	32376	1.65	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296344 5'
6173	19230	32377	1.65	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296344 5'
7281	20234	33484	6.39	7.1E-01	U36232.1	NT	Drosophila melanogaster 6-pyruvoyltryptophan synthase (pr) gene, complete cds
8769	21699	35044	0.58	7.1E-01	H54244.1	EST_HUMAN	yq89d09.s1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:202981 3'
9295	22223	35581	0.95	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-301299-011-d09 BT0567 Homo sapiens cDNA
9295	22223	35582	0.95	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-301299-011-d09 BT0567 Homo sapiens cDNA
10369	23258	36680	1.56	7.1E-01	BE904405.1	EST_HUMAN	601498330F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898495 5'
10894	23779	37208	1.29	7.1E-01	M12661.1	NT	Human T-cell receptor gamma chain J2 gene
12557	25768		2.16	7.1E-01	AA421492.1	EST_HUMAN	zu06h11.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:731109 3'
1257	14292	27237	0.86	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
1257	14292	27238	0.86	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
2473	15476	28476	1.54	7.0E-01	N62412.1	EST_HUMAN	yz73e07.s1 Soares multiple sclerosis_2NBHMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element;
2473	15476	28477	1.54	7.0E-01	N62412.1	EST_HUMAN	yz73e07.s1 Soares multiple sclerosis_2NBHMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element;
5189	18181		2.5	7.0E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
6177	19234		0.86	7.0E-01	AB021316.1	NT	Arabidopsis thaliana mRNA for chlorophyll b synthase, complete cds
8949	21879		7.02	7.0E-01	AE000253.1	NT	Escherichia coli K-12 MG1655 section 143 of 400 of the complete genome
11560	24469	37634	1.62	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
11560	24469	37635	1.62	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
13065	25800	31581	2.36	7.0E-01	8630494	NT	Bacteriophage N15 virion, complete genome
998	14046	26889	66.92	6.9E-01	U69874.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
998	14046	26890	66.92	6.9E-01	U69874.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
1336	14370	27320	2.26	6.9E-01	AA503550.1	EST_HUMAN	nm28e09.s1 NC1_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085176 3'
3268	16314	29217	1.93	6.9E-01	AE002271.2	NT	Chlamydia muridarum, section 3 of 85 of the complete genome
5992	19057	32184	0.79	6.9E-01	AB035662.1	NT	Branchiostoma belcheri BtNA3 mRNA for notochord actin, complete cds



Page 43 of 545  
Table 4  
Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6221	19276	32430	0.63	6.9E-01	Y18276.1	NT	Drosophila melanogaster mRNA for A-kinase anchor protein DAKAP550, partial
6630	19670	32855	1.62	6.9E-01	BE296188.1	EST_HUMAN	601177333F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532328 5'
8291	21185	34532	1.23	6.9E-01	AF248863.1	NT	Strongylocentrotus purpuratus myosin V, complete cds
8559	21490	34830	2.83	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
8959	21490	34831	2.63	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
9713	22638		0.72	6.9E-01	AF118046.1	NT	Entamoeba dispar cation transporting ATPase (atpase) gene, partial cds
10217	23108	36508	0.61	6.9E-01	AF206319.1	NT	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds
10217	23108	36509	0.61	6.9E-01	AF206319.1	NT	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds
11705	24607	38083	2.1	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
11705	24607	38084	2.1	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
12239	25763		1.75	6.9E-01	Q99958	SWISSPROT	FORKHEAD BOX PROTEIN C2 (FORKHEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK HEAD PROTEIN 1) (MFI-1 PROTEIN) (TRANSCRIPTION FACTOR FKHL14)
983	14034	26977	1.36	6.8E-01	AF017784.1	NT	Glardia intestinalis carbamate kinase gene, complete cds
2723	15716		2.04	6.8E-01	D60917.1	NT	Synechocystis sp. PCC6803 complete genome, 2727, 3418852-3573470
2877	14698	27631	1.19	6.8E-01	AA854475.1	EST_HUMAN	q76a03.s1 Soares_papillary tumor_NbHPA Homo sapiens cDNA clone IMAGE:1402256 3' similar to gb:X86411.1_mai1 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN);
4687	17692	30569	1.56	6.8E-01	J00762.1	NT	Rat(hooded) prolactin gene : exon iii and flanks
4966	17964	30822	0.7	6.8E-01	4758521	NT	Homo sapiens hevin (HEVIN) mRNA
10164	23056	36454	1.65	6.8E-01	AB037766.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
11529	24439	37897	2.17	6.8E-01	AJ276675.1	NT	Stagonospora avenae bgf1 gene for beta-glucosidase, exons 1-4
11529	24439	37898	2.17	6.8E-01	AJ276675.1	NT	Stagonospora avenae bgf1 gene for beta-glucosidase, exons 1-4
11554	24463	37928	2.65	6.8E-01	AF038939.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
11554	24463	37929	2.65	6.8E-01	AF038939.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
11745	24646	38126	1.39	6.8E-01	AF164151.1	NT	Anopheles gambiae strain M2 translation initiation factor 4C (TA) (eIF-4C) mRNA, complete cds
12035	24877	38382	1.46	6.8E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
12035	24877	38383	1.46	6.8E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
318	13410	26328	24.93	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
359	13446	26358	25.65	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds

Page 44 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1928	14943		1.17	6.7E-01	M12132.1	NT	Quail fast skeletal muscle troponin I gene, complete cds
2161	15173	28177	2.08	6.7E-01	AA451084.1	EST_HUMAN	zkl2g12.e1 Soares, total_fetus_NB2HF8_gw Homo sapiens cDNA clone IMAGE:786310 3' similar to contains element TAR1 repetitive element;
2179	15913	28197	3.88	6.7E-01	AF186073.1	NT	Drosophila melanogaster Mst85C gene, complete cds; NMDMC isoform (Nmdmc) gene, complete cds, alternatively spliced; and transcription factor (Relish) gene, complete cds, alternatively spliced
3039	16091	28993	4.6	6.7E-01	6878580	NT	Mus musculus Wiskott-Aldrich syndrome protein (Wasp), mRNA
4563	17571	30434	0.67	6.7E-01	X74421.1	NT	S. tuberosum mRNA for glucose-6-phosphate dehydrogenase
5080	18077	30928	1.11	6.7E-01	AW079110.1	EST_HUMAN	xa95g12.x1 NCL CGAP_Co17 Homo sapiens cDNA clone IMAGE:2574598 3'
5699	18772	31700	0.87	6.7E-01	J04836.1	NT	M. bakeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
5699	18772	31701	0.87	6.7E-01	J04836.1	NT	M. bakeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
6189	19243	32392	0.89	6.7E-01	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
6579	19623	32804	1.86	6.7E-01	9635035	NT	Gallid herpesvirus 2, complete genome
6579	19620	32805	1.86	6.7E-01	9635035	NT	Gallid herpesvirus 2, complete genome
6907	19937	33165	0.48	6.7E-01	BE986241.2	EST_HUMAN	601660177R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3905778 3'
6907	19937	33166	0.48	6.7E-01	BE986241.2	EST_HUMAN	601660177R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3905778 3'
7699	20631		3.77	6.7E-01	AE004606.1	NT	Pseudomonas aeruginosa PA01, section 167 of 529 of the complete genome
7728	20658	33955	0.98	6.7E-01	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
10642	23528		0.89	6.7E-01	M34046.1	NT	Human placental protein 14 (PP14) gene, complete cds
11392	24308	37754	2.29	6.7E-01	BF354649.1	EST_HUMAN	GM3-HT0769-010600-197-c03 HT0769 Homo sapiens cDNA
11891	23991	37430	3.38	6.7E-01	O14357	SWISSPROT	N-ACETYLGLUCOSAMINYL-PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN GPI1
2624	15525	28528	1.41	6.6E-01	AF075240.1	NT	Homo sapiens SLIT1 protein (SLIT2) mRNA, partial cds
2751	15742	28737	1.44	6.6E-01	AF199339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3548	16596	29491	1.25	6.6E-01	4506880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 9A (SEMA9A) mRNA
3728	16758	29846	2.9	6.6E-01	Y07669.1	NT	C. albicans random DNA marker, 282bp
6167	18159	31007	0.83	6.6E-01	Z28337.1	NT	M. aeruginosa (HUB 5-2-4) DNA from plasmid PMA1
5167	18159	31008	0.83	6.6E-01	Z28337.1	NT	M. aeruginosa (HUB 5-2-4) DNA from plasmid PMA1
6589	19630	32812	4.16	6.6E-01	6880577	NT	Mus musculus kinesin light chain 2 (Klc2), mRNA
7482	20422	33701	0.68	6.6E-01	AE004488.1	NT	Pseudomonas aeruginosa PA01, section 19 of 529 of the complete genome
7482	20422	33702	0.68	6.6E-01	AE004488.1	NT	Pseudomonas aeruginosa PA01, section 19 of 529 of the complete genome
8138	21047	34377	3.09	6.6E-01	AV680506.1	EST_HUMAN	AV680506 GLC Homo sapiens cDNA clone GLGID04 3'
9129	22057	35417	0.72	6.6E-01	AV704700.1	EST_HUMAN	AV704700 ADB Homo sapiens cDNA clone ADBCAF11 5'
10189	23080		1.14	6.6E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078

Page 45 of 645  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
647	13708	26615	1.33	6.9E-01	M75140.1	NT	H.vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
647	13708	26616	1.33	6.9E-01	M75140.1	NT	H.vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
3494	16533	29433	5.85	6.9E-01	AB041225.1	NT	Mus musculus gene for Tob2, complete cds
4121	17144	30017	1.01	6.9E-01	4504632	NT	Homo sapiens interleukin 10 receptor, alpha (IL10RA) mRNA
4380	17394	30259	4.79	6.9E-01	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
5197	18189	31030	2.9	6.9E-01	U28921.1	NT	Phaseolus vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds
5915	18984	32103	0.56	6.9E-01	AL163249.2	NT	Homo sapiens chromosome 21 segment H521C049
7026	20052	33284	1.31	6.9E-01	D88348.1	NT	Chicken mRNA for 115-kDa melanosomal matrix protein, complete cds
8025	20941	34256	0.78	6.9E-01	X04789.1	NT	Murine Ig-related lambda(50) gene (exon 1) transcribed selectively in pre-B lymphocytes
8119	21030	34357	0.9	6.9E-01	A1768892.1	EST_HUMAN	wo46a02.x1 NCI_CGAP_Pt28 Homo sapiens cDNA clone IMAGE:2321642 3'
10362	23241		0.85	6.9E-01	T78904.1	EST_HUMAN	yv21b04.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108847 3'
10823	23709	37138	4.51	6.9E-01	AF119676.1	NT	Mus musculus small GTP-binding protein RAB25 (Rab25) gene, complete cds
11079	24011	37452	2.87	6.9E-01	H87583.1	EST_HUMAN	yw17106.r1 Soares placenta_8to8weeks_2NbHP80sW Homo sapiens cDNA clone IMAGE:252515 5'
11128	24058	37504	3.7	6.9E-01	AA801287.1	EST_HUMAN	nc15c07.s1 NCI_CGAP_Pher1 Homo sapiens cDNA clone IMAGE:1100748 3'
11230	24158		3.97	6.9E-01	AU138078.1	EST_HUMAN	AU138078 PLACE1 Homo sapiens cDNA clone PLACE1007810 5'
12029	24871	38374	2.3	6.9E-01	AF014115.1	NT	Plasmodium berghei cytochrome c oxidase subunit III, cytochrome c oxidase subunit I, and cytochrome b genes, mitochondrial genes encoding mitochondrial proteins, complete cds
12606	25301		4.15	6.9E-01	BE465050.1	EST_HUMAN	hv74e10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3170130 3'
12828	25715		3.67	6.9E-01	Z74145.1	NT	S.cerevisiae chromosome IV reading frame ORF_YDL097c
271	13366	26282	6.03	6.4E-01	U48848.1	NT	Drosophila melanogaster 8kd dynein light chain mRNA, complete cds
2628	15624	28817	1.03	6.4E-01	AF161184.1	NT	Pseudomonas fluorescens typtophan halogenase (pmA) gene, complete cds
3516	16554	28455	1.4	6.4E-01	U48854.2	NT	Mus musculus dystroglycan 1 (DAG1) gene, exons 1 and 2 and complete cds
3928	16956	29839	1.39	6.4E-01	AB048827.1	NT	Homo sapiens mRNA for KIAA1607 protein, partial cds
4358	17372		0.96	6.4E-01	Z74155.1	NT	S.cerevisiae chromosome IV reading frame ORF_YDL107w
4605	17613	30473	0.75	6.4E-01	Y12488.1	NT	M.musculus whn gene
4605	17613	30474	0.75	6.4E-01	Y12488.1	NT	M.musculus whn gene
5055	18052	30905	1.04	6.4E-01	AF239978.1	NT	Salmonella enteritidis SefR (sefR), hypothetical protein 7, and Dlp (dip) genes, complete cds
9173	22101	35461	1.73	6.4E-01	AE001247.1	NT	Treponema pallidum section 63 of 87 of the complete genome
10591	23477	36905	10.78	6.4E-01	U82828.1	NT	Homo sapiens alaxia telangiectasia (ATM) gene, complete cds
10605	23491	36920	1.35	6.4E-01	BF670405.1	EST_HUMAN	602150289F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4281126 5'
12718	25366		12.84	6.4E-01	AV759212.1	EST_HUMAN	AV759212 MDS Homo sapiens cDNA clone MDSG008 5'
457	13529	26452	5.03	6.9E-01	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)

Page 46 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
558	13627	26535	144.48	6.3E-01	U32689.1	NT	Haemophilus influenzae Rd section 4 of 163 of the complete genome
2175	16187	28192	2.6	6.3E-01	U81136.1	NT	Shigella flexneri multi-antibiotic resistance locus
2616	15614	28608	3.63	6.3E-01	U75333.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2616	15614	28610	3.63	6.3E-01	U75333.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
3081	16113		0.86	6.3E-01	Y17275.1	NT	Lycopodium esculentum p68a gene, complete cds
6299	19350	32518	0.87	6.3E-01	BE093906.1	EST_HUMAN	PMO-BT0757-010500-002-a05 BT0757 Homo sapiens cDNA
6885	19915	33131	1.02	6.3E-01	L27798.1	NT	Streptococcus dysgalactiae (mag) gene, complete cds
6885	19915	33132	1.02	6.3E-01	L27798.1	NT	Streptococcus dysgalactiae (mag) gene, complete cds
9086	22015		3.21	6.3E-01	BE02044.1	EST_HUMAN	601676889F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959351 5'
9443	22371	35735	0.98	6.3E-01	S62927.1	NT	glycoprotein IIIa (Alu 1 and 3 fusion junction) [human, Genomic Mutant, 300 nt]
9761	22685	36072	0.67	6.3E-01	BF216984.1	EST_HUMAN	601884050F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4102596 5'
8954	22659	36247	3.73	6.3E-01	9627621	NT	Varola virus, complete genome
9994	22859	36248	3.73	6.3E-01	9627621	NT	Varola virus, complete genome
10447	23336		0.75	6.3E-01	AE002329.2	NT	Chlamydia muridarum, section 59 of 85 of the complete genome
10909	23794	37223	1.46	6.3E-01	Z73003.1	NT	S. cerevisiae chromosome VII reading frame ORF YGR218w
11008	23822	37326	0.72	6.3E-01	AE000313.1	NT	Escherichia coli K-12 MG1655 section 203 of 400 of the complete genome
11500	24411	37665	2.1	6.3E-01	AA877715.1	EST_HUMAN	n09h06.s1 NCL_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1181371 3' similar to TR:002916 O02916 HLARK.
11778	24678	38167	8.4	6.3E-01	AI604160.1	EST_HUMAN	CM-BT043-080299-046 BT043 Homo sapiens cDNA
11887	24747	38239	1.75	6.3E-01	P47003	SWISSPROT	HYPOTHETICAL 13.7 KD PROTEIN IN INO1-IDS2 INTERGENIC REGION
12019	24861	38361	2.14	6.3E-01	P36073	SWISSPROT	HYPOTHETICAL 13.3 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION
12219	25053		1.56	6.3E-01	BF333356.1	EST_HUMAN	RCO-C10037-250900-031-e09 C10037 Homo sapiens cDNA
12341	25005	31365	13.98	6.3E-01	9910293	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
12425	25188		1.61	6.3E-01	AF105227.1	NT	Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthetase (PAPSS) mRNA, complete cds
12623	25830		1.74	6.3E-01	X83528.1	NT	C. limicola pscD gene
6158	18151	30907	0.74	6.2E-01	AF157898.1	NT	Spermophilus euilicus isolate S47 cytochrome b (cytb) gene, complete cds; mitochondrial gene for mitochondrial product
6085	19146	32281	2.06	6.2E-01	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME I
7916	20840		2.84	6.2E-01	AF022253.1	NT	Mus musculus calcium-sensing receptor related protein 4 (Casr-rs4) mRNA, partial cds
7973	25681	34207	1.15	6.2E-01	AL021127.2	NT	Mus musculus chromosome X contigA, putative Mago89 gene, Caltractin, NAD(P) steroid dehydrogenase and Zinc finger protein 185
8876	21806	35159	5.59	6.2E-01	H72255.1	EST_HUMAN	Ys01e08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213542 3'
9415	22343	35708	0.63	6.2E-01	AF034411.1	NT	Lycopodium esculentum cytosolic Cu,Zn superoxide dismutase (Sod) gene, partial cds; and dehydroquinase dehydratase/shikimate:NADP oxidoreductase gene, complete cds

Page 47 of 545  
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9981	21339	34876	1.67	6.2E-01	BE562687.1	EST_HUMAN	601336148F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690010 5'
10041	22941		3.87	6.2E-01	M24461.1	NT	Human pulmonary surfactant-associated protein SP-B (SFTPB) mRNA, complete cds
10580	23436	36991	7.61	6.2E-01	AL161611.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
10717	23603	37031	0.6	6.2E-01	11420793	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1), mRNA
10717	23603	37032	0.6	6.2E-01	11420793	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1), mRNA
11015	23999	37335	5.73	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPEPTIDE [CONTAINS: RNA-DIRECTED RNA POLYMERASE; THIOL PROTEASE P3C; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
11015	23999	37336	5.73	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPEPTIDE [CONTAINS: RNA-DIRECTED RNA POLYMERASE; THIOL PROTEASE P3C; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
2417	15421		7.14	6.1E-01	6678076	NT	Mus musculus secreted acidic cytosine rich glycoprotein (Sparc), mRNA
4681	17657	30523	12.86	6.1E-01	4557538	NT	Homo sapiens solute carrier family 26 (sulfate transporter), member 2 (SLC26A2) mRNA
5726	18799	31892	1.21	6.1E-01	M59940.1	NT	Caenorhabditis elegans N2 CeliMyoD (hlt-1) alternatively spliced genes, complete cds
7195	20195	33439	3.56	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
7195	20195	33440	3.56	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
7365	20359	33528	0.81	6.1E-01	AW105653.1	EST_HUMAN	xd60103.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2597237 3' similar to gb:X12671_rna1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN); SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
7464	20404	33680	0.53	6.1E-01	Q63769	SWISSPROT	Arabidopsis thaliana putative zinc transporter (ZIP1) mRNA, complete cds
8811	21741	35090	3.73	6.1E-01	AF035353.1	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
9353	22281	35641	1.39	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
9353	22281	35642	1.39	6.1E-01	11431065	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
9949	22854	36241	23.9	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
9949	22854	36242	23.9	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
10357	23246	36565	1.08	6.1E-01	AE004452.1	NT	Pseudomonas aeruginosa PAO1, section 13 of 529 of the complete genome
10549	23435	36855	1.48	6.1E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
12166	24935	38494	2.24	6.1E-01	S83182.1	NT	hyaluronan-binding protein-hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
12166	24935	38495	2.24	6.1E-01	S83182.1	NT	hyaluronan-binding protein-hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
517	13587	26500	6.03	6.0E-01	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
583	13661		2.78	6.0E-01	5802999	NT	Homo sapiens adaptor-related protein complex 3, mu 2 subunit (CLA20), mRNA
1389	14420	27375	1.87	6.0E-01	AF065253.1	NT	Human respiratory syncytial virus strain CH63-63b attachment protein (G) gene, complete cds

Page 48 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon: SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3885	16914	29792	0.93	6.0E-01	AJ233396.1	NT	Viral hemorrhagic septicemia virus N, P, M, G, Nv, L genes, French strain 07-71
5463	18544	31384	3.6	6.0E-01	P20288	SWISSPROT	D(2) DOPAMINE RECEPTOR
5625	18701	31600	2.44	6.0E-01	AW130713.1	EST_HUMAN	U1-H-B11-eeb-a-10-0-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718619 3'
6818	19851	33062	2.9	6.0E-01	U38813.1	NT	Musca domestica insecticide-susceptible strain voltage-sensitive sodium channel mRNA, complete cds
6956	19884	33208	0.79	6.0E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON)
7127	20331	33594	0.82	6.0E-01	L10234.1	NT	(CDW136) (CD136 ANTIGEN)
7127	20331	33595	0.82	6.0E-01	L10234.1	NT	Strongylocentrotus purpuratus kinesin light chain isoform 2 mRNA, complete cds
7742	20673	33971	6.6	6.0E-01	AJ277681.1	NT	Strongylocentrotus purpuratus kinesin light chain isoform 2 mRNA, complete cds
8701	21632	34977	4.43	6.0E-01	P02835	SWISSPROT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
8701	21632	34978	4.43	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
10338	23227	36643	1.76	6.0E-01	AB008193.1	NT	SEGMENTATION PROTEIN FUSHI TARAZU
10760	23652		1.55	6.0E-01	Q01497	SWISSPROT	Homo sapiens genes for leukotriene B4 receptor BLT2, leukotriene B4 receptor BLT1, complete cds
10871	23757		0.52	6.0E-01	BE837779.1	EST_HUMAN	PEROXISOMAL MEMBRANE PROTEIN PER8 (PEROXIN-3)
11497	24408	37862	1.77	6.0E-01	AJ131892.1	NT	RC2-FN0094-190700-017-408 FN0094 Homo sapiens cDNA
11497	24408	37863	1.77	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
11984	24827	38324	3.16	6.0E-01	AJ420623.1	EST_HUMAN	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
12688	26345	31826	1.62	6.0E-01	11421663	NT	t0807.x1 NCL_CGAP_P728 Homo sapiens cDNA clone IMAGE:2095621 3'
12960	29771	31576	2.29	6.0E-01	9056303	NT	Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA
12986	25709		5.41	6.0E-01	BE157617.1	EST_HUMAN	Mus musculus cGMP-inhibited phosphodiesterase (Pde3a), mRNA
1028	14077	27017	0.95	6.0E-01	U32701.1	NT	RC1-HT0375-030500-016-c03 HT0375 Homo sapiens cDNA
1427	14458	27411	1.18	5.9E-01	6680232	NT	Haemophilus influenzae Rd section 16 of 163 of the complete genome
3314	16361	29261	6.06	6.0E-01	AL163287.2	NT	Mus musculus 3-hydroxy-3-methylglutaryl-Coenzyme A lyase (Hmgcl), mRNA
3314	16361	29262	6.06	6.0E-01	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C087
4319	17333		3.5	6.0E-01	AF162756.1	NT	Homo sapiens chromosome 21 segment HS21C087
5236	18223	31072	2.12	5.9E-01	L27316.1	NT	Rattus norvegicus cenexin 2 mRNA, partial cds
5328	18310	31160	2.5	5.9E-01	AF026566.1	NT	Oryzotagus culiculus immunoglobulin YDJ region gene
6738	19772	32983	2.3	5.9E-01	AF065440.2	NT	Ovis aries SRY gene promoter region
7042	20577	33871	3.8	5.9E-01	AB023486.1	NT	Homo sapiens low density lipoprotein receptor-related protein II (LRP2) gene, exon 1 and partial cds
7795	20724		0.56	5.9E-01	X68801.1	NT	Homo sapiens gene for histamine H2 receptor, promoter region and complete cds
8578	21509	34855	0.61	5.9E-01	D90911.1	NT	G gallus gene for skeletal alpha-actinin, exon EF2
						NT	Synchozoetia sp. PCC8803 complete genome, 13/27, 1675593-1710843

Page 49 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E- Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9197	22125	35481	0.64	5.9E-01	D12922.1	NT	Legionella pneumophila gene for iron superoxide dismutase, complete cds
10072	22987	36382	0.59	5.9E-01	AF063204.2	NT	Chlamydia trachomatis strain K10W31/Cx major outer membrane protein (omp1) gene, complete cds
10424	23313		0.6	5.9E-01	P06463	SWISSPROT	E6 PROTEIN
10885	23571	37001	1.62	5.9E-01	P55284	SWISSPROT	VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (CADHERIN-5)
11115	24045	37491	2.77	5.9E-01	Q9X0I3	SWISSPROT	THYMIDYLATE KINASE (DTMP KINASE)
11120	24050	37495	1.7	5.9E-01	AF107944.1	NT	Xenopus laevis receptor protein tyrosine phosphatase delta (XPTP-D) mRNA, complete cds
11398	24314	37760	3.48	5.9E-01	AW937175.1	EST_HUMAN	PM1-DT0041-180100-002-H03 DT0041 Homo sapiens cDNA
11639	24545	38019	2.85	5.9E-01	AF084626.1	NT	Mus spretus strain SPRET/Ei CD48 antigen (Cd48) gene, partial cds
11909	24757	38251	1.47	5.9E-01	P47135	SWISSPROT	JSN1 PROTEIN
11909	24757	38252	1.47	5.9E-01	P47135	SWISSPROT	JSN1 PROTEIN
12376	25156	31870	1.8	5.9E-01	L42320.1	NT	Oryctolagus cuniculus alpha 1 anti-trypsin (alpha 1 AT) gene, promoter region
12593	25289		3.38	5.9E-01	A5017705.1	NT	Aspergillus oryzae pyrG gene for orotidine-5'-phosphate decarboxylase, complete cds
12764	25421		5.68	5.9E-01	P34926	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN LC2]
1925	14946	27922	1.05	5.8E-01	P40472	SWISSPROT	SIM1 PROTEIN
4069	17095	29978	1.22	5.8E-01	BF695738.1	EST_HUMAN	601852474F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076131 5'
4635	17641	30504	5.31	5.8E-01	A5009077.1	NT	Vigna radiata mRNA for protein pyrophosphatase, complete cds
4912	17911		1.23	5.8E-01	AF110846.1	NT	Megascella scalaris sex-lethal homolog (Megsx) gene, partial cds, alternatively spliced products
5559	18537		0.62	5.8E-01	AE002152.1	NT	Ureaplasma urealyticum section 53 of 58 of the complete genome
5721	18784	31886	3.69	5.8E-01	Q10699	SWISSPROT	POTENTIAL 5'-3' EXONUCLEASE
6423	19472	32046	2.18	5.8E-01	D78699.1	EST_HUMAN	HUM500E06B Human placenta polyA+ (TFJivara) Homo sapiens cDNA clone GEN-500E06 5'
6567	19608	32793	0.7	5.8E-01	D50601.1	NT	Shigella sonnei DNA for 28 ORFs, complete cds
7124	20328		2	5.8E-01	S85081.1	NT	cyclic AMP-regulated phosphoprotein [rats, mRNA, 1030 nt]
8467	21398		2.69	5.8E-01	H41571.1	EST_HUMAN	Yn91b03 s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:175767 3' similar to
8865	21596	34935	0.78	5.8E-01	A1280051.1	EST_HUMAN	gb:S78187 M-PHASE INDUCER PHOSPHATASE 2 (HUMAN);
8865	21596	34936	0.78	5.8E-01	A1280051.1	EST_HUMAN	qh85d10.x1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:1853779 3'
8768	21698	35042	2.74	5.8E-01	P14328	SWISSPROT	qh85d10.x1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:1853779 3'
8768	21698	35043	2.74	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP96
9448	22376	36739	11.31	5.8E-01	A1270774.1	NT	SPORE COAT PROTEIN SP96
9524	22451	36914	1.05	5.8E-01	Q27399	SWISSPROT	Homo capiene partial TCF-4 gene for T-cell transcription factor-4, exons 6-11
10123	23014		0.64	5.8E-01	BF031606.1	EST_HUMAN	TRANSSCRIPTION FACTOR E2F
11428	24344	37789	7.78	5.8E-01	AJ243213.1	NT	601557774F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827298 5'
11475	24388		3.57	5.8E-01	BF700092.1	EST_HUMAN	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
							602121577F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4284403 5'

Page 50 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11582	24491		1.97	5.8E-01	BF700092.1	EST_HUMAN	602127577F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5'
1512	14543	27504	1.03	5.7E-01	P06727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
1512	14543	27505	1.03	5.7E-01	P06727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
3090	16141		0.96	5.7E-01	G755253	NT	Mus musculus plasmacytoma variant translocation 1 (Pvt1), mRNA
3270	16318	29221	1.89	5.7E-01	Q8W1J2	SWISSPROT	PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOYO1) (MOYO1A)
3591	16598		3.73	5.7E-01	AB033503.1	NT	Populus euramericana peaces-2 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
6613	19554	32838	4.16	5.7E-01	BF035413.1	EST_HUMAN	601454962F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858580 5'
7008	20035	33268	0.78	5.7E-01	AA194201.1	EST_HUMAN	Zf38c06.11 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:665874 5'
7183	18455	31325	1.24	5.7E-01	AL111440.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
8233	21138	34470	2	5.7E-01	P00373	SWISSPROT	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE)
8548	21479		0.57	5.7E-01	AJ251835.1	NT	Mus musculus Kcnq1, Ltrpc5, Mash2, Tape-1, Tssc4 and Tssc6 genes, alternative transcripts
8951	21881		0.84	5.7E-01	AI065061.1	EST_HUMAN	HA0385 Human fetal liver cDNA library Homo sapiens cDNA
10316	23205	36815	1.24	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
10316	23205	36816	1.24	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
11048	23932	37372	1.07	5.7E-01	BF540992.1	EST_HUMAN	602067712F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4088810 5'
3419	16461	29367	1.11	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3419	16461	29368	1.11	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3952	16980	29864	0.85	5.6E-01	AL161501.2	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
8159	21060	34396	0.41	5.6E-01	L44513.1	EST_HUMAN	HUMEST4B9 Human thymus NSTH II Homo sapiens cDNA
9361	22289	35654	4.78	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GK Homo sapiens cDNA clone GKCF5F05 5'
9361	22289	35655	4.78	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GK Homo sapiens cDNA clone GKCF5F05 5'
9914	22902	36289	1.51	5.6E-01	AB038782.1	NT	Homo sapiens MUC3A gene for intestinal mucin, partial cds
12244	25068		3.53	5.6E-01	BE888280.1	EST_HUMAN	601514007F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915457 5'
12886	16980	29864	3.48	5.6E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
12715	25365		2.95	5.6E-01	P50505	SWISSPROT	HIGH AFFINITY POTASSIUM TRANSPORTER
13074	25598		3.35	5.6E-01	BF573829.1	EST_HUMAN	602132029F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271334 5'
1239	14276	27218	1.54	5.6E-01	8303912	NT	Rattus norvegicus Protonyl Coenzyme A carboxylase, beta polypeptide (Pccb), mRNA
2752	15743	28738	4.81	5.5E-01	P03341	SWISSPROT	PROTEIN P30; NUCLEOPROTEIN P10J
2752	15743	28739	4.81	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL
2961	16013	28911	1.09	5.5E-01	5902085	NT	GAG POLYPROTEIN [CONTAINS: NUCLEOPROTEIN P10J
3114	16165		1.76	5.6E-01	H46219.1	EST_HUMAN	Homo sapiens superkiller viralicidal activity 2 (S_cervisiae homolog)-like (SKIV2L), mRNA
							yo18a10.s1 Soares adult brain N25HB55Y Homo sapiens cDNA clone IMAGE:178286 3'



Page 51 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3281	16329	29234	2.75	5.5E-01	AF227240.1	NT	Rabbit oral papillomavirus, complete genome
3757	16769	29679	1.22	5.5E-01	P48755	SWISSPROT	FOS-RELATED ANTIGEN-1
7626	20561	33854	0.56	5.5E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region: butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete>
7628	20561	33855	0.56	5.5E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region: butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete>
7668	20600		0.66	5.5E-01	AB015596.1	NT	Carassius auratus gene for gonadotropin II beta subunit, complete cds
9017	21946	35302	0.61	5.5E-01	A1791766.1	EST_HUMAN	cr2c01.y5 NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1602336 5'
10287	23177		0.77	5.5E-01	U88415.1	NT	Grmean-Congo hemorrhagic fever virus strain SPU 415/85 nucleoprotein gene, complete cds
10865	23751	37176	1.06	5.5E-01	T05047.1	EST_HUMAN	EST02935 Fetal brain, Stragene (cat#9330206) Homo sapiens cDNA clone HFB0035
11580	24469	37958	1.66	5.5E-01	BF120507.1	EST_HUMAN	601811077R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4054003 3'
150	13250	26167	7.75	5.4E-01	7657266	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
150	13250	26168	7.75	5.4E-01	7657266	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
606	13672	26575	1.71	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and Gsta (gsta) genes, complete cds, and unknown genes
606	13672	26576	1.71	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and Gsta (gsta) genes, complete cds, and unknown genes
1298	14331	27277	2.28	5.4E-01	AW896087.1	EST_HUMAN	QV4-NN004D-070400-160-c04 NN0040 Homo sapiens cDNA
2118	15131		1.71	5.4E-01	AE002247.2	NT	Chlamydomonas reinhardtii AR39, section 74 of 94 of the complete genome
2271	15281	28288	2.29	5.4E-01	AJ276882.1	NT	Drosophila melanogaster mRNA for 15,15' bala carotene dioxygenase (bala-diox gene)
5360	13672	26575	0.7	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and Gsta (gsta) genes, complete cds, and unknown genes
5360	13672	26576	0.7	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and Gsta (gsta) genes, complete cds, and unknown genes
5384	18366		0.91	5.4E-01	X85973.1	NT	A. thaliana mRNA for phosphorothioate-specific phospholipase C
5864	18925	32041	0.79	5.4E-01	AW842327.1	EST_HUMAN	PM2-CN0030-030200-003-c10 CN0030 Homo sapiens cDNA
6432	19479	32656	1.52	5.4E-01	AB025017.1	NT	Rattus norvegicus gene for TIS11, complete cds
6890	19728	32928	0.41	5.4E-01	11559624	NT	Homo sapiens hypothetical protein LOC63929 (LOC63929), mRNA
7376	20370	33639	0.63	5.4E-01	BE966592.2	EST_HUMAN	601650276R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906090 3'
7721	20653	33948	0.69	5.4E-01	Z21619.1	NT	S. cerevisiae RIB3 gene encoding DBP synthase

Page 52 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7721	20653	33949	0.69	5.4E-01	Z21619.1	NT	S.cerevisiae RIB3 gene encoding DBP synthase
7723	20655	33952	1.67	5.4E-01	Q64428	SWISSPROT	MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA SUBUNIT PRECURSOR (TP-ALPHA)
10496	23394		2.35	5.4E-01	BF572536.1	EST_HUMAN	[INCLUDES: LONG-CHAIN ENOYL-COA HYDRATASE; LONG CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE]
11518	24428	37886	2.8	5.4E-01	P36858	SWISSPROT	NITRATE REDUCTASE [NADPH] (NR)
12045	24886	38390	2.58	5.4E-01	Q60876	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
12045	24886	38391	2.58	5.4E-01	Q60875	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
12161	19479	32658	5.55	5.4E-01	AB025017.1	NT	Rattus norvegicus gene for TIS11, complete cds
12301	25110		3.13	5.4E-01	A1858398.1	EST_HUMAN	w137g04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2427126 3' similar to gb:M13452 LAMIN A (HUMAN);
539	13608	26518	2.16	5.3E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (B), and complement component C2 (C2) genes;>
2154	15168	29168	0.94	5.3E-01	AF113919.1	NT	Brassica oleracea var. capitata phospholipase D2 (PLD2) gene, complete cds
2154	15168	29169	0.94	5.3E-01	AF113919.1	NT	Brassica oleracea var. capitata phospholipase D2 (PLD2) gene, complete cds
2833	15822	28817	7.36	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
3289	16336	29239	4.03	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
4307	17321		2.5	5.3E-01	U39887.1	NT	Homo sapiens secreted C-type lectin precursor (SLC) gene, complete cds
5843	18718	31621	1.43	5.3E-01	A1820921.1	EST_HUMAN	Mycoplasma genitalium section 9 of 51 of the complete genome
5843	18718	31622	1.43	5.3E-01	A1820921.1	EST_HUMAN	zu42h12.y5 Soares ovary tumor NHOT Homo sapiens cDNA clone IMAGE:740711 5'
5745	18818	31914	0.85	5.3E-01	AA193672.1	EST_HUMAN	zu42h12.y5 Soares ovary tumor NHOT Homo sapiens cDNA clone IMAGE:740711 5'
5745	18818	31915	0.85	5.3E-01	AA193672.1	EST_HUMAN	zu42g09.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:666112 5'
5842	18913	32029	1.93	5.3E-01	BE645620.1	EST_HUMAN	zu42g09.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:666112 5'
5842	18913	32030	1.93	5.3E-01	BE645620.1	EST_HUMAN	7e73c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783
9461	22389		1.81	5.3E-01	L01950.2	NT	PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
9510	22437	35801	0.84	5.3E-01	BF433956.1	EST_HUMAN	PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
9510	22437	35802	0.84	5.3E-01	BF433956.1	EST_HUMAN	Roridula gorgonias ribulose 1,5-bisphosphate carboxylase (rbcl) gene, partial cds; chloroplast gene for chloroplast product
							7q71c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains element MER29 repetitive element;
							7q71c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains element MER29 repetitive element;

Page 53 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10707	23593	37020	0.8	5.3E-01	AI954210.1	EST_HUMAN	w894602.x1 NCL_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2551275 3' similar to SW:COXA_HUMAN P20874 CYTOCHROME C OXIDASE POLYPEPTIDE VA PRECURSOR ;
11073	23957	37393	0.52	5.3E-01	11428833	NT	Homo sapiens nucleoporin 214KD (CAN) (NUP214), mRNA
11993	24835	38333	5.76	6.3E-01	BE669291.1	EST_HUMAN	601339867F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682168 5'
12238	25769		4.27	5.3E-01	AA916053.1	EST_HUMAN	cg30e05.s1 NCL_CGAP_Br7 Homo sapiens cDNA clone IMAGE:1441376 3' similar to gb:J02611
841	13898	26833	13.59	5.2E-01	L20770.1	NT	APOLIPOPROTEIN D PRECURSOR (HUMAN);
1191	14230	27189	7.63	5.2E-01	Q9WV30	SWISSPROT	Drosophila melanogaster helix-loop-helix mRNA, complete cds
1219	14257	27197	2.31	5.2E-01	AF24492.1	NT	NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5)
1908	14927		2.81	5.2E-01	AL163285.2	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
2160	15172	28176	2.02	5.2E-01	AB018283.2	NT	Homo sapiens chromosome 21 segment HS21C085
3164	16214	29103	1.48	5.2E-01	U65942.1	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3465	16505		1.84	5.2E-01	AL116780.1	NT	Chlamydomonas abortus strain S2673 POMF91A and POMF90A precursor, genes, complete cds
3505	16543	29443	2.26	5.2E-01	AA984165.1	EST_HUMAN	Bolivian cinerea strain T4 cDNA library under conditions of nitrogen deprivation
3899	16731		1.03	5.2E-01	AF020289.1	NT	am77g05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1616504 3'
4717	17722	30584	0.69	5.2E-01	6752947	NT	Medicago sativa chloroplast malate dehydrogenase precursor (p1mdh) mRNA, nuclear gene encoding chloroplast protein, complete cds
5850	18921	32035	0.92	5.2E-01	AA284261.1	EST_HUMAN	Mus musculus acetylcholine receptor beta (Acrb), mRNA
10251	25693	36549	0.82	5.2E-01	X02218.1	NT	zc44d09.T7 Soares_senescent_fibroblasts NBHSF Homo sapiens cDNA clone IMAGE:325169 3'
10251	25693	36550	0.82	5.2E-01	X02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
10530	23416	36830	1.28	5.2E-01	AF143952.2	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
13051	25583		4.1	5.2E-01	P18516	SWISSPROT	Homo sapiens PELOTA (PELOTA) gene, complete cds
640	13701	26508	1.85	5.1E-01	M58509.1	NT	RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR-DELTA)
671	13733	26544	3.66	5.1E-01	AJ233944.1	NT	Human adrenodoxin reductase gene, exons 3 to 12
671	13733	26546	3.66	5.1E-01	AJ233944.1	NT	Polyangium vitellinum (strain PI vt1) 16S rRNA gene
1679	14709		1.08	5.1E-01	X87885.1	NT	Polyangium vitellinum (strain PI vt1) 16S rRNA gene
4163	17184	30057	5.45	5.1E-01	AB58495.1	EST_HUMAN	R.norvegicus mRNA for mammalian fusca protein
4283	17297	30163	3.04	5.1E-01	P96380	SWISSPROT	w39b12.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2427283 3'
6467	19512	32687	0.64	5.1E-01	BE541068.1	EST_HUMAN	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)
6528	19572		0.91	5.1E-01	AV712326.1	EST_HUMAN	801063606F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3450000 5'
7246	20155	33395	1.3	5.1E-01	R80873.1	EST_HUMAN	AY712328 DCA Homo sapiens cDNA clone DCAUF07 5'
8956	21786	35135	0.52	5.1E-01	BE772052.1	EST_HUMAN	y94409.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:146872 3'
							CM4-F10103-220600-210-e12 FT0103 Homo sapiens cDNA

Page 54 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9135	22063	35422	0.81	5.1E-01	AW809881.1	EST_HUMAN	QV4-ST0023-160400-172-a01 ST0023 Homo sapiens cDNA
9135	22063	35423	0.81	5.1E-01	AW809881.1	EST_HUMAN	QV4-ST0023-160400-172-a01 ST0023 Homo sapiens cDNA
10209	23100	36500	4.79	5.1E-01	J05412.1	NT	Human regenerating protein (reg) gene, complete cds
10211	23102	36503	3.8	5.1E-01	W22302.1	EST_HUMAN	65B1 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional
10856	23542	36976	1.02	5.1E-01	M94578.1	NT	Human carboxyl ester lipase (CEL) gene, complete cds
12434	25702		2.66	5.1E-01	BF030207.1	EST_HUMAN	601555863F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3828767 5'
12664	25335		1.86	5.1E-01	BF439982.1	EST_HUMAN	hac51110.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3406218 3' similar to contains element TAR1 repetitive element:
2148	18161	28162	0.98	5.0E-01	4885552	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA
2148	15161	28163	0.98	5.0E-01	4885552	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA
2159	15171	28174	1.28	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFE), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
2159	15171	28175	1.28	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFE), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
3904	18933	29812	1.11	5.0E-01	L38483.1	NT	Rattus norvegicus jagged protein mRNA, complete cds
3942	16970	29852	3.68	5.0E-01	AB033010.1	NT	Homo sapiens mRNA for KIAA1184 protein, partial cds
6776	18848	31952	0.44	5.0E-01	U30320.1	NT	Sperua aurea gonadotropin-releasing hormone (bGnRH) precursor mRNA, complete cds
6776	18848	31953	0.44	5.0E-01	U30320.1	NT	Sperua aurea gonadotropin-releasing hormone (bGnRH) precursor mRNA, complete cds
6936	19965		0.62	5.0E-01	BF575199.1	EST_HUMAN	902132642F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271939 5'
7029	20055	33288	0.55	5.0E-01	AF042848.1	NT	Homo sapiens EMMPRIN gene, promoter and exon 1
8115	21026	34351	0.73	5.0E-01	AL161549.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
8115	21026	34352	0.73	5.0E-01	AL161549.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
8371	21275		0.44	5.0E-01	Z71560.1	NT	S. cerevisiae chromosome XIV reading frame ORF YNL284c
9094	22023		1.97	5.0E-01	M92304.1	NT	Xenopus laevis smooth muscle beta-tropomyosin mRNA, complete cds
9228	22156	35509	0.69	5.0E-01	BF107848.1	EST_HUMAN	601823850R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:403486 3'
9990	21348	34682	3.39	5.0E-01	BF317212.1	EST_HUMAN	601903871F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4136632 5'
10151	23042	36441	1.63	5.0E-01	P35573	SWISSPROT	(GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)])
10151	23042	36442	1.63	5.0E-01	P35573	SWISSPROT	(GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)])

Page 55 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10878	23764		0.86	5.0E-01	BE869218.1	EST_HUMAN	601445024F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849436 5'
11086	23950	37386	0.59	5.0E-01	AW845172.1	EST_HUMAN	QV0-CT0010-100699-009 CT0010 Homo sapiens cDNA
12380	25160		4.42	5.0E-01	AF029215.1	NT	Mus musculus MRC OX-2 antigen homolog gene, exons 2-5, and complete cds
13028	25503		3.91	5.0E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
13039	25576		3	5.0E-01	O13961	SWISSPROT	NUCLEAR ENVELOPE PROTEIN CUT11
816	13871	26808	1.95	4.9E-01	BF571482.1	EST_HUMAN	602076649F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243860 5'
1686	14716	27677	1.09	4.9E-01	AJ243955.1	EST_HUMAN	Xenopus laevis mRNA for o-Jun protein, 1978 BP
4788	17792		0.99	4.9E-01	AW968780.1	EST_HUMAN	EST380866 MAGe resequences, MAGJ Homo sapiens cDNA
5591	18667	31545	1.38	4.9E-01	Q61554	SWISSPROT	FIBRILLIN 1 PRECURSOR
6270	19321	32485	2.64	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
6270	19321	32486	2.64	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
7856	20783	34086	1.65	4.9E-01	AB040051.1	NT	Oryza sativa subsp. Japonica mEF-G mRNA for mitochondrial elongation factor G, complete cds
8164	21071	34400	0.7	4.9E-01	Q10806	SWISSPROT	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE
8164	21071	34401	0.7	4.9E-01	Q10806	SWISSPROT	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE
9541	22408		2.01	4.9E-01	BF209791.1	EST_HUMAN	601874964F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4102503 5'
9729	22654	36037	1.17	4.9E-01	AW339905.1	EST_HUMAN	hc90c02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2907288 3' similar to TR:095714
9836	25992		2.07	4.9E-01	10946863	NT	Mus musculus unc13 homolog (C. elegans) 1 (Unc13h1), mRNA
10807	26693	37120	1.11	4.9E-01	AF039880.1	NT	Mus musculus adenyl cyclase 1 (Adcy1) cDNA, partial cds
11002	28866	37319	0.53	4.9E-01	X90000.1	NT	H. sapiens DNA for BCL7A gene and BCL7AIGH locus fusion
13020	25942		4.94	4.9E-01	AA613562.1	EST_HUMAN	nc22611.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1144652 3'
13029	25569	31738	1.58	4.9E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
4440	17451		0.72	4.8E-01	4504850	NT	Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5) mRNA, and translated products
4787	17451		0.8	4.8E-01	4504850	NT	Homo sapiens potassium channel, subfamily K, member 6 (TASK-2) (KCNK6) mRNA, and translated products
5697	18770	31698	8.47	4.8E-01	J02987.1	NT	Saccharomyces cerevisiae sporulation protein (SPO11) gene required for meiotic recombination, complete cds
6975	20002	33234	0.75	4.8E-01	U92882.1	NT	Mus musculus slow skeletal muscle troponin T (Tnni1) gene, complete cds
6985	20012		4.23	4.8E-01	AA659878.1	EST_HUMAN	nu85f09.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1217513
7700	20692		2	4.8E-01	5031650	NT	Homo sapiens reproduction 8 (D8S2288E) mRNA
8118	21029	34356	0.88	4.8E-01	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8229	21134	34465	3.51	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
8229	21134	34466	3.51	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4

Page 56 of 545  
Table 4  
Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8484	21415	34752	1.2	4.8E-01	AB20744.1	EST_HUMAN	Y17710.y5 Soares breast 2NBH8at Homo sapiens cDNA clone IMAGE:154795 5' similar to contains element
9787	22761		1.05	4.8E-01	BE155148.1	EST_HUMAN	MER6 repetitive element;
10513	23400		0.58	4.8E-01	BF508633.1	EST_HUMAN	PM11-HT0350-201299-004-b04 HT0350 Homo sapiens cDNA
11170	24098		2.4	4.8E-01	X83502.1	NT	60218/267F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300048 5'
12357	25146		1.66	4.8E-01	AL163227.2	NT	S.cerevisiae ORF's from chromosome X
12561	25735		4.16	4.8E-01	AF227665.1	NT	Homo sapiens chromosome 21 segment HS21C027
3123	16174		0.74	4.7E-01	AF192387.1	NT	Trypanosoma cruzi transposon VIP II SIRE repeat region
6793	19826	33036	8.84	4.7E-01	BF217173.1	EST_HUMAN	Felis catus feline leukemia virus subgroup C receptor (FLVCR1) mRNA, complete cds
7392	20091	33325	0.74	4.7E-01	AI204374.1	EST_HUMAN	601883890F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096387 5'
8446	21378	34719	0.88	4.7E-01	T11414.1	EST_HUMAN	qf72a09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755544 3'
8446	21378	34720	0.68	4.7E-01	T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5' end
11282	24203		5.26	4.7E-01	AF102873.1	NT	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5' end
11525	24435	37893	2.11	4.7E-01	U41069.1	NT	Influenza A virus isolate h51697 hemagglutinin (HA) gene, partial cds
11728	24630	38110	1.4	4.7E-01	BF529658.1	EST_HUMAN	Human collagen alpha2(XI) (COL11A2) gene, exon 6 through 16, and partial cds
11815	24736	38227	1.58	4.7E-01	AW889448.1	EST_HUMAN	602043899F1 MGI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4181303 5'
12463	25210		2.06	4.7E-01	BE887763.1	EST_HUMAN	RC6-NT0029-240400-011-E08 NT0029 Homo sapiens cDNA
3806	16837	28723	2.16	4.6E-01	BF693300.1	EST_HUMAN	601511333F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912488 5'
3806	16837	28724	2.16	4.6E-01	BF693300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
5604	18680	31557	0.93	4.6E-01	BF313593.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
5604	18680	31558	0.93	4.6E-01	BF313593.1	EST_HUMAN	601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5'
5659	18733	31639	3.46	4.6E-01	Q30843	SWISSPROT	601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5'
5659	18733	31640	3.46	4.6E-01	Q30843	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5737	18810	31904	2.35	4.6E-01	BE734781.1	EST_HUMAN	INTERFERON REGULATORY FACTOR 3 (IRF-3)
							601568755F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843637 5'
5751	18824	31921	2.32	4.6E-01	AI247679.1	EST_HUMAN	qh59h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to
5751	18824	31922	2.32	4.6E-01	AI247679.1	EST_HUMAN	qh59h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to
5759	18832	31933	1.52	4.6E-01	P20050	SWISSPROT	TR-O15338 O15338 BUTYRPHILIN.1
5843	18914		0.66	4.6E-01	AF212124.1	NT	qh59h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to
5934	19001		0.85	4.6E-01	BE817247.1	EST_HUMAN	MEIOSIS SPECIFIC PROTEIN HOP1
6117	19176	32311	0.46	4.6E-01	D26215.1	NT	Ancolie schwartzii cytochrome b gene, partial cds; mitochondrial gene for mitochondrial product
							PM0-BN0260-120600-001-F07 BN0260 Homo sapiens cDNA
							Unidentified soil bacteria 16S rRNA gene encoding 16S ribosomal RNA
6506	19590	32730	0.95	4.6E-01	AE000894.1	NT	Methanobacterium thermoautotrophicum from bases 1165751 to 1176238 (section 100 of 148) of the complete genome

Page 57 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7020	20048	33281	0.48	4.8E-01	AF115340.1	NT	Bacillus subtilis Bbma (bbma) gene, complete cds
7073	20279	33533	1.66	4.8E-01	U62332.1	NT	Emicella nidulans NEMPA (nempa) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
7073	20279	33534	1.66	4.8E-01	U62332.1	NT	Emicella nidulans NEMPA (nempa) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
7600	25672	33824	0.63	4.8E-01	L07320.1	NT	Murine cytomegalovirus e1 protein gene, complete cds
8192	21089	34429	0.74	4.8E-01	AA463577.1	EST_HUMAN	h04h05.s1 NCL_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:843353 similar to contains Alu repetitive element; contains element L1 repetitive element
8226	21131		0.49	4.8E-01	Q90069	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (HC-PRO); PROTEIN P3; 6 KD PROTEIN 1 (9K1); CYTOPLASMIC INCLUSION PROTEIN (CI); 6 KD PROTEIN 2 (9K2); GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NI-A) (NI>
8300	21204		0.55	4.8E-01	AE004031.1	NT	Xyella fastidiosa, section 177 of 229 of the complete genome
8895	21825	35177	19.05	4.8E-01	BF697399.1	EST_HUMAN	602130953F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287828 5'
9308	22234	35594	0.51	4.8E-01	AA932237.1	EST_HUMAN	cc78b08.s1 NCL_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1572087 3' similar to gb:M36341 ADP-RIBOSYLATION FACTOR 4 (HUMAN);
9308	22234	35595	0.51	4.8E-01	AA932237.1	EST_HUMAN	cc78b08.s1 NCL_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1572087 3' similar to gb:M36341 ADP-RIBOSYLATION FACTOR 4 (HUMAN);
9841	22746	36128	1.04	4.8E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
9841	22746	36129	1.04	4.8E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
10482	23370	36782	1.64	4.8E-01	A015634.1	EST_HUMAN	wg73e12.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766 3'
10482	23370	36783	1.64	4.8E-01	A015634.1	EST_HUMAN	wg73e12.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766 3'
11429	24345		2.78	4.8E-01	P98163	SWISSPROT	PUTATIVE VITELLOGENIN RECEPTOR PRECURSOR (VL)
11438	24354	37801	5.16	4.8E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
11438	24354	37802	5.16	4.8E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
11903	24003	37442	5.82	4.8E-01	AF019369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
11903	24003	37443	5.82	4.8E-01	AF019369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
12209	25043	38546	1.43	4.8E-01	M20080.1	EST_HUMAN	Hordeum vulgare alpha-hordothionin (Hth-1) gene, complete cds
1733	14760		1.89	4.8E-01	BE311420.1	EST_HUMAN	801142105F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505993 5'
1927	14948	27924	1	4.8E-01	AE001931.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
1927	14948	27925	1	4.8E-01	AE001931.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
2913	15966	28665	5.98	4.8E-01	AA677085.1	EST_HUMAN	q55402.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:454179 3'

Page 58 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3362	16406	29307	6.69	4.5E-01	Q05793	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
3435	16476	29382	1.71	4.5E-01	AF126378.1	NT	PRECURSOR (HSPG) (PERLECAN) (PLC)
4112	17136		1.38	4.5E-01	Q28247	SWISSPROT	Mus musculus DNA polymerase epsilon catalytic subunit (Pde) gene, exons 2 through 12
4161	17182	30055	0.89	4.5E-01	AI108908.1	EST_HUMAN	COLLAGEN ALPHA 5(V) CHAIN
4272	18412		4.09	4.5E-01	AW873495.1	EST_HUMAN	ho60g22.x1 Soares_NFL_T_GBC_ST Homo sapiens cDNA clone IMAGE:2353480 3'
5057	18054	30907	1.33	4.5E-01	BE963445.2	EST_HUMAN	601657229R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866023 3'
5740	18813	31609	1.49	4.5E-01	AW608814.1	EST_HUMAN	QV2.PT0012-140100-031-c09 PT0012 Homo sapiens cDNA
6892	19922		1.6	4.5E-01	Q00956	SWISSPROT	COAT PROTEIN
7813	20742	34046	0.68	4.5E-01	M37036.1	NT	Rat nuclear proteins B23.1 and B23.2
8053	20966	34281	2.54	4.5E-01	A1838849.1	EST_HUMAN	wk3e02.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2428618 3' similar to TR:Q92923 Q92923
8882	21812		1.43	4.5E-01	M32681.1	NT	SWISNF COMPLEX 170 KDA SUBUNIT..
8974	21904	35260	2.98	4.5E-01	A1648596.1	EST_HUMAN	D melanogaster Shaw2 protein mRNA, complete cds
							t256g11.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2292644 3'
9122	22050	35410	0.8	4.5E-01	Q52728	SWISSPROT	POLY-BETA-HYDROXYBUTYRATE POLYMERASE (POLY(3-HYDROXYBUTYRATE) POLYMERASE)
9340	22268		2.07	4.5E-01	11444788	NT	(PHB POLYMERASE) (PHB SYNTHASE) (POLY(3-HYDROXYALKANOATE) POLYMERASE) (PHA
9551	22478	35837	0.83	4.5E-01	AE000218.1	NT	POLYMERASE) (PHA SYNTHASE) (POLYHYDROXYALKANOIC ACID SYNTHASE)
10450	23339		1.02	4.5E-01	9630816	NT	Homo sapiens hypodermal protein DKFZp547G183 (DKFZp547G183), mRNA
10973	23857	37284	24.91	4.5E-01	M86006.1	EST_HUMAN	Escherichia coli K-12 MG1655 section 108 of 400 of the complete genome
10973	23857	37285	24.91	4.5E-01	M86006.1	EST_HUMAN	Bombay mod nuclear polyhedrosis virus, complete genome
11298	24217	37667	2.63	4.5E-01	AW591271.1	EST_HUMAN	EST02531 Fetal brain, Stratiogene (cat#636206) Homo sapiens cDNA clone HFBCY17
11899	24601		1.43	4.5E-01	AV719382.1	EST_HUMAN	EST02531 Fetal brain, Stratiogene (cat#636206) Homo sapiens cDNA clone HFBCY17
12253	25932		4.79	4.5E-01	BE871481.1	EST_HUMAN	xc14h01.x1 NCI_CGAP_U3 Homo sapiens cDNA clone IMAGE:2703985 3' similar to SW:INT6_MOUSE
12935	25503		5.32	4.5E-01	11422099	NT	Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6, [1];
2050	15067		0.95	4.4E-01	6680503	NT	AV719382 GLC Homo sapiens cDNA clone GLCED12 6'
							601449201F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852961 5'
							Homo sapiens testis-specific kinase 2 (TESK2), mRNA
							Mus musculus integral membrane-associated protein 1 (Imap1), mRNA
2412	15416	28418	4.14	4.4E-01	P49765	SWISSPROT	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)
3360	16404	29305	1.59	4.4E-01	AF058790.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3360	16404	29308	1.59	4.4E-01	AF058790.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3364	16408	28309	2.86	4.4E-01	BF056726.1	EST_HUMAN	7J91402.Y1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3393765 5'



Page 59 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4334	17348		1.95	4.4E-01	BE378707.1	EST_HUMAN	601237139F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609393 5'
5605	18681	31559	1.37	4.4E-01	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5605	18681	31560	1.37	4.4E-01	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5883	18955	32072	1.57	4.4E-01	S65019.1	NT	much [rats, Sprague-Dawley, sulfur-dioxide-treated tracheal epithelium, mRNA Partial, 360 nt]
5904	18973	32091	1.92	4.4E-01	AV720408.1	EST_HUMAN	AV720408 GLC Homo sapiens cDNA clone GLCSC12 5'
6179	19233	32382	1.09	4.4E-01	AI188413.1	EST_HUMAN	q162h11.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29188 Q29188 UNKNOWN PROTEIN ;
6179	19233	32383	1.09	4.4E-01	AI188413.1	EST_HUMAN	q162h11.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29188 Q29188 UNKNOWN PROTEIN ;
6488	19532	32711	1.6	4.4E-01	AW080795.1	EST_HUMAN	xc27e08.x1 NCL_CGAP_Cc18 Homo sapiens cDNA clone IMAGE:2585510 3' similar to TR:O96154 O96154 AFLATOXIN B1-ALDEHYDE REDUCTASE. ;
6585	19823		0.98	4.4E-01	AA776132.1	EST_HUMAN	TYROSINE-PROTEIN KINASE LYN (HUMAN);
7766	20725	34027	0.86	4.4E-01	AE000671.1	NT	lae5411.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:970965 3' similar to gb:M16038
8361	25837		0.84	4.4E-01	AE001188.1	NT	Halobacter pflor 26595 section 49 of 134 of the complete genome
8423	21355		13.12	4.4E-01	Z11679.1	NT	Treponema pallidum section 4 of 87 of the complete genome
9322	22253	35614	1	4.4E-01	AA056427.1	EST_HUMAN	z69a03.s1 Stralagene colon (8937204) Homo sapiens cDNA clone IMAGE:508836 3'
9694	22619	35997	0.78	4.4E-01	AF112540.1	NT	HIV-1 isolate 08107v6 from USA, envelope glycoprotein (env) gene, partial cds
9725	22650	36032	0.58	4.4E-01	AW612578.1	EST_HUMAN	h05c08.x1 NCL_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2854222 3' similar to SW:IMSH6 HUMAN P52701 DNA MISMATCH REPAIR PROTEIN MSH6 ;
9830	22736	36118	1.27	4.4E-01	O62838	SWISSPROT	ZINC FINGER X-CHROMOSOMAL PROTEIN
10468	23356	36771	2.12	4.4E-01	AI269650.1	EST_HUMAN	q39109.x1 NCL_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1910921 3'
10468	23357		2.33	4.4E-01	P28822	SWISSPROT	GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14)
10599	23485	36914	4.95	4.4E-01	P35590	SWISSPROT	TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR
10862	23748	37172	1.99	4.4E-01	S78404.1	NT	beta -HKA-H,K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
10862	23748	37173	1.99	4.4E-01	S78404.1	NT	beta -HKA-H,K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
12491	26232	31889	4.51	4.4E-01	6677874	NT	Mus musculus sodium channel, type X, alpha polypeptide (Scn10a), mRNA
12501	26873		15.77	4.4E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
434	13505	26429	1.87	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
434	13505	26430	1.87	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
1626	14656	27620	1.25	4.3E-01	AW866550.1	EST_HUMAN	QV4-SN0024-200400-183-b01 SN0024 Homo sapiens cDNA
2915	15993		1.02	4.3E-01	AW835268.1	EST_HUMAN	CM2-DT0003-010200-077-c01 DT0003 Homo sapiens cDNA
4249	17265	30132	1.59	4.3E-01	J00306.1	NT	Human somatostatin 1 gene and flanks
4512	13505	26429	1.01	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region

Page 60 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4612	13505	28430	1.01	4.3E-01	AF155218.1	NT	Calitrix jacchus MW/LW qpsn gene, upstream flanking region
5281	18247		1.11	4.3E-01	9635250	NT	Xeslia c-nigrum granulovirus, complete genome
5549	18627	31503	0.9	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
5549	18627	31504	0.9	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
6105	19168	32289	1.15	4.3E-01	BE181655.1	EST_HUMAN	QV1-H10638-070500-191-d08 HT0638 Homo sapiens cDNA
6125	19184	32319	2.07	4.3E-01	AF179625.1	NT	Salimiri sciureus olfactory receptor (SSC186) gene, partial cds
7005	20032	33284	4.36	4.3E-01	AJ001878.1	NT	Coturnix coturnix japonica ifnG gene
7094	20300	33561	0.66	4.3E-01	AF076629.1	NT	Equus caballus microsatellite LEX027
7191	20191		0.7	4.3E-01	Q33367	SWISSPROT	DNA GYRASE SUBUNIT B
7832	20761		1.55	4.3E-01	BF348001.1	EST_HUMAN	602023134FT NCI_CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4158296 5'
8333	21238		0.44	4.3E-01	M58643.1	NT	Human lipoprotein associated coagulation inhibitor (LACI) gene, exon 2
8897	21926		3.19	4.3E-01	U97040.1	NT	Methanococcus voltae flagella-related protein C-1 (flaC-fla) genes, complete cds
9797	22761	36146	1.17	4.3E-01	Y14804.1	NT	Erwinia amylovora rcsV gene
10247	23138	36543	1.91	4.3E-01	AW630048.1	EST_HUMAN	Hh74e10.Y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2988554 5'
10247	23138	36544	1.91	4.3E-01	AW630048.1	EST_HUMAN	Hh74e10.Y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2988554 5'
10723	23609	37039	0.68	4.3E-01	AW170559.1	EST_HUMAN	xn63e05.x1 Soares_NHCeC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698400 3' similar to
10991	23875	37304	0.59	4.3E-01	H65292.1	EST_HUMAN	Yr45b05.s1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:208209 3'
11369	20300	33561	2.26	4.3E-01	AF075628.1	NT	Equus caballus microsatellite LEX027
12163	24699	38500	1.53	4.3E-01	A1874332.1	EST_HUMAN	t264d04.x1 NCI_CGAP_OV65 Homo sapiens cDNA clone IMAGE:2293351 3'
1385	15699	27371	1.38	4.2E-01	Q39102	SWISSPROT	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
3673	18706	28598	6.15	4.2E-01	AE003947.1	NT	Xylella fastidiosa, section 93 of 229 of the complete genome
3705	18737	26626	1.13	4.2E-01	A1280338.1	EST_HUMAN	qj94b01.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1879945 3'
3774	18411		0.7	4.2E-01	N81203.1	EST_HUMAN	788E1 fetal brain cDNA Homo sapiens cDNA clone 788E1-K similar to R07879, Z40498
4067	17053	29977	1.16	4.2E-01	Q04886	SWISSPROT	SOX-B PROTEIN
4810	17811	30677	6.24	4.2E-01	AA534093.1	EST_HUMAN	n169h01.s1 NCI_CGAP_P10 Homo sapiens cDNA clone IMAGE:997777 similar to gb:M33600 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN);
4894	17853	30759	4.12	4.2E-01	R13497.1	EST_HUMAN	yf77e01.t1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28278 5'
5914	19983	32102	1.58	4.2E-01	BF242055.1	EST_HUMAN	601979721F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108493 5'
5990	19055	32182	1.71	4.2E-01	AW854162.1	EST_HUMAN	RC3-C10254-060400-028-g04 CT0254 Homo sapiens cDNA
6446	19492	32659	1.05	4.2E-01	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
7283	20236	33486	9.31	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
7283	20236	33487	9.31	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
7355	25668	33618	2.39	4.2E-01	S82504.1	NT	Brcal=breast cancer gene [rats, W/F, spleen, Genomic, 418 nt, segment 2 of 2]

Page 61 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7452	20393	33663	6.45	4.2E-01	AL161547.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47
8005	20922	34238	0.47	4.2E-01	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
8572	21603	34846	3.88	4.2E-01	AW957448.1	EST_HUMAN	EST369413 IMAGE resequencing, MAGG Homo sapiens cDNA
8572	21503	34847	3.88	4.2E-01	AW957448.1	EST_HUMAN	EST369413 IMAGE resequencing, MAGG Homo sapiens cDNA
8784	21714	35061	0.58	4.2E-01	4758039	NT	Homo sapiens cytochrome c oxidase subunit VIc (COX6C), nuclear gene encoding mitochondrial protein, mRNA
9851	22766	36150	0.53	4.2E-01	U57431.1	NT	Human cytomegalovirus early phosphoprotein p50 mRNA, complete cds
9851	22766	36151	0.53	4.2E-01	U57431.1	NT	Human cytomegalovirus early phosphoprotein p50 mRNA, complete cds
10478	23364		0.66	4.2E-01	AA705007.1	EST_HUMAN	Z958101.s1 Soares fetal_liver_spleen_TNFLS_S1 Homo sapiens cDNA clone IMAGE:462849 3'
10677	23563	36993	0.65	4.2E-01	AF181854.1	NT	Laesa virus strain 803213 glycoprotein precursor and nucleoprotein genes, complete cds
10974	23858	37286	1.67	4.2E-01	AW863866.1	EST_HUMAN	MR3-SN0010-280300-103-H07 SN0010 Homo sapiens cDNA
11478	24392	37842	1.83	4.2E-01	AB023489.1	NT	Onyias latipes OIGG7 mRNA for membrane guanylyl cyclase, complete cds
11833	24684	38173	2.4	4.2E-01	BE665485.2	EST_HUMAN	601660352R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3806085 3'
1121	14163	27100	1.72	4.1E-01	A1905481.1	EST_HUMAN	RG-BT091-210189-142 BT091 Homo sapiens cDNA
1130	14172	27109	1.01	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1632	14682	27625	1.02	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
2760	15751	28747	1.51	4.1E-01	A1905949.1	EST_HUMAN	PM-BT103-270499-684 BT103 Homo sapiens cDNA
2882	16033	28934	2.77	4.1E-01	7705283	NT	Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA
2882	16033	28935	2.77	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
3347	16393	29294	1.07	4.1E-01	AL161536.2	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
3839	16868	29751	1.67	4.1E-01	AA906344.1	EST_HUMAN	q94b08.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1505943 3'
3839	16868	29752	1.67	4.1E-01	AW961292.1	EST_HUMAN	EST373364 IMAGE resequencing, MAGG Homo sapiens cDNA
4373	17387	30251	3.51	4.1E-01	AW961292.1	EST_HUMAN	EST373364 IMAGE resequencing, MAGG Homo sapiens cDNA
4409	17421		0.69	4.1E-01	AJ249207.1	NT	Rhodococcus sp. AD45 isoG, isoH, isoI, isoJ, isoK, isoL, isoM, isoN, isoO, isoP, isoQ, isoR, isoS, isoT, isoU, isoV, isoW, isoX, isoY, isoZ, isoAA, isoAB, isoAC, isoAD, isoAE, isoAF, isoAG, isoAH, isoAI, isoAJ, isoAK, isoAL, isoAM, isoAN, isoAO, isoAP, isoAQ, isoAR, isoAS, isoAT, isoAU, isoAV, isoAW, isoAX, isoAY, isoAZ, isoBA, isoBB, isoBC, isoBD, isoBE, isoBF, isoBG, isoBH, isoBI, isoBJ, isoBK, isoBL, isoBM, isoBN, isoBO, isoBP, isoBQ, isoBR, isoBS, isoBT, isoBU, isoBV, isoBW, isoBX, isoBY, isoBZ, isoCA, isoCB, isoCC, isoCD, isoCE, isoCF, isoCG, isoCH, isoCI, isoCJ, isoCK, isoCL, isoCM, isoCN, isoCO, isoCP, isoCQ, isoCR, isoCS, isoCT, isoCU, isoCV, isoCW, isoCX, isoCY, isoCZ, isoDA, isoDB, isoDC, isoDD, isoDE, isoDF, isoDG, isoDH, isoDI, isoDJ, isoDK, isoDL, isoDM, isoDN, isoDO, isoDP, isoDQ, isoDR, isoDS, isoDT, isoDU, isoDV, isoDW, isoDX, isoDY, isoDZ, isoEA, isoEB, isoEC, isoED, isoEE, isoEF, isoEG, isoEH, isoEI, isoEJ, isoEK, isoEL, isoEM, isoEN, isoEO, isoEP, isoEQ, isoER, isoES, isoET, isoEU, isoEV, isoEW, isoEX, isoEY, isoEZ, isoFA, isoFB, isoFC, isoFD, isoFE, isoFF, isoFG, isoFH, isoFI, isoFJ, isoFK, isoFL, isoFM, isoFN, isoFO, isoFP, isoFQ, isoFR, isoFS, isoFT, isoFU, isoFV, isoFW, isoFX, isoFY, isoFZ, isoGA, isoGB, isoGC, isoGD, isoGE, isoGF, isoGG, isoGH, isoGI, isoGJ, isoGK, isoGL, isoGM, isoGN, isoGO, isoGP, isoGQ, isoGR, isoGS, isoGT, isoGU, isoGV, isoGW, isoGX, isoGY, isoGZ, isoHA, isoHB, isoHC, isoHD, isoHE, isoHF, isoHG, isoHH, isoHI, isoHJ, isoHK, isoHL, isoHM, isoHN, isoHO, isoHP, isoHQ, isoHR, isoHS, isoHT, isoHU, isoHV, isoHW, isoHX, isoHY, isoHZ, isoIA, isoIB, isoIC, isoID, isoIE, isoIF, isoIG, isoIH, isoII, isoIJ, isoIK, isoIL, isoIM, isoIN, isoIO, isoIP, isoIQ, isoIR, isoIS, isoIT, isoIU, isoIV, isoIW, isoIX, isoIY, isoIZ, isoJA, isoJB, isoJC, isoJD, isoJE, isoJF, isoJG, isoJH, isoJI, isoJJ, isoJK, isoJL, isoJM, isoJN, isoJO, isoJP, isoJQ, isoJR, isoJS, isoJT, isoJU, isoJV, isoJW, isoJX, isoJY, isoJZ, isoKA, isoKB, isoKC, isoKD, isoKE, isoKF, isoKG, isoKH, isoKI, isoKJ, isoKK, isoKL, isoKM, isoKN, isoKO, isoKP, isoKQ, isoKR, isoKS, isoKT, isoKU, isoKV, isoKW, isoKX, isoKY, isoKZ, isoLA, isoLB, isoLC, isoLD, isoLE, isoLF, isoLG, isoLH, isoLI, isoLJ, isoLK, isoLL, isoLM, isoLN, isoLO, isoLP, isoLQ, isoLR, isoLS, isoLT, isoLU, isoLV, isoLW, isoLX, isoLY, isoLZ, isoMA, isoMB, isoMC, isoMD, isoME, isoMF, isoMG, isoMH, isoMI, isoMJ, isoMK, isoML, isoMN, isoMO, isoMP, isoMQ, isoMR, isoMS, isoMT, isoMU, isoMV, isoMW, isoMX, isoMY, isoMZ, isoNA, isoNB, isoNC, isoND, isoNE, isoNF, isoNG, isoNH, isoNI, isoNJ, isoNK, isoNL, isoNM, isoNO, isoNP, isoNQ, isoNR, isoNS, isoNT, isoNU, isoNV, isoNW, isoNX, isoNY, isoNZ, isoOA, isoOB, isoOC, isoOD, isoOE, isoOF, isoOG, isoOH, isoOI, isoOJ, isoOK, isoOL, isoOM, isoON, isoOO, isoOP, isoOQ, isoOR, isoOS, isoOT, isoOU, isoOV, isoOW, isoOX, isoOY, isoOZ, isoPA, isoPB, isoPC, isoPD, isoPE, isoPF, isoPG, isoPH, isoPI, isoPJ, isoPK, isoPL, isoPM, isoPN, isoPO, isoPP, isoPQ, isoPR, isoPS, isoPT, isoPU, isoPV, isoPW, isoPX, isoPY, isoPZ, isoQA, isoQB, isoQC, isoQD, isoQE, isoQF, isoQG, isoQH, isoQI, isoQJ, isoQK, isoQL, isoQM, isoQN, isoQO, isoQP, isoQQ, isoQR, isoQS, isoQT, isoQU, isoQV, isoQW, isoQX, isoQY, isoQZ, isoRA, isoRB, isoRC, isoRD, isoRE, isoRF, isoRG, isoRH, isoRI, isoRJ, isoRK, isoRL, isoRM, isoRN, isoRO, isoRP, isoRQ, isoRR, isoRS, isoRT, isoRU, isoRV, isoRW, isoRX, isoRY, isoRZ, isoSA, isoSB, isoSC, isoSD, isoSE, isoSF, isoSG, isoSH, isoSI, isoSJ, isoSK, isoSL, isoSM, isoSN, isoSO, isoSP, isoSQ, isoSR, isoSS, isoST, isoSU, isoSV, isoSW, isoSX, isoSY, isoSZ, isoTA, isoTB, isoTC, isoTD, isoTE, isoTF, isoTG, isoTH, isoTI, isoTJ, isoTK, isoTL, isoTM, isoTN, isoTO, isoTP, isoTQ, isoTR, isoTS, isoTT, isoTU, isoTV, isoTW, isoTX, isoTY, isoTZ, isoUA, isoUB, isoUC, isoUD, isoUE, isoUF, isoUG, isoUH, isoUI, isoUJ, isoUK, isoUL, isoUM, isoUN, isoUO, isoUP, isoUQ, isoUR, isoUS, isoUT, isoUU, isoUV, isoUW, isoUX, isoUY, isoUZ, isoVA, isoVB, isoVC, isoVD, isoVE, isoVF, isoVG, isoVH, isoVI, isoVJ, isoVK, isoVL, isoVM, isoVN, isoVO, isoVP, isoVQ, isoVR, isoVS, isoVT, isoVU, isoVV, isoVW, isoVX, isoVY, isoVZ, isoWA, isoWB, isoWC, isoWD, isoWE, isoWF, isoWG, isoWH, isoWI, isoWJ, isoWK, isoWL, isoWM, isoWN, isoWO, isoWP, isoWQ, isoWR, isoWS, isoWT, isoWU, isoWV, isoWW, isoWX, isoWY, isoWZ, isoXA, isoXB, isoXC, isoXD, isoXE, isoXF, isoXG, isoXH, isoXI, isoXJ, isoXK, isoXL, isoXM, isoXN, isoXO, isoXP, isoXQ, isoXR, isoXS, isoXT, isoXU, isoXV, isoXW, isoXX, isoXY, isoXZ, isoYA, isoYB, isoYC, isoYD, isoYE, isoYF, isoYG, isoYH, isoYI, isoYJ, isoYK, isoYL, isoYM, isoYN, isoYO, isoYP, isoYQ, isoYR, isoYS, isoYT, isoYU, isoYV, isoYW, isoYX, isoYY, isoYZ, isoZA, isoZB, isoZC, isoZD, isoZE, isoZF, isoZG, isoZH, isoZI, isoZJ, isoZK, isoZL, isoZM, isoZN, isoZO, isoZP, isoZQ, isoZR, isoZS, isoZT, isoZU, isoZV, isoZW, isoZX, isoZY, isoZZ

Page 62 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7016	20043	33277	0.88	4.1E-01	U02298.1	NT	Mus musculus NIH 3T3 chemokine raties (Scya5) gene, complete cds
7836	20764	34067	2.97	4.1E-01	U87535.1	NT	Methanococcus jannaschii section 77 of 150 of the complete genome
8387	21291		0.47	4.1E-01	M84594.1	NT	Homo sapiens aromatic decarboxylase gene, exon 4
8613	21544	34886	1.69	4.1E-01	BF674604.1	EST_HUMAN	802133261F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288238 5'
9636	22562	35932	1.34	4.1E-01	6755521	NT	Mus musculus signaling intermediate in Toll pathway-evolutionarily conserved (Slpec-pending), mRNA
10094	22944		0.84	4.1E-01	AF160597.1	NT	Volavio gymnocaudus Vaym560 cytochrome b (cyb) gene, complete cds; mitochondrial gene for
10756	23642		1.52	4.1E-01	AL139076.2	NT	Campylobacter jejuni NGTC11168 complete genome; segment 3/8
10895	23780	37207	1.13	4.1E-01	AV649579.1	EST_HUMAN	AV649579 GLC Homo sapiens cDNA clone GLCBVD12 3'
10885	23869	37297	0.58	4.1E-01	P18594	SWISSPROT	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK56)
10885	23869	37298	0.58	4.1E-01	P18594	SWISSPROT	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK56)
11051	23935		1.01	4.1E-01	BF349382.1	EST_HUMAN	GM2-HT0137-200999-010-e08 HT0137 Homo sapiens cDNA
11277	24109	37651	80.3	4.1E-01	X58700.1	NT	Zea mays ZMFM52 gene for 19 kDa zein protein
11830	23966	37400	2.12	4.1E-01	Q09470	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (HUK1) (HBK1)
12803	25912		2.53	4.1E-01	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
148	15887		3.81	4.0E-01	AW847123.1	EST_HUMAN	RC2-CT0201-290999-012-d10 CT0201 Homo sapiens cDNA
1065	14108	27046	0.97	4.0E-01	8404656	NT	Laqueus rubellus mitochondrion, complete genome
1367	14399	27353	1.49	4.0E-01	AF203478.1	NT	Drosophila melanogaster Dalmation (dmt) mRNA, complete cds
1503	14534		5.87	4.0E-01	6679258	NT	Mus musculus platelet derived growth factor receptor, beta polypeptide (Pdgfrb), mRNA
2852	13247	26165	1.46	4.0E-01	6678480	NT	Mus musculus ubiquitin-protein ligase c3 componen n-recogin (Ubr1), mRNA
3009	16061	28964	1.35	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
		28965	1.35	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
3760	16792	29883	2.47	4.0E-01	AF068903.1	NT	Streptococcus pneumoniae Y1C (Y1C), penicillin-binding protein 2x (pbp2x), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide phospho-MurNAc-pentapeptide transferase (mraY) genes, complete cds
3901	16930	29808	4.68	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3901	16930	29809	4.68	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
4931	17930		11.58	4.0E-01	Q31849	SWISSPROT	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 6, CHLOROPLAST
6130	19189	32325	1.08	4.0E-01	AW070610.1	EST_HUMAN	EST1382691 MAGE sequences, MAGK Homo sapiens cDNA
6706	19742	32944	0.75	4.0E-01	P27285	SWISSPROT	STRUCTURAL POLYPEPTIDE (P130) [CONTAINS: COAT PROTEIN C ; SPIKE GLYCOPROTEINS E3, E2 AND E1; 6 KD PEPTIDE]
8507	21438	34778	0.51	4.0E-01	BF092834.1	EST_HUMAN	MR4-TN0110-180800-202-g02 TN0110 Homo sapiens cDNA
8590	21521	34866	1.1	4.0E-01	AB019625.1	NT	Homo sapiens OCTN2 gene, complete cds

Page 63 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9558	22485	35845	1.27	4.0E-01	AA323269.1	EST_HUMAN	EST26068 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
12001	24843		2.28	4.0E-01	BF030262.1	EST_HUMAN	601558283F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3828092 5'
12143	24863		2.52	4.0E-01	L76080.1	NT	Synechocystis sp. PCC 9413 transposase gene, complete cds
12503	25785		1.58	4.0E-01	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
1404	14435	27391	1.88	3.9E-01	AF206618.1	NT	Gorilla gorilla carboxyl-ester lipase (CEL) gene, complete cds
2690	15684	28683	3.5	3.9E-01	AB033019.1	NT	Homo sapiens mRNA for KIAA1193 protein, partial cds
2755	15746	28740	6.31	3.9E-01	X82032.1	NT	H. sapiens B-myb gene
2755	15745	28741	6.31	3.9E-01	X82032.1	NT	H. sapiens B-myb gene
3144	16184	28087	6.19	3.9E-01	AJ225896.1	NT	Sinorhizobium meliloti egf, syB2, cya3 genes and orf3
4168	17187	30060	1.82	3.9E-01	BF692611.1	EST_HUMAN	7161d01.x1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3339169 3'
5112	18109	30954	1.59	3.9E-01	BE728667.1	EST_HUMAN	601563948F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833699 5'
6157	19215	32355	4.8	3.9E-01	BF208036.1	EST_HUMAN	601862362F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4082055 5'
6532	19579	32758	0.56	3.9E-01	U82895.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
8532	21463	34803	1.02	3.9E-01	U79415.1	NT	Homo sapiens prepro dipeptidyl peptidase I (DPP-I) gene, complete cds
9420	22348	35713	0.83	3.9E-01	AW177011.1	EST_HUMAN	GM3-CT0105-170869-004-b08 CT0105 Homo sapiens cDNA
9428	22356		0.76	3.9E-01	BF348634.1	EST_HUMAN	602019944F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4155322 5'
9776	22700	36086	1.93	3.9E-01	AW196898.1	EST_HUMAN	xn86d04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701351 3' similar to TR:094821 O64821 KIAA0713 PROTEIN ;
10074	22889	36384	1.68	3.9E-01	AI937337.1	EST_HUMAN	wp76a02.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2467658 3' similar to SW:RFX6 HUMAN P49382 BINDING REGULATORY FACTOR ;
10390	23279	36700	3.46	3.9E-01	M19879.1	NT	Human clabindin 27 gene, exons 10 and 11, and L1 and Alu repeats
10662	23548	36992	0.7	3.9E-01	D66722.1	NT	Nicotiana tabacum mRNA for TATA binding protein (TBP), complete cds
10840	23726	37149	1.14	3.9E-01	BF381856.1	EST_HUMAN	GM2-NN0034-030600-218-h04 NN0034 Homo sapiens cDNA
10840	23726	37150	1.14	3.9E-01	BF381856.1	EST_HUMAN	GM2-NN0034-030600-218-h04 NN0034 Homo sapiens cDNA
11068	23952	37387	0.55	3.9E-01	M18440.1	NT	Human beta-B2-crystallin (B2-1) gene, exon 4, partial cds
11259	24182		2.64	3.9E-01	AV695974.1	EST_HUMAN	AV695974 GKO Homo sapiens cDNA clone GKO8QCC11 5'
12170	26006	36509	1.64	3.9E-01	AV702623.1	EST_HUMAN	AV702623 ADB Homo sapiens cDNA clone ADBD8E06 5'
12305	26851		3.39	3.9E-01	AF304354.1	NT	Homo sapiens proteoglycan 3 (PRG3) gene, complete cds
12888	25480		1.63	3.9E-01	11433335	NT	Homo sapiens hypothetical protein FLJ10583 (FLJ10583), mRNA
170	13271		3.69	3.8E-01	7019488	NT	Homo sapiens protein kinase PKNbeta (pkribeta), mRNA
528	13597		4.86	3.8E-01	AB029291.1	NT	Mus musculus pcm-1 mRNA for pericentriolar material-1, complete cds
1893	14814		1.11	3.8E-01	AE003870.1	NT	Xydia fastidiosa, section 16 of 229 of the complete genome

Page 64 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2606	15804	28598	1.22	3.8E-01	AF214117.1	NT	Arabidopsis thaliana putative c-myc-like transcription factor (MY33R-3) mRNA, complete cds
2679	15930	28673	5.44	3.8E-01	6878002	NT	Mus musculus solute carrier family 1, member 6 (Slc1a6), mRNA
3046	16098		22.67	3.8E-01	AJ251057.1	NT	Human immunodeficiency virus type 1 complete genome (isolate 98SE-MP1213)
3095	16149	29044	2.06	3.8E-01	AF043383.1	NT	Pleurocetes americanus aminopeptidase N (ampN) gene, partial cds
3542	16380	29483	10.02	3.8E-01	AL161518.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30
3599	16636		0.69	3.8E-01	AL161518.2	NT	wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3614	16636		1.21	3.8E-01	AI807219.1	EST_HUMAN	wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3820	16850	29734	1.38	3.8E-01	BE154080.1	EST_HUMAN	PMO-HT0339-200400-010-G01 HT0339 Homo sapiens cDNA
3900	17017	29906	0.98	3.8E-01	6754095	SWISSPROT	Mus musculus general transcription factor II (GTF2), mRNA
5804	18878	31983	1.03	3.8E-01	Q04899	NT	TRANSCRIPTION FACTOR SOX-10
6596	19637		0.5	3.8E-01	S46825.1	NT	p10n protein [pink, Genomic, 2448 nt]
6914	19944	33163	4.65	3.8E-01	BE072399.1	EST_HUMAN	QV3-BT0537-271299-049-a02 BT0537 Homo sapiens cDNA
7095	20271	33527	4.54	3.8E-01	AI374601.1	EST_HUMAN	ta54411.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2047917 3' similar to contains Alu repetitive element;
7270	20178	33421	1.15	3.8E-01	AL161513.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 25
7922	20845	34150	4.03	3.8E-01	AA626274.1	EST_HUMAN	zu88c05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745084 3'
7939	20851		4.31	3.8E-01	XG1597.1	NT	M. musculus gene for kallikrein-binding protein
8189	21096	34427	0.63	3.8E-01	V00693.1	NT	Yeast mitochondrial gene for ATPase (genes oil-2 and oil-4)
9120	22048	36407	3.24	3.8E-01	AB046851.1	NT	Homo sapiens mRNA for KIAA1631 protein, partial cds
9185	22113	35471	0.82	3.8E-01	11441264	NT	Homo sapiens FOS-like antigen-1 (FOSL1), mRNA
9376	22304	35665	1.45	3.8E-01	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
10090	22883		5.51	3.8E-01	T95413.1	EST_HUMAN	ye43h06.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120539 5' similar to contains Alu repetitive element; contains PTR5 repetitive element;
10190	23081	36492	0.84	3.8E-01	7305518	NT	Mus musculus Sfp1/PU.1 interaction partner (Sp1b), mRNA
11235	24161		1.72	3.8E-01	AV755814.1	EST_HUMAN	AV755814 BM Homo sapiens cDNA clone BMFCE07 5'
11965	24808		3.55	3.8E-01	BE719219.1	EST_HUMAN	RCO-HT0841-040800-032-b12 HT0841 Homo sapiens cDNA
12117	24958	38481	2.41	3.8E-01	R42950.1	EST_HUMAN	yf92h11.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30288 3'
12117	24958	38462	2.41	3.8E-01	R42950.1	EST_HUMAN	yf92h11.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30288 3'
12402	25233		2	3.8E-01	AE001124.1	NT	Borrelia burgdorferi (section 10 of 70) of the complete genome
12609	25870		1.71	3.8E-01	U94788.1	NT	Human p53 (TP53) gene, complete cds
12720	25368		1.88	3.8E-01	BE829256.1	EST_HUMAN	QV3-ET0063-190700-271-a05 ET0063 Homo sapiens cDNA
2504	15505	28507	10.48	3.7E-01	AB037831.1	NT	Homo sapiens mRNA for KIAA1410 protein, partial cds
3521	16559	29461	12.37	3.7E-01	AF056336.1	NT	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds
3539	16967	29850	0.64	3.7E-01	AA319482.1	EST_HUMAN	EST21715 Adrenal gland tumor Homo sapiens cDNA 5' end

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4329	17343	30209	12.09	3.7E-01	A1218707.1	EST_HUMAN	ok39c07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1510188 3'
4426	17437	30297	1.66	3.7E-01	AW878037.1	EST_HUMAN	MR3-OT0007-080300-704-502 OT0007 Homo sapiens cDNA
4497	17507	30373	2.68	3.7E-01	AE002408.1	NT	Neisseria meningitidis serogroup B strain MC58 section 50 of 206 of the complete genome
5971	19037	32158	1.22	3.7E-01	AF135187.1	NT	Homo sapiens interferon-induced protein p78 (MX1) gene, complete cds
6175	19232	32379	1	3.7E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6788	19821	33033	0.96	3.7E-01	M10806.1	NT	Chicken (White leghorn) delta-1 and delta-2 crystallin genes, complete cds
6809	19842		0.86	3.7E-01	L10363.1	NT	Mus saxicola heptoglobin mRNA, complete cds
7503	20442	33725	5.21	3.7E-01	11525843	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
7828	20757	34081	0.51	3.7E-01	BE873743.1	EST_HUMAN	601483887F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886652 5'
7828	20757	34082	0.51	3.7E-01	BE873743.1	EST_HUMAN	601483887F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886652 5'
8263	21188	34502	0.86	3.7E-01	T68802.1	EST_HUMAN	ye50a07.r3 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:65324 5'
8349	21254	34589	0.48	3.7E-01	AW511326.1	EST_HUMAN	hd45605.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912457 3' similar to contains Alu repetitive element-contains L1 L2 L1 repetitive element;
8904	21834	35189	2.31	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (G12ORF4), mRNA
8904	21834	35190	2.31	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (G12ORF4), mRNA
8937	21867	36226	0.76	3.7E-01	AA902912.1	EST_HUMAN	ok43b11.s1 NCI_CGAP_L12 Homo sapiens cDNA clone IMAGE:1516701 3'
8743	22867		1.67	3.7E-01	AJ271386.1	NT	Gallus gallus mRNA for beta-carotene 15,15'-dioxygenase (bcdo gene)
10666	23552		0.55	3.7E-01	X00691.1	NT	mouse Ig germline alpha membrane exons region
10706	23592	37019	4.2	3.7E-01	A1336411.1	EST_HUMAN	q45b07.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1950997 3'
11291	24211	37660	1.8	3.7E-01	X05958.1	NT	Rabbit mRNA for fast skeletal muscle myosin heavy chain (MHC)
11471	24384	37832	5.03	3.7E-01	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
11471	24384	37833	5.03	3.7E-01	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
11898	23998	37436	2.46	3.7E-01	X04122.1	NT	Bovine mRNA for terminal deoxynucleotidyltransferase (TdT) (EC 2.7.7.31)
12100	24941	38444	2.93	3.7E-01	D78348.1	EST_HUMAN	HUM230A08B Human aorta polyA+ (TF-ujwara) Homo sapiens cDNA clone GEN-230A08 5'
12126	24967		1.9	3.7E-01	AA973540.1	EST_HUMAN	cc46d03.s1 NCI_CGAP_Lu8 Homo sapiens cDNA clone IMAGE:1569221 3' similar to gb:M77698
12182	25018		3.08	3.7E-01	6877678	NT	TRANSCRIPTIONAL REPRESSOR PROTEIN YY1 (HUMAN);
12386	25164		4.15	3.7E-01	AJ243525.1	NT	Mus musculus retinoblastoma 1 (Rb1), mRNA
12470	25216		1.98	3.7E-01	D86076.1	NT	Chlamydomonas reinhardtii partial omp1 gene for outer membrane protein 1
12613	25435		2.7	3.7E-01	AL121154.1	EST_HUMAN	Human mRNA for KIAA0223 gene, partial cds
12876	25475	31162	2.36	3.7E-01	Y18000.1	NT	DKFZp762k075_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762k075 6'
280	13374	26289	0.75	3.6E-01	AJ009609.1	NT	Homo sapiens NF2 gene
1023	14072		6.82	3.6E-01	U89241.1	NT	Brassica napus mRNA for MAPK alpha2 protein
1340	14373	27325	4.1	3.6E-01	T80255.1	EST_HUMAN	Human mbp gene, partial cds
							yc03e05.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443 5'

Page 66 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1340	14373	27326	4.1	3.6E-01	T80265.1	EST_HUMAN	y03e05.t1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443 5'
1932	14953	27929	5.21	3.6E-01	AW590184.1	EST_HUMAN	hg3302.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2947419 3'
1932	14953	27930	5.21	3.6E-01	AW590184.1	EST_HUMAN	hg3302.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2947419 3'
1966	14984	27968	4.68	3.6E-01	AF216207.1	NT	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds
2288	16266		1.56	3.6E-01	AB002321.1	NT	Human mRNA for KIAA0323 gene, partial cds
2413	15417		2.44	3.6E-01	X76725.1	NT	P. irregularis (P3804) gene for actin
2497	15489	28489	1.31	3.6E-01	L05435.1	NT	Rattus norvegicus synaptic vesicle protein (SV2) mRNA, complete cds
2497	15489	28500	1.31	3.6E-01	L05435.1	NT	Rattus norvegicus synaptic vesicle protein (SV2) mRNA, complete cds
2510	15511	28514	1.77	3.6E-01	AW812033.1	EST_HUMAN	RC5-ST0171-181099-011-g07 ST0171 Homo sapiens cDNA
							PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)
2677	15673	28671	1.69	3.6E-01	P24206	SWISSPROT	Drosophila melanogaster sugar transporter 3 (sut3) mRNA, complete cds
2942	18409		10.87	3.6E-01	AF199485.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
3530	16568	29471	1.92	3.6E-01	X76758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
3530	16568	29472	1.92	3.6E-01	X76758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
4514	17523	30388	1.24	3.6E-01	BE707883.1	EST_HUMAN	RC1-HT0545-156600-014-b12 HT0545 Homo sapiens cDNA
4854	17856	30721	0.8	3.6E-01	AJ00609.1	NT	Brassica napus mRNA for MAP4K alpha2 protein
5131	18127	30969	3.83	3.6E-01	AW339393.1	EST_HUMAN	ha02g04.x1 NCI_CGAP_LU24 Homo sapiens cDNA clone IMAGE:2872566 3'
5240	18227	31076	0.88	3.6E-01	BE067698.1	EST_HUMAN	MR4-BT0358-270300-005-c10 BT0358 Homo sapiens cDNA
5567	18645	31523	0.75	3.6E-01	AJ006565.1	NT	Homo sapiens lipo gene intron 5
							FORMATE HYDROGENLYASE SUBUNIT 5 PRECURSOR (PHL SUBUNIT 5) (HYDROGENASE-3 COMPONENT E)
6323	19373	32541	0.92	3.6E-01	P16431	SWISSPROT	Homo sapiens PHX gene
6752	19766	32998	1.55	3.6E-01	Y10136.1	NT	y174a08.t1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:275987 5'
7508	20447		3.84	3.6E-01	R94090.1	EST_HUMAN	wf72c10.x1 Soares thymus_NHFTn Homo sapiens cDNA clone IMAGE:2513010 3' similar to TR:O15117
							O15117 FYN BINDING PROTEIN. [1];
7662	20596	33895	1.47	3.6E-01	AW027174.1	EST_HUMAN	xa94h12.x1 NCI_CGAP_Cot17 Homo sapiens cDNA clone IMAGE:2574503 3' similar to contains element
							MER5 repetitive element;
8270	21175	34510	0.47	3.6E-01	AW079100.1	EST_HUMAN	SCO-SPONDIN
8802	21732	35081	0.74	3.6E-01	P98167	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79
8855	21785	35134	8.06	3.6E-01	AL161583.2	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (-HLA-H) gene, RoRat gene, and sodium phosphate transporter (NP T3) gene, complete cds
9530	22457	35819	0.57	3.6E-01	U91328.1	NT	



Page 67 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9530	22457	35820	0.57	3.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
9554	22481	35840	3.22	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
9554	22481	35841	3.22	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
9734	22859	36042	1.47	3.6E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9935	22840	36228	1.05	3.6E-01	X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
9935	22840	36229	1.05	3.6E-01	X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
10002	22819		0.7	3.6E-01	X62825.1	NT	C. perfringens plc gene for phospholipase C upstream region containing bent DNA fragment
10377	23268	36688	20.27	3.6E-01	Q53194	SWISSPROT	PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TS
11383	24299	37745	1.94	3.6E-01	BE002390.1	EST_HUMAN	601676418F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958897 5'
11550	24459	37622	3.81	3.6E-01	AB004293.1	NT	Arabidopsis thaliana mRNA for Sig8, complete cds
11877	23977	37415	2.68	3.6E-01	AE000659.1	NT	Methanobacterium thermoautotrophicum from bases 702375 to 714311 (section 62 of 148) of the complete genome
12260	25970		4.08	3.6E-01	Y19210.1	NT	Homo sapiens hrb5 gene for hair keratin, exons 1 to 9
12340	25135		7.58	3.6E-01	AE000335.1	NT	Escherichia coli K-12 MG1655 section 225 of 400 of the complete genome
12478	25222		3.44	3.6E-01	U66888.1	NT	Mus musculus Emr1 mRNA, complete cds
12819	25439		1.61	3.6E-01	11432598	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 10 (AF10), mRNA
119	13227	26139	1.45	3.5E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
222	13321	26237	2.31	3.5E-01	8678933	NT	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA
701	13760	26677	4.76	3.5E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
748	13805	26730	1.48	3.5E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
748	13805	26731	1.48	3.5E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
806	13882	26787	3.87	3.5E-01	BF129796.1	EST_HUMAN	601811060R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053951 3'
1642	14673	27638	1.06	3.5E-01	BF310688.1	EST_HUMAN	601894653F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124244 5'
1566	14696	27656	0.95	3.5E-01	U35776.1	NT	Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds
2302	15310	28316	0.99	3.5E-01	P06799	SWISSPROT	HOMEOBOX PROTEIN HOX-A4 (HOX-1.4) (MH-3)
2848	15929	28643	1.14	3.5E-01	AA223252.1	EST_HUMAN	zr08a08.s1 Sitalagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650872 3'
3873	16902		0.91	3.5E-01	AA642138.1	EST_HUMAN	tr50d03.s1 NCL CGAP_Lym3 Homo sapiens cDNA clone IMAGE:1172957 3'

Page 68 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4362	17376	30239	2.6	3.5E-01	AF071253.1	NT	Danio rerio homeobox protein (hoxb5b) gene, complete cds
5044	18041	30997	4.88	3.5E-01	M18349.1	NT	Rat leukocyte common antigen (L-CA) gene, exons 1 through 5
5328	18312	31161	1.47	3.5E-01	H12004.1	EST_HUMAN	ym1h12.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:47811 3'
5517	18596	31444	1.21	3.5E-01	Q86987	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5517	18596	31445	1.21	3.5E-01	Q86687	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5741	18814	31910	1.31	3.5E-01	D42045.1	NT	Human mRNA for KIAA0086 gene, complete cds
6485	19530		1.02	3.5E-01	AW863918.1	EST_HUMAN	PM4-SN0012-030400-001-af1 SN0012 Homo sapiens cDNA
6673	19710	32905	0.59	3.5E-01	AA431833.1	EST_HUMAN	zw78f03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782428 5' similar to TR:G1066935 G1066935 F10F2.1
6721	19757	32964	0.64	3.5E-01	U37150.1	NT	Bos taurus peptide methionine sulfoxide reductase (msrA) mRNA, complete cds
6958	19987	33211	0.92	3.5E-01	O24357	SWISSPROT	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHLOROPLAST PRECURSOR (G6PD)
7409	20108	34205	2.9	3.5E-01	X98505.1	NT	S.scrofa mRNA for CD31 protein (PECAM-1)
7971	20893	34206	0.55	3.5E-01	P47281	SWISSPROT	HISTIDYL-TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS)
8214	21119	34452	0.54	3.5E-01	X06091.1	NT	HISTIDYL-TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS)
8849	21580		2.72	3.5E-01	11448042	NT	E. coli L-arabinose transport operon with genes araF, araG and araH
8852	21583	34918	0.69	3.5E-01	BF359871.1	EST_HUMAN	Homo sapiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA
9036	21965		0.79	3.5E-01	AF051561.1	NT	RC4-ET0024-260600-014-007 ET0024 Homo sapiens cDNA
9482	22410	35771	1.34	3.5E-01	4507610	NT	Rattus norvegicus Na-K-Cl cotransporter (Nkccl) mRNA, complete cds
10256	23146	36554	1.96	3.5E-01	Q02294	SWISSPROT	Homo sapiens tyrosine kinase non-receptor 1 (TNK1), mRNA
10398	23287	36709	5.09	3.5E-01	Z26825.1	NT	VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L
10473	23361	36775	0.89	3.5E-01	BE174794.1	EST_HUMAN	TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL III) (BII)
11176	24102	37548	3.66	3.5E-01	X51084.1	NT	X.laevis gene for albumin including HP1 enhancer
11462	24377	37826	2.05	3.5E-01	AJ243178.1	NT	QV2-HT0577-090400-128-c07 HT0577 Homo sapiens cDNA
11462	24377	37827	2.06	3.5E-01	AJ243178.1	NT	C.griseus rhodopsin gene for opsin protein
11953	24797	38297	1.51	3.5E-01	U07000.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
12022	24884	38365	1.98	3.5E-01	N77597.1	EST_HUMAN	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
12044	24885		1.74	3.5E-01	M82885.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
12109	24950	38453	1.62	3.5E-01	L05145.1	NT	yz90h12.r1 Soares_multiple_sclerosis_2NBHMSF Homo sapiens cDNA clone IMAGE:290375 5'
12351	25973		2.69	3.5E-01	AF297488.1	NT	Drosophila melanogaster dual bar protein (BarH2) gene, exon 1
12413	25182		4.57	3.5E-01	X64595.1	NT	Human glucokinase (GCK) gene, repeat polymorphism
12559	25271		1.93	3.5E-01	AE001774.1	NT	Schistosoma mansoni strain NMRI chromatin assembly factor 1 small subunit-like protein (RBAP48) mRNA, complete cds
						NT	B.taurus atpA1 gene for F10F1(1) ATP synthase alpha-subunit
						NT	Thermotoga maritima section 88 of 136 of the complete genome

Page 69 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13094	25827	31486	2.82	3.5E-01	H80814.1	EST_HUMAN	y56411.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5'
13094	25827	31487	2.82	3.5E-01	H80814.1	EST_HUMAN	y56411.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5'
730	13788		1.78	3.4E-01	AJ242956.1	NT	Homo sapiens partial N-myo (exon 3), HPV45 L2, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line
1002	14051	26995	5.28	3.4E-01	Y09798.2	NT	Pseudomonas fluorescens colR, colS genes, orf222 and partial lhaA gene
1004	14053	26997	21.9	3.4E-01	AW380120.1	EST_HUMAN	Q73-HT0261-241199-019-g10 HT0261 Homo sapiens cDNA
1354	14386	27339	1.3	3.4E-01	Y00554.1	NT	Azotobacter vinelandii nifA gene for NifA protein (positive regulatory element)
2423	15427	28428	2.47	3.4E-01	D90909.1	NT	Synechocystis sp. PCC8803 complete genome, 11/27, 1311235-1430418
3044	16096	28998	0.72	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3044	16096	28999	0.72	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3181	16240	29135	0.98	3.4E-01	D90909.1	NT	Synechocystis sp. PCC8803 complete genome, 11/27, 1311235-1430418
3204	16252	29148	7.69	3.4E-01	U83905.1	NT	Canis familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNGC1) mRNA, complete cds
3382	16435	29338	0.94	3.4E-01	AF034862.1	NT	Homo sapiens pulmonary surfactant protein D, promoter region and exon 1
3593	16630	29534	5.01	3.4E-01	AF106835.1	NT	Methylovorus sp. strain S81 putative GrpE (grpE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds
3855	16884		1.31	3.4E-01	BF449010.1	EST_HUMAN	7n94a01.x1 NCL_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q9UJ15
4136	17157		1.82	3.4E-01	AA584198.1	EST_HUMAN	Q9UJ15 DJ1809.1
4614	17622	30485	1.13	3.4E-01	AF166341.1	NT	nc11b10.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100347 3'
4755	17780	30822	2.1	3.4E-01	BE069912.1	EST_HUMAN	Homo sapiens integrin alpha 6 (ITGA6) gene, exons 12 through 23
4771	17776	30644	1.42	3.4E-01	BF314689.1	EST_HUMAN	MIR4-BT0403-230200-202-c01 BT0403 Homo sapiens cDNA
5067	18064		6.1	3.4E-01	A1240973.1	EST_HUMAN	601801632F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130835 5'
5256	18242		0.66	3.4E-01	AA587031.1	EST_HUMAN	q95c05.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1867208 3' similar to contains Alu repetitive element
5373	18355	31195	1.16	3.4E-01	AW002545.1	EST_HUMAN	hnr73g04.s1 NCL_CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1089558 3' similar to gb:M98776_rna1
5882	18951	32037	2.72	3.4E-01	AL161594.2	NT	KERATIN, TYPE II CYTOSKELETAL 1 (HUMAN);
6022	19084		4.43	3.4E-01	AA085313.1	EST_HUMAN	wu10012.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2516587 3' similar to TR:Q13537 Q13537 SIMILAR TO POGO ELEMENT.;
6239	19293		2.27	3.4E-01	U02971.1	NT	AraBidopsis thaliana DNA chromosome 4, contig fragment No. 90
6263	19314	32479	0.83	3.4E-01	BE748912.1	EST_HUMAN	zn12d11.s1 Stralagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:547221 3'
6346	19396	32563	2.27	3.4E-01	AW204505.1	EST_HUMAN	Echovirus 22 1AB, 1C, 1D, 2A, 2B, 2C, 3A, 3B, 3C, 3D proteins RNA, complete mature peptides and cds
							601571811T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838826 3'
							UI-P-B11-aa1-e-12-0-UI.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2710682 3'

Page 70 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6482	19527	32705	1.82	3.4E-01	AL120544.1	EST_HUMAN	DKFZp761A249_1 761 (synonym: hamy2) Homo sapiens cDNA clone IMAGE:4249365 5'
7047	20073		1.3	3.4E-01	N95225.1	EST_HUMAN	Z63612.s1 Soares fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:307342 3'
7279	20232	33482	1.22	3.4E-01	AI468082.1	EST_HUMAN	Im63p05.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162840 3' similar to gb:S37431
7473	20112	33346	0.48	3.4E-01	BF678702.1	EST_HUMAN	LAMININ RECEPTOR (HUMAN);
7886	20812	34118	0.41	3.4E-01	BE971699.1	EST_HUMAN	602085283F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249365 5'
8485	21416		0.61	3.4E-01	AE000493.1	NT	601651613R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934947 3'
8814	21744	35092	0.77	3.4E-01	Y14930.1	NT	Escherichia coli K-12 MG1695 section 383 of 400 of the complete genome
9056	21985		2	3.4E-01	AA337083.1	EST_HUMAN	Homo sapiens TORAY28 gene, allele A4, partial
9126	22054	35414	1.25	3.4E-01	L04890.1	NT	EST141765 Endometrial tumor Homo sapiens cDNA 5' end
9411	22339	35703	1.9	3.4E-01	P26013	SWISSPROT	Oriculus griseus cholesterol 7-alpha-hydroxylase gene, complete cds
9753	22677	36062	4.32	3.4E-01	P26013	SWISSPROT	Bovine enterovirus strain K2577, complete genome
9956	22860		0.63	3.4E-01	AB017510.1	NT	INTEGRIN BETA-8 PRECURSOR
9979	21337	34672	5.71	3.4E-01	U19492.1	NT	INTEGRIN BETA-8 PRECURSOR
9978	21337	34673	5.71	3.4E-01	U19492.1	NT	Ephydaria fluviatilis mRNA for PLC-gammaS, complete cds
10218	23109	36510	0.93	3.4E-01	U68763.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
10401	23290	36713	1.51	3.4E-01	AJ225084.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
10956	23840		0.74	3.4E-01	AE004096.1	NT	Glycine max putative transcription factor SCOF-1 (scf-1) mRNA, complete cds
11455	24371		4.38	3.4E-01	AE000881.1	NT	Homo sapiens FAA gene, exon 16, 17 and 18
11491	24403	37854	3.01	3.4E-01	P06925	SWISSPROT	Vibrio cholerae chromosome I, section 4 of 251 of the complete chromosome
11534	24444	37905	2.43	3.4E-01	AF045981.1	NT	Methanobacterium thermoautotrophicum from bases 1018444 to 1029212 (section 87 of 148) of the complete genome
11729	24631	38111	1.82	3.4E-01	M25856.1	NT	PROBABLE E4 PROTEIN
11729	24631	38112	1.82	3.4E-01	M25856.1	NT	Rutillus arcasii cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11930	24775	38273	2.47	3.4E-01	AB035507.1	NT	Human von Willebrand factor gene, exons 36 and 37
11958	24801	38299	3.9	3.4E-01	AL161515.2	NT	Human von Willebrand factor gene, exons 36 and 37
12192	25027	38528	1.84	3.4E-01	BF061948.1	EST_HUMAN	Rattus norvegicus mRNA for s-glycerolMUC18, complete cds
12242	25066		2.46	3.4E-01	U93604.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
12344	25137		1.49	3.4E-01	Z21621.1	NT	7k69d12.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:3480646 3'
12433	25733		1.82	3.4E-01	AF254351.1	NT	Citrus variegata virus putative replicase gene, partial cds
12541	25261		12.67	3.4E-01	L26339.1	NT	S.cerevisiae RIB5 gene encoding Riboflavin synthase
						NT	Schizosaccharomyces pombe Cwf8p (cwf8) gene, complete cds
						NT	Human autoantigen mRNA, complete cds

Page 71 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12568	25758		3.15	3.4E-01	BE218652.1	EST_HUMAN	hV42H08.X1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176127 3' similar to contains PTR5.13
12620	25847		2.91	3.4E-01	9838361	NT	PTR5 repetitive element ;
12725	25370	31801	1.9	3.4E-01	AJ297131.1	NT	Beta vulgaris mitochondrion, complete genome
12921	25930		1.45	3.4E-01	AJ288948.1	NT	Mus musculus SIL_MAP_17, CYP_5, SCL & CYP_b genes
							Clostridium cellulosilyticum partial spoIVB gene and spoOA gene, strain ATCC 35319
							Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK2W), RD, complement factor B (Bf), and complement component C2 (C2) genes;>
13002	25554		2.08	3.4E-01	AF019413.1	NT	Naegleria gruberi mitochondrion, complete genome
13101	25616		1.62	3.4E-01	11466174	NT	Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene
16	13130	26016	5.42	3.3E-01	X07890.1	NT	Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene
109	13130	26016	4.93	3.3E-01	X07890.1	NT	Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene
470	13541	26464	0.93	3.3E-01	AL161545.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
656	13718	26629	2.53	3.3E-01	7862485	NT	Homo sapiens KIAA1100 protein (KIAA1100), mRNA
1228	14265	27209	3.64	3.3E-01	Q12446	SWISSPROT	PROLINE-RICH PROTEIN LAS17
1333	14367	27317	4.03	3.3E-01	BF588880.1	EST_HUMAN	602184016T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300251 3'
1628	14658	27621	1	3.3E-01	6753685	NT	Mus musculus uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase) (UMPS) mRNA
2428	15432		4.56	3.3E-01	4507834	NT	Bacteriophage phi-Yeo3-12 complete genome
2991	16043	28947	1.96	3.3E-01	AJ251805.1	NT	INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 35 KD SUBUNIT) (CLMF P35)
3060	16112		0.72	3.3E-01	O02743	SWISSPROT	Streptomyces argillaceus mithramycin biosynthetic genes
3103	16154	29050	0.99	3.3E-01	AJ007632.2	NT	Homo sapiens MTA1-L1 gene, complete cds
3554	16582	29497	1.71	3.3E-01	AB012922.1	NT	EXODEOXYRIBONUCLEASE V BETA CHAIN
3877	16906	29787	2.5	3.3E-01	O84845	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (HC-PRO); PROTEIN P3]
3889	16918	29795	1.01	3.3E-01	P22602	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4048	17075	29951	1.57	3.3E-01	AL161499.2	NT	Hypoxylon fragiforme chitin synthase gene, partial cds
4087	17112	29990	1.92	3.3E-01	AF200448.1	NT	Homo sapiens RAS protein activator like 1 (GAP1 like) (RASAL1) mRNA
4389	17403		1.1	3.3E-01	4759026	NT	Rattus norvegicus DNA for regucalcin, partial cds
4474	17485		1.79	3.3E-01	D31662.1	NT	ip78b12.x1 NCL CGAP_U03 Homo sapiens cDNA clone IMAGE:2205407 3' similar to gb.X57522 ANTIGEN PEPTIDE TRANSPORTER 1 (HUMAN);
4800	17801		1.4	3.3E-01	AJ539114.1	EST_HUMAN	Synechocystis sp. PCC6803 complete genome, 22/27, 2755703-2868766
4952	17950	30808	1.12	3.3E-01	D64003.1	NT	

Page 72 of 545  
Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5354	18337		0.97	3.3E-01	AF038547.2	NT	Bacillus stearothermophilus beta-1, 4-mannanase (manF), esterase (esA), transcription regulator (repA), and
5507	18586	31434	2.28	3.3E-01	X89819.1	NT	alpha-galactosidase (galA) genes, complete cds
5507	18586	31435	2.28	3.3E-01	X89819.1	NT	R.norvegicus mRNA for 3'UTR of ubiquitin-like protein
5777	18849	31954	0.97	3.3E-01	P39055	SWISSPROT	R.norvegicus mRNA for 3'UTR of ubiquitin-like protein
5777	18849	31955	0.97	3.3E-01	P39055	SWISSPROT	DYNAMIN
5997	19062	32190	0.64	3.3E-01	BF213873.1	EST_HUMAN	DYNAMIN
6171	19228	32373	1.45	3.3E-01	BE619650.1	EST_HUMAN	601848090F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:4078823 5'
6171	19228	32374	1.45	3.3E-01	BE619650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
6271	19322	32487	49.51	3.3E-01	P05691	SWISSPROT	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
7101	20307	33566	0.69	3.3E-01	AB034233.1	NT	CIRCUMSPOROZOITE PROTEIN (CS)
7101	20307	33567	0.69	3.3E-01	AB034233.1	NT	Flexibacter littoralis gyrB gene for DNA gyrase B subunit, partial cds
7216	20216	33462	4.71	3.3E-01	AI628131.1	EST_HUMAN	Flexibacter littoralis gyrB gene for DNA gyrase B subunit, partial cds
7218	20216	33463	4.71	3.3E-01	AI628131.1	EST_HUMAN	ty84h01.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2288809 3' similar to contains Alu repetitive element; contains element L1 repetitive element ; repetitive element; contains element L1 repetitive element ;
8258	21161	34494	1.95	3.3E-01	N85146.1	EST_HUMAN	ty84h01.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2288809 3' similar to contains Alu repetitive element; contains element L1 repetitive element ;
9125	22053	35413	21.18	3.3E-01	BF683954.1	EST_HUMAN	J2488F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2498 5' similar to TEGT
9288	22216	35574	0.62	3.3E-01	BF210322.1	EST_HUMAN	602140372F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301800 5'
9320	22248	35511	0.54	3.3E-01	AU126115.1	EST_HUMAN	601879281F1 NIH_MGC_64 Homo sapiens cDNA clone IMAGE:4097180 5'
9320	22248	35512	0.54	3.3E-01	AU126115.1	EST_HUMAN	AU126115 NT2RP1 Homo sapiens cDNA clone NT2RP1000130 5'
9658	22584	35955	0.86	3.3E-01	Q52925	SWISSPROT	AU126115 NT2RP1 Homo sapiens cDNA clone NT2RP1000130 5'
9917	22905	36293	1.28	3.3E-01	BE828461.1	EST_HUMAN	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 (MAPK/ERK KINASE 1) (MEK KINASE 1) (MEKK 1)
9917	22905	36294	1.28	3.3E-01	BE828461.1	EST_HUMAN	KINASE 1) (MEKK 1)
10042	22942	36330	3.16	3.3E-01	N69866.1	EST_HUMAN	CM3-ET0041-180500-187-410 ET0041 Homo sapiens cDNA
10081	22874	36262	2.52	3.3E-01	BF376745.1	EST_HUMAN	CM3-ET0041-180500-187-410 ET0041 Homo sapiens cDNA
10497	23385		1.56	3.3E-01	L41044.1	NT	za67h01.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:297649 3'
11164	24092	37530	2.42	3.3E-01	X63953.1	NT	RC4-TN0077-250800-011-g04 TN0077 Homo sapiens cDNA
11465	24379		2.27	3.3E-01	BF526498.1	EST_HUMAN	Homo sapiens high-mobility group phosphoprotein (HMG1-C) gene, exons 1-3, complete cds
11680	24584	38061	8.39	3.3E-01	BE219331.1	EST_HUMAN	D.mauritiana Adh gene
						NT	D.mauritiana Adh gene
						EST_HUMAN	602070802F1 NCL_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4213585 5'
						EST_HUMAN	hvs1g02.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176978 3'

Page 73 of 545  
Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descripbr
11785	24707	38199	4.62	3.3E-01	P47953	SWISSPROT	GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (ICE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (CBP30)
12140	24980		3.98	3.3E-01	AA806621.1	EST_HUMAN	ab71902.s1 NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336850 3'
12159	13130	26016	1.87	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5.J1 nodX gene
12995	25549		25.89	3.3E-01	AF000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position (277)
479	13550		1.75	3.2E-01	AF018261.1	NT	Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds
741	13799		1.34	3.2E-01	AL161591.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
1189	14228	27167	15.88	3.2E-01	AF047013.1	NT	Fusarium poae virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds
1308	14341	27289	2.22	3.2E-01	Z50202.1	NT	P.vulgaris arc5-1 gene
1417	14448	27402	5.67	3.2E-01	Q48624	SWISSPROT	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1659	14689		0.98	3.2E-01	AF209730.1	NT	Arabidopsis thaliana cultivar Columbia RPP13 (RPP13) gene, complete cds
1799	14825	27193	1.19	3.2E-01	Z35041.1	NT	S.cerevisiae chromosome II reading frame ORF YBR172c
1808	14834	27804	4.71	3.2E-01	AW957194.1	EST_HUMAN	EST369264 MAGE resequencing, MAGD Homo sapiens cDNA
1808	14834	27805	4.71	3.2E-01	AW957194.1	EST_HUMAN	EST369264 MAGE resequencing, MAGD Homo sapiens cDNA
1868	14890	27870	1.33	3.2E-01	AL111655.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2173	15185	28190	2.66	3.2E-01	BF203817.1	EST_HUMAN	801868804F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111612 5'
2572	15570		2.76	3.2E-01	7710079	NT	Mus musculus Pbx/knotted 1 homeobox (Pbxox1), mRNA
2759	15750	28746	1.72	3.2E-01	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
3671	16704		1.03	3.2E-01	D10872.1	NT	Human h NAT allele 3-2 gene for arylamine N-acetyltransferase
4501	17511	30377	1.77	3.2E-01	M18818.1	NT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4587	17595	30453	0.74	3.2E-01	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
4619	17627	30491	1.69	3.2E-01	Q10268	SWISSPROT	HYPOTHETICAL 81.7 KD PROTEIN C13G7.04C IN CHROMOSOME 1 PRECURSOR
4850	17852		6.43	3.2E-01	BF693617.1	EST_HUMAN	602081972F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246505 5'
5153	18146	30991	0.94	3.2E-01	BE762748.1	EST_HUMAN	601465591F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3668799 5'
5464	18535	31377	3.04	3.2E-01	BE173994.1	EST_HUMAN	CMO-HT0669-060300-289-f10 HT0669 Homo sapiens cDNA
6183	19240	32387	1.24	3.2E-01	L27221.1	NT	Giardia intestinalis pyruvate:flavodoxin oxidoreductase and flanking genes
6477	19522	32699	0.52	3.2E-01	BE383518.1	EST_HUMAN	601297331F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3627462 5'
6477	19522	32700	0.52	3.2E-01	BE383518.1	EST_HUMAN	601297331F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3627462 5'
6558	19600	32786	0.76	3.2E-01	AF016494.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c?

Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6881	19911	33127	0.67	3.2E-01	AV718037.1	EST_HUMAN	A/718037 FHTA Homo sapiens cDNA clone FHTAABH01 5'
7037	20063		1.44	3.2E-01	AB002359.1	NT	Human mRNA for KIAA0361 gene, KIAA0361 protein
8439	21371	34712	0.57	3.2E-01	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
8750	21680	35023	1.69	3.2E-01	M60266.1	NT	Rat ISO-alpha natriuretic factor gene, complete cds
8842	21772	35119	0.56	3.2E-01	AJ231001.1	NT	Rattus norvegicus repeat; map NOS-D12Wox1
8939	21869	35227	15.44	3.2E-01	X02508.1	NT	H. sapiens gene fragment for acetylcholine receptor (AChR) alpha subunit exons 8, 9 and 3' flanking region
8942	21872	35232	15.28	3.2E-01	BF311635.1	EST_HUMAN	601897107F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126633 5'
9030	21959		1.7	3.2E-01	AL161574.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 70
9067	21998	36349	1.42	3.2E-01	BF248771.1	EST_HUMAN	601855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4076627 5'
9087	21998	35350	1.42	3.2E-01	BF248771.1	EST_HUMAN	601855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4076627 5'
9136	22084	35424	1.47	3.2E-01	AE002015.1	NT	Dainococcus radiodurans R1 section 152 of 228 of the complete chromosome 1
9239	22157	35510	0.85	3.2E-01	U51026.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH6-a2) gene, partial cds
9229	22157	35511	0.85	3.2E-01	U51026.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH6-a2) gene, partial cds
9619	22545	35918	0.62	3.2E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9625	22551		2.39	3.2E-01	M86511.1	NT	Human monocyte antigen CD14 (CD14) mRNA, complete cds
9693	22618	35995	0.62	3.2E-01	AF041829.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
9693	22618	35996	0.62	3.2E-01	AF041829.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
10499	23387	36797	3.21	3.2E-01	U44914.1	NT	Borrelia burgdorferi plasmid op32-2, erpC and erpD genes, complete cds; and unknown genes
10695	23581	37011	0.68	3.2E-01	BE326230.1	EST_HUMAN	h99f05.x1 NCL CGAP Lu24 Homo sapiens cDNA clone IMAGE:3181599 3'
10800	23686		3.96	3.2E-01	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
11112	24042	37487	3.28	3.2E-01	T06813.1	EST_HUMAN	EST04702 Fetal brain, Striatum (cat#936206) Homo sapiens cDNA clone HFB0221
12365	25872		4.58	3.2E-01	L07289.1	NT	Drosophila melanogaster laminin A (Lam-A) mRNA, complete cds
12844	25456		3.57	3.2E-01	O83217	SWISSPROT	ELONGATION FACTOR TU (EF-TU)
12934	25716		1.71	3.2E-01	AF157825.1	NT	Bos taurus Insulin 1,4-5-trisphosphatase receptor type I mRNA, complete cds
12977	25537		1.49	3.2E-01	L39874.1	NT	Homo sapiens deoxydicyclate deaminase gene, complete cds
13024	25904	31364	1.48	3.2E-01	BE385778.1	EST_HUMAN	601275480F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3616746 5'
2720	15713	28712	3.72	3.1E-01	R18051.1	EST_HUMAN	ye90h06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125051 5' similar to
2748	15862	28733	3.75	3.1E-01	7661971	NT	gib:M64241 QM PROTEIN (HUMAN)
2748	15862	28734	3.75	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2800	15954		1.33	3.1E-01	AW629036.1	EST_HUMAN	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA



Single Exon Probes Expressed in Adult Liver

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3216	18264		4.39	3.1E-01	AB029069.1	NT	Mus musculus gene for Ser/Thr kinase KKIAMRE, exon 6
3981	17009	29897	0.95	3.1E-01	AJ251886.1	NT	Daucus carota mRNA for transcription factor E2F (E2F gene)
5034	18031	30888	0.89	3.1E-01	S68245.1	NT	carbonic anhydrase IV [rats, Sprague-Dawley, lung, mRNA, 1205 nt]
5076	18073	30922	0.86	3.1E-01	AE003894.1	NT	Xylella fastidiosa, section 130 of 229 of the complete genome
5184	18176	31021	0.95	3.1E-01	AL161603.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
5666	18740	31649	10.28	3.1E-01	AF176111.1	NT	Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3A) gene, exon 1
5794	18966	31974	0.67	3.1E-01	P44132	SWISSPROT	HYPOTHETICAL PROTEIN H11238
5795	18987	31975	0.85	3.1E-01	Z74883.1	NT	S. cerevisiae chromosome XV reading frame ORF YOL141w
5806	18978		0.89	3.1E-01	Y13278.1	NT	Mus musculus mRNA for polyeyelin
5980	19045	32168	2.26	3.1E-01	AF184122.1	NT	Homo sapiens filamin 2 (FLN2) gene, exons 10 through 22
6537	25650	32764	0.53	3.1E-01	R94322.1	EST_HUMAN	y44104.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:198367 5'
6739	19773	32984	1.41	3.1E-01	AW983549.1	EST_HUMAN	RC3-HN0001-310300-011-b04 HN0001 Homo sapiens cDNA
6812	19845	33055	0.98	3.1E-01	A1264458.1	EST_HUMAN	q359d01.x1 NCL_CGAP_Cos8 Homo sapiens cDNA clone IMAGE:1874689 3'
6979	20006	33238	0.62	3.1E-01	X71887.1	NT	H. sapiens gene for immunoglobulin kappa light chain variable region A8 and A9
7071	20277		1.1	3.1E-01	AW373564.1	EST_HUMAN	MR2-CT0222-281093-005-h05 CT0222 Homo sapiens cDNA
7307	25625	31297	2.34	3.1E-01	BE737392.1	EST_HUMAN	601308121F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640420 5'
8132	21042	34372	0.71	3.1E-01	4885390	NT	Homo sapiens hyaluronan synthase 2 (HAS2), mRNA
8230	21135	34467	0.45	3.1E-01	AF242431.1	NT	Mus musculus neuronal apoptosis inhibitory protein 6 (Nalip6) gene, complete cds; and Nalip3 gene, exons 2-9 and 11-16
8408	21311	34642	0.5	3.1E-01	AW850168.1	EST_HUMAN	IL3-CT0219-271099-022-E03 CT0219 Homo sapiens cDNA
8408	21311	34643	0.5	3.1E-01	AW850168.1	EST_HUMAN	IL3-CT0219-271099-022-E03 CT0219 Homo sapiens cDNA
8207	22135	35492	0.91	3.1E-01	R46318.1	EST_HUMAN	y546f01.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:35639 3'
10589	23455	36875	1.21	3.1E-01	BF696639.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
10589	23455	36876	1.21	3.1E-01	BF696639.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
10628	23514	36947	2.28	3.1E-01	A1244001.1	EST_HUMAN	q616f11.x1 NCL_CGAP_K63 Homo sapiens cDNA clone IMAGE:1863980 3' similar to gb:S55700
10792	23678		0.54	3.1E-01	T55325.1	EST_HUMAN	HYDROXYMETHYL-GLUTARYL-COA LYASE PRECURSOR (HUMAN);
11384	24300	37746	1.42	3.1E-01	AL021127.2	NT	y647h08.s1 Strategene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:74387 3' similar to similar
11967	24810	38305	2.2	3.1E-01	7662291	NT	to gb:M91036_ina2 HEMOGLOBIN GAMMA-A AND GAMMA-G CHAINS (HUMAN)
12508	25242		1.44	3.1E-01	AF304162.1	NT	Stizostedion vitreum 40S ribosomal protein S11 mRNA, partial cds
12648	26322		4.24	3.1E-01	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds

Page 76 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
12983	25542		4.75	3.1E-01	AF198779.1	NT	Homo sapiens transcription factor TGHM enhancer 3, JM11 protein, JM5 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a2
13011	25900		1.53	3.1E-01	10946823	NT	Mus musculus peptidoglycan recognition protein-like (Pglyp1-pending), mRNA
75	15840	26100	7.93	3.0E-01	6755083	NT	Mus musculus protein kinase C, epsilon (Pkcε), mRNA
273	13368	26284	9.5	3.0E-01	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
1251	14287	27230	1.77	3.0E-01	AW300400.1	EST_HUMAN	xs83f08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2774343 3'
1527	14558	27518	5.53	3.0E-01	AJ006755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
2160	15162	28164	1.17	3.0E-01	AF237778.1	NT	Rattus norvegicus Ca2+/calmodulin-dependent protein kinase II, alpha subunit mRNA, 3' untranslated region
3256	16306		1.85	3.0E-01	AB030481.1	NT	Corynebacterium sp. ALY-1 alyPG gene for polyglutamate lyase, complete cds
3454	16495	29399	0.8	3.0E-01	P23825	SWISSPROT	GATA BINDING FACTOR-3 (TRANSCRIPTION FACTOR NF-E1C) (GATA-3)
3933	16961	29844	1.83	3.0E-01	AW817785.1	EST_HUMAN	PM1-ST0262-261195-001-g01 ST0262 Homo sapiens cDNA
4634	17640	30503	2.9	3.0E-01	AJ006755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
4842	17843		1	3.0E-01	AF157835.1	NT	Bacteriophage APSE-1, complete genome
5297	16495	29399	0.75	3.0E-01	P23825	SWISSPROT	GATA BINDING FACTOR-3 (TRANSCRIPTION FACTOR NF-E1C) (GATA-3)
5536	18615	31465	5.08	3.0E-01	BE741629.1	EST_HUMAN	601594960F1 NIH_MGC_e Homo sapiens cDNA clone IMAGE:3948734 5'
5617	18693	31589	0.48	3.0E-01	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
5621	18697	31594	0.92	3.0E-01	AF229247.1	NT	Canis lupus familiaris hemagglutinin gene, complete cds
5694	18767	31691	3.73	3.0E-01	BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-a03 BT0333 Homo sapiens cDNA
5694	18767	31692	3.73	3.0E-01	BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-a03 BT0333 Homo sapiens cDNA
5731	18804	31898	5.41	3.0E-01	U01247.1	NT	Mus musculus 129/sv Clara cell 10 kd protein (mCC10) gene, complete cds
7144	20262	33504	2.95	3.0E-01	D16313.1	NT	Mouse cyclodextrin 15 gene, complete cds
7182	18454	31324	0.82	3.0E-01	U02369.1	NT	Strongylocentrotus purpuratus 34/67 kDa laminin-binding protein mRNA, partial cds
7255	20164	33403	1.03	3.0E-01	AF229247.1	NT	Canis lupus familiaris hemagglutinin gene, complete cds
7343	20339	33606	0.55	3.0E-01	X63941.1	NT	S. cerevisiae GAC1
7480	20420	33699	0.68	3.0E-01	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
7712	20644	33941	6.72	3.0E-01	10947007	NT	Mus musculus midline (Midn-pending), mRNA
7923	20846	34151	2.35	3.0E-01	AF071810.1	NT	Streptococcus pneumoniae strain DBL5 PspA (pspA) gene, partial cds
8505	21493	34777	1.19	3.0E-01	AE001755.1	NT	Thermotoga maritima section 67 of 136 of the complete genome
8645	21875		3.79	3.0E-01	9910161	NT	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Clec5f9), mRNA
9032	21951	35321	0.54	3.0E-01	Z70200.1	NT	H. sapiens gene for U5 snRNP-specific 200kD protein

Page 77 of 545  
Table 4  
Single Exon Probes Expressed In Adult Liver

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9045	21974	35332	1.63	3.0E-01	BE566083.1	EST_HUMAN	601339079F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681694 5'
9388	22316	35678	0.69	3.0E-01	AF141676.1	NT	Streptomyces sulfonofaciens isopenicillin N synthase (pcbC) gene, partial cds
9429	22357		0.92	3.0E-01	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
9759	22683	36069	1.14	3.0E-01	AF220507.1	NT	Anabaena POC7120 cytosine-specific DNA methyltransferase (dmnB) gene, complete cds; putative
10102	22993	36388	0.61	3.0E-01	P76389	SWISSPROT	enthrinate phosphoribosyltransferase gene, partial cds; and unknown gene
10474	23362	36776	0.86	3.0E-01	BF574612.1	EST_HUMAN	HYPOTHETICAL 59.5 KD PROTEIN IN WZA-ASMA INTERGENIC REGION
10882	23767	37192	2.27	3.0E-01	AB030231.1	NT	602133271F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4286335 5'
12183	25019	38520	2.77	3.0E-01	H51029.1	EST_HUMAN	Aspergillus oryzae btpA gene for ER chaperone BIP, complete cds
12183	25019	38521	2.77	3.0E-01	H51029.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5'
12522	25247		1.64	3.0E-01	P54660	SWISSPROT	yp84b10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5'
12752	25857		2.88	3.0E-01	AJ297631.1	NT	PONTICULIN PRECURSOR
13005	25897		6.88	3.0E-01	8677766	NT	Rattus norvegicus mRNA for glyceroldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene)
2037	15054	28053	1.52	2.9E-01	AE000736.1	NT	Mus musculus ribose 5-phosphate isomerase A (RpiA), mRNA
2263	15275	28278	1.03	2.9E-01	AF222718.1	NT	Aquifex aeolicus section 68 of 109 of the complete genome
3227	16275	29178	1.4	2.9E-01	AF078111.1	NT	Chrysodidymus synurideus mitochondrion, complete genome
3296	16343	29246	1.16	2.9E-01	AW754239.1	EST_HUMAN	Xenopus laevis transcription factor E2F mRNA, complete cds
3296	16343	29247	1.16	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0328-171299-001-112 CT0328 Homo sapiens cDNA
3966	16994	29878	0.82	2.9E-01	AI610836.1	EST_HUMAN	PM1-CT0328-171299-001-112 CT0328 Homo sapiens cDNA
4173	17194		0.71	2.9E-01	AW002902.1	EST_HUMAN	PM1-CT0328-171299-001-112 CT0328 Homo sapiens cDNA
4599	17607	30484	1.16	2.9E-01	AA284468.1	EST_HUMAN	PM1-CT0328-171299-001-112 CT0328 Homo sapiens cDNA
4603	17611	30470	0.79	2.9E-01	AF134119.1	NT	PM1-CT0328-171299-001-112 CT0328 Homo sapiens cDNA
4603	17611	30471	0.79	2.9E-01	AF134119.1	NT	PM1-CT0328-171299-001-112 CT0328 Homo sapiens cDNA
5132	18126	30970	1.1	2.9E-01	7662169	NT	PM1-CT0328-171299-001-112 CT0328 Homo sapiens cDNA
5367	18346		1.11	2.9E-01	AL161885.2	NT	PM1-CT0328-171299-001-112 CT0328 Homo sapiens cDNA
5439	18521		1.63	2.9E-01	R37495.1	EST_HUMAN	PM1-CT0328-171299-001-112 CT0328 Homo sapiens cDNA
5580	20184	33428	0.82	2.9E-01	AF321001.1	NT	PM1-CT0328-171299-001-112 CT0328 Homo sapiens cDNA
5972	19038	32169	5.29	2.9E-01	X56098.1	NT	PM1-CT0328-171299-001-112 CT0328 Homo sapiens cDNA
5972	19038	32160	5.29	2.9E-01	X56098.1	NT	PM1-CT0328-171299-001-112 CT0328 Homo sapiens cDNA
5985	19060	32175	4.94	2.9E-01	6679662	NT	PM1-CT0328-171299-001-112 CT0328 Homo sapiens cDNA

### Single Exon Probes Expressed in Adult Liver

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6291	19342	32510	1.3	2.9E-01	AA418145.1	EST_HUMAN	z197D12.r1 Soares_NhlhPpu_S1 Homo sapiens cDNA clone IMAGE:767711 5'
6533	19577	32759	0.93	2.9E-01	A1797128.1	EST_HUMAN	we27C05.x1 NCJ_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2342312 3' similar to contains L1.t1 L1
6582	19623	32808	2.55	2.9E-01	U03420.1	NT	repetitive element :
6728	19764	32971	0.43	2.9E-01	R69194.1	EST_HUMAN	Bos taurus myosin I mRNA, complete cds
6728	19764	32972	0.43	2.9E-01	R69194.1	EST_HUMAN	y39d08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:141615 5'
7022	20048	33072	0.53	2.9E-01	Z60155.1	NT	y39d08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:141615 5'
7184	20184	33428	0.59	2.9E-01	AF321001.1	NT	D discoidium gene for 34 kD actin binding protein
7327	18495	31270	1.57	2.9E-01	AF142328.1	NT	Suaeda maritima subsp. salina S-adenosylmethionine synthetase 2 mRNA, complete cds
7455	20395	33666	2.87	2.9E-01	Q04399	SWISSPROT	Mus musculus Filin protein (Filin) gene, complete cds; and Ugh protein (Ugh) gene, partial cds
7521	20460	33746	1.76	2.9E-01	AF100956.1	NT	PUTATIVE MULTICOPPER OXIDASE YDR506C
8493	21429	34769	1.78	2.9E-01	BE540422.1	EST_HUMAN	Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bing1 (BING1), lapasin (lapasin), RelGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1), 3-galactosyl t-
8498	21429	34770	1.78	2.9E-01	BE540422.1	EST_HUMAN	601065930F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
8728	21658	35004	0.85	2.9E-01	AJ237937.1	NT	601065930F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
8728	21658	35005	0.55	2.9E-01	AJ237937.1	NT	Bos taurus partial slat5A gene, exons 5-19
8740	21670		1.12	2.9E-01	BF217743.1	EST_HUMAN	Bos taurus partial slat5A gene, exons 5-19
9167	22085	35444	0.77	2.9E-01	AJ150970.1	EST_HUMAN	601882570F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4085113 5'
9481	22409	35770	1.11	2.9E-01	AF225908.1	NT	AU150910 NT2RP2 Homo sapiens cDNA clone NT2RP2003901 3'
9584	22511	35874	0.88	2.9E-01	M22452.1	NT	Arabidopsis thaliana sulfonylurea receptor-like protein mRNA, complete cds
9788	22752	36133	0.89	2.9E-01	AJ248287.1	NT	Baboon lymphocyte homing/adhesion receptor mRNA, complete cds
9788	22752	36134	0.89	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
11332	24251	37688	1.76	2.9E-01	AF128843.1	NT	Pyrococcus abyssi complete genome; segment 5/6
11602	24511	37978	2.08	2.9E-01	V01394.1	NT	Trypanosoma cruzi stage-specific surface glycoprotein gp82 (gp82) mRNA, partial cds
11602	24511	37979	2.08	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
12013	24855	38355	1.9	2.9E-01	AA935373.1	EST_HUMAN	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
12017	24859	38359	3.68	2.9E-01	AL139078.2	NT	n35h02.s1 NCL_CGAP_P12 Homo sapiens cDNA clone IMAGE:1273779 similar to contains LTR8.12 LTR8
12030	24872	38375	1.53	2.9E-01	U35025.1	NT	repetitive element :
12030	24872	38376	1.53	2.9E-01	U35025.1	NT	Campylobacter jejuni NCTC:11168 complete genome; segment 5/6
12704	25369	31786	1.55	2.9E-01	AW005671.1	EST_HUMAN	Rattus norvegicus activin receptor-like kinase 7 (ALK7) mRNA, complete cds
12785	25414	31787	2.61	2.9E-01	AF092493.1	NT	Rattus norvegicus activin receptor-like kinase 7 (ALK7) mRNA, complete cds
							Rattus norvegicus activin receptor-like kinase 7 (ALK7) mRNA, complete cds
							w28h05.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2565921 3' similar to contains element
							MER29 repetitive element :
							Homo sapiens TNF-a-inducible RNA binding protein (TIRP) gene, complete cds

Page 79 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12823	25442		1.55	2.9E-01	BE788199.1	EST_HUMAN	601492059F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884558 5'
500	13658		1.3	2.8E-01	U67136.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds
595	13682		0.72	2.8E-01	L28145.1	NT	Prune dwarf virus movement protein, complete cds; coat protein, complete cds
1110	14152	27093	2.47	2.8E-01	AF168050.1	NT	Gulaia guira oocyte maturation factor Mos (c-mos) gene, partial cds
1303	14336	27283	1.41	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1303	14336	27284	1.41	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1317	14350	27298	0.91	2.8E-01	D86550.1	NT	Human mRNA for serine/threonine protein kinase, complete cds
1757	14784	27755	1.69	2.8E-01	AW88020.1	EST_HUMAN	QV1-CT0364-120200-066-005 CT0364 Homo sapiens cDNA
2025	15043	28037	1.41	2.8E-01	AL047620.1	EST_HUMAN	DKFZp5662321_r1 586 (synonym: hule1) Homo sapiens cDNA clone DKFZp5662321
2145	15158	28160	1.16	2.8E-01	AW511195.1	EST_HUMAN	hcd44503.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912333 3'
2494	15496	28496	2.51	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2494	15496	28497	2.51	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2578	15577		2.16	2.8E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 66
2714	15708	28703	1.07	2.8E-01	AB020975.1	NT	Arabidopsis thaliana mRNA for lipoyltransferase, complete cds
3011	16063		1.92	2.8E-01	AF179480.1	NT	Toxoplasma gondii 90kDa heat-shock protein (HSP90) mRNA, partial cds
3012	16064	28967	2.41	2.8E-01	Z14037.1	NT	B. taurus microsatellite (ETH121)
3012	16064	28968	2.41	2.8E-01	Z14037.1	NT	B. taurus microsatellite (ETH121)
3436	16477	29383	0.98	2.8E-01	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (4/7)
4082	17107	29985	2.55	2.8E-01	AE001180.1	NT	Borrelia burgdorferi (section 66 of 70) of the complete genome
4220	17236		0.68	2.8E-01	AE004450.1	NT	Pseudomonas aeruginosa PA01, section 11 of 529 of the complete genome
4294	17308		2.98	2.8E-01	AI090888.1	EST_HUMAN	ov44g10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640226 3' similar to contains Alu repetitive element; contains element MER22 repetitive element ;
4568	17574	30437	1.22	2.8E-01	AL021127.2	NT	Mus musculus chromosome X contig; putative Mage9 gene, Caltractin, NAD(P) sterold dehydrogenase and Zinc finger protein 185
4571	17575	30441	3	2.8E-01	P13615	SWISSPROT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L PROTEIN)
4936	17935	30792	1.11	2.8E-01	AF075238.1	NT	Hepatitis G virus isolate 80 (SZNAE12) polyprotein precursor, gene, partial cds
4943	17942	30800	3.99	2.8E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
4971	17968	30828	1.41	2.8E-01	BF528188.1	EST_HUMAN	602042601F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4180129 5'
4984	17993	30950	3.14	2.8E-01	AI272669.1	EST_HUMAN	q159c11.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1876628 3' similar to contains Alu repetitive element; contains element LTR5 repetitive element ;
5408	18389	31227	0.91	2.8E-01	AI805265.1	EST_HUMAN	te32c02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2087618 3' similar to TR:O60392
5408	18389	31228	0.91	2.8E-01	AI805266.1	EST_HUMAN	te32c02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2087618 3' similar to TR:O60392

Page 80 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

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5494	25628	31419	23.22	2.8E-01	AA349997.1	EST_HUMAN	EST57072 Infant brain Homo sapiens cDNA 5' end
5800	18872	31980	2.53	2.8E-01	AB016625.1	NT	Homo sapiens OCTN2 gene, complete cds
6028	19090		0.85	2.8E-01	AV092583.1	EST_HUMAN	CV1-BN0024-150200-118-g12 BN0024 Homo sapiens cDNA
6143	19202	32339	0.54	2.8E-01	AA765298.1	EST_HUMAN	ca01d06.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1303691 3' similar to gb:M34539 FK506-BINDING PROTEIN (HUMAN).
6163	19220		0.61	2.8E-01	AA404576.1	EST_HUMAN	z44101.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:724921 5' similar to contains Alu repetitive element
6417	25978		0.83	2.8E-01	M36688.1	NT	Bovine 680 bp repeated unit of 1.723 satellite DNA
6482	19507	32882	1.52	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds
6482	19507	32883	1.52	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds
7035	20061	33295	9.12	2.8E-01	BF511215.1	EST_HUMAN	UHH-B14-ach-f-04-0-UJ.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085182 3'
7349	20345	33612	0.83	2.8E-01	U65300.1	NT	Orthocentrus heterodus cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
7745	20676	33974	0.47	2.8E-01	BE881465.1	EST_HUMAN	601490157F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:3992142 5'
7845	20772		1.02	2.8E-01	U05633.1	NT	Marsilea quadrifolia ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (tblL) gene, chloroplast gene encoding chloroplast protein, partial cds
8412	19220		0.53	2.8E-01	AA404576.1	EST_HUMAN	z44101.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:724921 5' similar to contains Alu repetitive element;
8671	21602	34941	1.53	2.8E-01	AI346126.1	EST_HUMAN	qp48h01.x1 NCL_CGAP_C08 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1
8671	21602	34942	1.53	2.8E-01	AI346126.1	EST_HUMAN	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8787	21717	35065	2.55	2.8E-01	U51688.1	NT	qp48h01.x1 NCL_CGAP_C08 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1
9080	22009	35365	0.63	2.8E-01	AA911629.1	EST_HUMAN	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
9151	22079		9.22	2.8E-01	BF347847.1	EST_HUMAN	Homo sapiens lanosterol 14-alpha demethylase cytochrome P450 (CYP51) gene, exon 5
9999	22816	36205	1.29	2.8E-01	U17251.1	NT	602022987F1 NCL_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4158525 5'
10233	23124		1.24	2.8E-01	L13654.1	NT	Neurospora crassa negative regulator sulfur controller-2 (econ-2) gene, complete cds
10400	23289	36711	1.44	2.8E-01	AF132728.1	NT	Lycopodium obscurum peroxidase (TPX1) mRNA, complete cds
10400	23289	36712	1.44	2.8E-01	AF132728.1	NT	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds
10457	23345	36762	0.71	2.8E-01	AF294993.1	NT	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds
10592	23448	36870	5.21	2.8E-01	7706163	NT	Rattus norvegicus glycerol-3-phosphate dehydrogenase gene, promoters A and B and exons 1a and 1b; nuclear gene for mitochondrial product
10902	23688		1.17	2.8E-01	9626154	NT	Homo sapiens hypothetical protein (LOC51319). mRNA
							Fujinami sarcoma virus, complete genome

Page 81 of 545  
Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
11184	24110	37557	2.61	2.8E-01	BF241082.1	EST_HUMAN	601880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
11184	24110	37558	2.61	2.8E-01	BF241062.1	EST_HUMAN	601880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
11211	24137	37587	2.96	2.8E-01	BF695970.1	EST_HUMAN	601852148F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076026 5'
11317	24236	37681	2.21	2.8E-01	AF051652.1	NT	Drosophila heteronema fruitless (fru) gene, alternative splice products, 5' flanking region, exons 1 through 7 and complete cds
11724	24626		3.63	2.8E-01	BF674023.1	EST_HUMAN	602137418F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273853 5'
12222	25056	38555	2.52	2.8E-01	R22890.1	EST_HUMAN	YH21H11.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130437 5' similar to contains LTR3 repetitive element
12738	25378		12.34	2.8E-01	D68329.1	NT	Mus musculus DNA for prostaglandin D2 synthase, complete cds
12834	25449	31776	6.3	2.8E-01	BE178699.1	EST_HUMAN	PM4-HT0606-030400-001-a07 HT0606 Homo sapiens cDNA
499	13569	28487	4.49	2.7E-01	Y17324.1	NT	Rattus norvegicus GDIK104 mRNA
636	13697	28602	2.7	2.7E-01	AA150061.1	EST_HUMAN	z339610.s1 Soares fetal_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:788827 3' similar to contains Alu repetitive element
1288	14321	27267	1.38	2.7E-01	AB004906.1	NT	Ipomoea purpurea transposable element Tip100 gene for transposase, complete cds
1044	14675		1.92	2.7E-01	X79815.1	NT	G. lamblia SR2 gene
1759	14786	27756	2.77	2.7E-01	W58087.1	EST_HUMAN	z422h10.1 Soares fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341443 5'
1801	14827	27795	1.34	2.7E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2149	15917		2.21	2.7E-01	AF047575.1	NT	Rattus norvegicus vesicular monocamine transporter type 2, promoter region and exon 1
2390	15995	28997	6.69	2.7E-01	Y13968.1	NT	Feline immunodeficiency virus env gene, isolate ITT C088PIU (M86), partial
2479	15481	28482	3.93	2.7E-01	A1310858.1	EST_HUMAN	ta43c11.x2 NCI_CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2049836 3' similar to contains element L1 repetitive element
2941	15994	28896	1.32	2.7E-01	AF251276.1	NT	Mus musculus serine protease inhibitor 14 (Spi14) mRNA, complete cds
3026	16078		0.81	2.7E-01	BF088294.1	EST_HUMAN	CM1-HT0875-060900-385-e05 HT0875 Homo sapiens cDNA
3899	16928	29806	0.86	2.7E-01	AJ290443.1	NT	Corynebacterium glutamicum mek gene, ORF1 (partial) and ORF2 (partial)
4097	17122	29999	2.58	2.7E-01	A1928015.1	EST_HUMAN	wo92e11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462828 3'
4108	17132	30006	0.78	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (aE6) gene, partial cds
4108	17132	30007	0.78	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (aE6) gene, partial cds
4113	17136	30010	2.67	2.7E-01	L77569.1	NT	Homo sapiens Digeorge syndrome critical region, telomeric end
4177	17197	30067	1.08	2.7E-01	A1701408.1	EST_HUMAN	wo20f05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2342620 3' similar to TR:Q13638 Q13638 ORF2: FUNCTION UNKNOWN.
5000	17998	30856	3.23	2.7E-01	L27516.1	NT	Triticum aestivum (Wcs66) gene, complete cds
5171	18163		4.27	2.7E-01	AW856131.1	EST_HUMAN	RC1-CT0286-230200-018-e03 CT0286 Homo sapiens cDNA
5191	18183	31026	0.92	2.7E-01	A1827753.1	EST_HUMAN	wf11g03.x1 Soares_NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:2360324 3'

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5449	18530	31256	2.42	2.7E-01	P17277	SWISSPROT	HOMEOBOX PROTEIN HOXA4 (HOXA4-1.4)
5678	18752		1.39	2.7E-01	AB033171.1	NT	Astrepore myriophthalma mitochondrial cyb gene for cytochrome b, partial cds
6599	19640	32820	0.71	2.7E-01	Q00918	SWISSPROT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT)
6599	19640	32821	0.71	2.7E-01	Q00918	SWISSPROT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT)
6897	19927	33143	1.08	2.7E-01	AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome
6897	19927	33144	1.08	2.7E-01	AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome
7056	20292	33552	1.99	2.7E-01	Q61554	SWISSPROT	FIBRILLIN 1 PRECURSOR
7361	20355	33625	0.5	2.7E-01	U15967.1	NT	Drosophila melanogaster rfc40 protein, Rop protein (Rop), and small GTP binding protein (Dras2) genes, complete cds
7405	20104		0.46	2.7E-01	A1540070.1	EST_HUMAN	h08h08.x1 NCL_OGAP_QLL1 Homo sapiens cDNA clone IMAGE:2076103 3'
7746	20577	33975	0.76	2.7E-01	Q11079	SWISSPROT	HYPOTHETICAL 20.9 KD PROTEIN B0563.3 IN CHROMOSOME X
7894	20912	34227	0.94	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7894	20912	34228	0.94	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
8141	21050	34381	2.24	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
8141	21050	34382	2.24	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
8203	21109	34439	0.9	2.7E-01	AA351121.1	EST_HUMAN	EST58740 Infant brain Homo sapiens cDNA 5' end similar to similar to myosin-binding protein H
8203	21109	34440	0.9	2.7E-01	AA351121.1	EST_HUMAN	EST58740 Infant brain Homo sapiens cDNA 5' end similar to similar to myosin-binding protein H
8263	21188	34528	0.51	2.7E-01	L01081.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
8445	21377	34718	0.71	2.7E-01	AA013147.1	EST_HUMAN	ze35b11.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360857 3' similar to contains Alu repetitive element
8604	21535		0.63	2.7E-01	AF048820.1	NT	Carassius auratus pituitary adenylate cyclase activating polypeptide type 1 receptor precursor mRNA, complete cds
8714	21645	34991	0.57	2.7E-01	AF048820.1	EST_HUMAN	MR1-SN0052-100500-002-409 SN0062 Homo sapiens cDNA
8764	21694	35036	0.84	2.7E-01	R39257.1	EST_HUMAN	yc91h06.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:23511 3'
8867	21797	35151	0.86	2.7E-01	AL161662.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
9318	22243	35608	0.76	2.7E-01	Q14764	SWISSPROT	MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN)
9578	22505	35869	0.59	2.7E-01	X03216.1	NT	Staphylococcus aureus transposon Tn554
9573	22783	36178	9.77	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)



Page 83 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9873	22788	36178	9.77	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9875	22780		2.78	2.7E-01	P37928	SWISSPROT	FIMBRIAE W PROTEIN
10317	23206	36617	0.8	2.7E-01	D89690.1	NT	Rattus norvegicus DNA for peroxisome assembly factor-2, exon 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 and complete cds
10583	23469	38895	1.14	2.7E-01	AF091848.1	NT	Oryzodagus cuticulus calgranulin C mRNA, partial cds
10618	23504	36938	0.86	2.7E-01	AF087434.1	NT	Mus musculus transcription factor NF-A1c isoform a (NF-A1c) mRNA, complete cds
10743	23629	37060	1.07	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10743	23629	37061	1.07	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
11070	23894		0.52	2.7E-01	AB011679.1	NT	Rattus norvegicus mRNA for class I beta-tubulin, complete cds
11251	24175	37622	1.55	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
11251	24175	37623	1.55	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
11261	24184	37633	3.26	2.7E-01	AJ133289.1	NT	Homo sapiens caveolin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
12887	26545		2.8	2.7E-01	AF217491.1	NT	Homo sapiens fragile 16D oxido reductase (FOR) gene, exon 6
492	16875	26480	1.46	2.6E-01	P78411	SWISSPROT	IRQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2
503	13574		1.31	2.6E-01	D16459.1	NT	Bos taurus mRNA for mb-1, complete cds
1420	14461	27405	1.41	2.6E-01	BE885087.1	EST_HUMAN	601510838F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912345 5'
1456	14488	27448	0.9	2.6E-01	AB013290.1	NT	Glycine max pseudogene for Bd 30K
1614	14935	27611	4.79	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
1614	14935	27612	4.79	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
2105	15119		9.35	2.6E-01	AW733152.1	EST_HUMAN	bb04d10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2958451 3' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN); gb:M14689_cds1 Mouse surfeit locus surfeit 3 protein gene (MOUSE);
2167	15179	28185	1.13	2.6E-01	M11844.1	NT	Human prealbumin gene, complete cds
2677	15576		11.59	2.6E-01	BE272440.1	EST_HUMAN	801126016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990043 5'
3641	16677	29575	1.02	2.6E-01	M22342.1	NT	Bacteriophage T2 DNA-(adenine-N6)methyltransferase (dam) gene, complete cds
3711	16743	29933	2.18	2.6E-01	AF229118.1	NT	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLQ) gene, exons 1A, 2, 3, 4, and 5
4190	17210	30076	0.71	2.6E-01	AW959510.1	EST_HUMAN	EST371580 IMAGE sequences; MAGF Homo sapiens cDNA
4252	17268	30137	17.02	2.6E-01	BE080508.1	EST_HUMAN	QV1-BT0630-040400-132-903 BT0630 Homo sapiens cDNA
4466	17477	30336	1.42	2.6E-01	AF175293.1	NT	Erterococcus faecium strain N97-330 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene
4611	17619	30481	0.72	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4611	17619	30482	0.72	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds

Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4664	17669	30539	1.47	2.6E-01	AA457617.1	EST_HUMAN	aa89d07.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838477 5'
4757	17762	30624	1.03	2.6E-01	U01103.1	NT	Arabidopsis thaliana PSI type III chlorophyll <i>ab</i> -binding protein (Lhca3*) mRNA, complete cds
4828	17829	30697	1.22	2.6E-01	AF142703.1	NT	Ophrestia radiosa maturase-like protein (matK) gene, complete cds; chloroplast gene for chloroplast product
5092	18089	30939	4.99	2.6E-01	H04858.1	EST_HUMAN	y51e05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:152288 5'
5258	18244	31085	1	2.6E-01	P08503	SWISSPROT	ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC, MITOCHONDRIAL PRECURSOR (MCAD)
5525	18604		1.14	2.6E-01	AB035972.1	NT	Paramedium caudatum gene for PAP, complete cds
5634	18710	31610	0.68	2.6E-01	M96060.1	NT	Acetobacter xylinum cellulose synthase (bcsA) gene, partial cds, CMCax and CopAx genes, complete cds
5763	18836		0.81	2.6E-01	AI892398.1	EST_HUMAN	td18a03.x1 NCL_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2075788 3' similar to contains element MER35 repetitive element ;
5983	19049	32172	0.67	2.6E-01	AF207650.1	NT	Homo sapiens protein translocase, JM28 protein, UDP-galactose translocator, pim-2 protooncogene homolog pim-2h, and ehal-type potassium channel genes, complete cds; JM12 protein and transcription factor IGHM enhancer 3 genes, partial cds; and unknown g>
6306	25975		2.34	2.6E-01	AE001811.1	NT	Thermotoga maritima section 123 of 136 of the complete genome
8442	19488	32865	2.01	2.6E-01	AI882557.1	EST_HUMAN	ts02e12.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW.NDF1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1 ; contains element LTR1 repetitive element ;
8442	19488	32866	2.01	2.6E-01	AI882557.1	EST_HUMAN	ts02e12.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW.NDF1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1 ; contains element LTR1 repetitive element ;
6689	19725	32925	1.01	2.6E-01	AL162757.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 6/7
6864	19902	33219	0.65	2.6E-01	BE792052.1	EST_HUMAN	601581754F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936156 5'
6964	19992	33220	0.65	2.6E-01	BE792052.1	EST_HUMAN	601581754F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936156 5'
7389	20382	33651	1.07	2.6E-01	AI914380.1	EST_HUMAN	wd48c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2331985 3' similar to gb.M37721 PEPTIDYL-GLYCINE ALPH-A-MIDATING MONOOXYGENASE PRECURSOR (HUMAN);
7787	20716	34019	0.74	2.6E-01	BE148961.1	EST_HUMAN	CM0-HT0245-031199-085-f04 HT0245 Homo sapiens cDNA
7833	25677		1.75	2.6E-01	AL139077.2	NT	Campylobacter jejuni NC1C11166 complete genome; segment 4/6
7875	20802		0.62	2.6E-01	AA186149.1	EST_HUMAN	zp92e01.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627672 5'
8204	21110	34441	1.63	2.6E-01	R10365.1	EST_HUMAN	y37a03.e1 Soares fetal liver spleen tNfLS Homo sapiens cDNA clone IMAGE:129004 3' similar to
8265	21170	34504	0.5	2.6E-01	Q09855	SWISSPROT	gb.X12617 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (HUMAN);
8346	21251		0.48	2.6E-01	AF314149.1	NT	HYPOPHYSICAL TRP-ASP REPEATS CONTAINING PROTEIN C29E6.01 IN CHROMOSOME 1
8432	21364	34703	1.41	2.6E-01	R02411.1	EST_HUMAN	Mus musculus telokin mRNA, complete cds
							y682a07.r1 Soares fetal liver spleen tNfLS Homo sapiens cDNA clone IMAGE:124212 5'

Page 85 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8483	21414	34751	1.35	2.6E-01	BE144331.1	EST_HUMAN	NR0-HT0168-181199-003-d12 HTD166 Homo sapiens cDNA
8719	21650	34906	0.63	2.6E-01	X82641.1	NT	D.melanogaster mRNA for alpha 1,2 mannosidase (Berlin)
8719	21650	34997	0.63	2.6E-01	X82641.1	NT	D.melanogaster mRNA for alpha 1,2 mannosidase (Berlin)
8909	21839	35184	3.16	2.6E-01	BF343588.1	EST_HUMAN	602014422F1 NCL CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4150396 5'
8981	21911	35266	2.35	2.6E-01	Q10199	SWISSPROT	HYPOTHETICAL 75.2 KD PROTEIN G11G11.02 IN CHROMOSOME II
9252	22180	35533	4.07	2.6E-01	BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
9252	22180	35534	4.07	2.6E-01	BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
10000	22817	36206	1.09	2.6E-01	X17804.1	NT	S. occidentalis INV gene for Invertase (EC 3.2.1.26)
10259	23149		0.57	2.6E-01	AF087121.1	NT	Lontra canadensis cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10381	23270	36692	1.28	2.6E-01	P87366	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KPH-G)
10381	23270	36693	1.28	2.6E-01	P87366	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KPH-G)
10687	23573		0.71	2.6E-01	Q28295	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
10687	23573		1.16	2.6E-01	Y10196.1	NT	Homo sapiens PHEX gene
11074	23958		0.56	2.6E-01	Y15874.2	NT	Danio rerio mRNA for RPTP-alpha protein
11855	24705	38196	1.81	2.6E-01	P48280	SWISSPROT	CELL DIVISION PROTEIN FTSW HOMOLOG
11956	24799		53.33	2.6E-01	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
12350	25142		1.61	2.6E-01	10190655	NT	Mus musculus Jerky (Jrk), mRNA
12520	25863		3.66	2.6E-01	BE883491.1	EST_HUMAN	601511052F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912612 5'
12580	25282	31841	3.08	2.6E-01	AF316896.1	NT	Homo sapiens Naik-ATPase gamma subunit (FXD2) gene, complete cds, alternatively spliced
12894	25484		1.79	2.6E-01	D88425.1	NT	Caixa cobaya mRNA for serine/threonine kinase, complete cds
12965	25531		1.95	2.6E-01	AE001713.1	NT	Thermotoga maritima section 25 of 136 of the complete genome
13038	25575		2.47	2.6E-01	P47285	SWISSPROT	HYPOTHETICAL PROTEIN MG039
260	13357	26272	2.76	2.5E-01	4502296	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
261	13357	26272	1.71	2.5E-01	4502296	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
274	13368		3.59	2.5E-01	M26501.1	NT	Starfish (P. ochraceus) cytoplasmic actin gene, complete cds
857	13911	26854	1.33	2.5E-01	U09064.1	NT	Mus musculus ICR/Swiss glyceroldehyde 3-phosphate dehydrogenase (Gapdh-S) gene, complete cds
1087	14131		1.24	2.5E-01	AE002156.1	NT	Ureaplasma urealyticum section 57 of 69 of the complete genome
1148	14190	27129	7.22	2.5E-01	T89837.1	EST_HUMAN	ye11907.11 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:117468 5'
1405	14436		0.93	2.5E-01	AB025343.1	NT	Olea europaea OEW mRNA for lupeol synthase, complete cds
1540	14570	27529	1.51	2.5E-01	AL115624.1	NT	Bakyrus cinerea strain T4 cDNA library under conditions of nitrogen deprivation

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1758	14785		4.13	2.5E-01	4885406	NT	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA
2431	15435		9.17	2.9E-01	AE000675.1	NT	Aquifex aeolicus section 7 of 109 of the complete genome
2518	15519		1.96	2.5E-01	AA251887.1	EST_HUMAN	zsl1a12.1 NCL_GGAP_GCB1 Homo sapiens cDNA clone IMAGE:684862 5'
2683	15577	28676	1.69	2.5E-01	X95310.1	NT	B. taurus mRNA for D-aspartate oxidase
3473	16513		4.87	2.5E-01	AW973471.1	EST_HUMAN	EST385464 IMAGE resequences, MAGM Homo sapiens cDNA
3608	16645	29544	8.3	2.5E-01	AL161517.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 29
4158	17177		1.54	2.5E-01	P32323	SWISSPROT	A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR
4423	17434		0.91	2.5E-01	Q03314	SWISSPROT	RHIB PROTEIN
4728	17733	30595	0.77	2.5E-01	AF242431.1	NT	Mus musculus neuronal apoptosis inhibitory protein 6 (Naiip6) gene, complete cds, and Naiip3 gene, exons 2-9 and 11-16
4863	17865		1.8	2.5E-01	Q27225	SWISSPROT	MOLT-INHIBITING HORMONE PRECURSOR (MIH)
4869	17869	30733	4.63	2.5E-01	AF007768.1	NT	Chlorostoma fumiferana diapause associated protein 2 (DAP2) mRNA, complete cds
4895	17894	30760	2.58	2.5E-01	AE004410.1	NT	Vibrio cholerae chromosome II, section 73 of 93 of the complete chromosome
4918	17917		3.27	2.5E-01	AJ230113.1	NT	Mus musculus annexin V gene, intron 4 segment containing 5' LTR and gag portion of MuERV-L (murine endogenous retrovirus) element
4947	17948	30804	0.78	2.5E-01	BE586785.1	EST_HUMAN	801437468F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922800 5'
5178	18170	31015	1.06	2.5E-01	AW873588.1	EST_HUMAN	h062111.X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041997 3' similar to WP:Y71F9A_294.D CE22858 :
5242	18229	31078	0.94	2.5E-01	P27023	SWISSPROT	MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G)
5242	18229	31079	0.94	2.5E-01	P27023	SWISSPROT	MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G)
5509	18588	31437	10.94	2.5E-01	S83390.1	NT	T3 receptor-associated cofactor-1 [human, fetal liver, mRNA, 2930 nt]
6188	19242	32389	0.59	2.5E-01	AJ006345.1	NT	Homo sapiens KVLQ11 gene
6188	19243		0.75	2.5E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
6649	19888	32880	0.68	2.5E-01	P22219	SWISSPROT	PROTEIN KINASE VPS15
6915	19945	33164	0.89	2.5E-01	AJ251873.1	NT	Homo sapiens partial steirin-1 gene
7396	20095	33328	0.71	2.5E-01	8394138	NT	Rattus norvegicus rab3 (RABIN3), mRNA
7740	20871	33969	0.91	2.5E-01	U13992.1	NT	Felina calicivirus CF168 RNA helicase/cysteine protease/RNA-dependent RNA polymerase polyprotein precursor and capsid protein precursor, genes, complete cds; and unknown gene
7771	20701		1.49	2.5E-01	AF134119.1	NT	Mus musculus SKOT (Skd1) gene, complete cds
8037	20952	34207	0.03	2.5E-01	AL161506.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
8085	20997	34317	4.95	2.5E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
8427	21369	34699	1.71	2.5E-01	BF109040.1	EST_HUMAN	7187a03.x1 Soares_NSIF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525389 3'
8438	21370	34711	0.78	2.5E-01	BE660712.1	EST_HUMAN	601653391R2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826198 3'

Page 87 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8804	21734	35083	2.25	2.9E-01	BF038595.1	EST_HUMAN	801459238F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3862809 5'
9195	22123	35479	4.58	2.9E-01	H53236.1	EST_HUMAN	X98407.1 Scars fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:202501 5'
9433	22361	35724	1.03	2.9E-01	M88626.1	NT	Mouse testis-specific protein (TPX-1) gene, exon 10
10047	22963	36351	22.51	2.9E-01	U96651.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
10047	22963	36352	22.51	2.9E-01	U96651.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
10101	22950	36339	1.58	2.9E-01	AF085164.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
10101	22950	36340	1.58	2.9E-01	AF085164.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
10500	23486	36915	1.69	2.9E-01	AW581997.1	EST_HUMAN	RC3-ST0186-130100-015-a07 ST0186 Homo sapiens cDNA
10830	23716	37141	0.52	2.9E-01	11456592	NT	Porphyria purpurea chloroplast, complete genome
11020	23904	37343	1.77	2.9E-01	AW152246.1	EST_HUMAN	xg40c10.x1 NCJ_CGAP_U1 Homo sapiens cDNA clone IMAGE:2830034 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
11023	23907	37347	1.81	2.9E-01	X58491.1	NT	Mouse LIMD LINE DNA
11516	24426	37884	4.42	2.9E-01	D50914.1	NT	Human mRNA for KIAA0124 gene, partial cds
12075	24916	38675	1.61	2.9E-01	AF027163.1	NT	Homo sapiens sodium/myo-inositol cotransporter (SLC5A3) gene, complete cds
12290	25101	38675	6.69	2.9E-01	AF200528.1	NT	Zea mays cellulose synthase-4 (Cesa-4) mRNA, complete cds
12316	25936		4.22	2.9E-01	AL161541.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41
575	13943	26550	1.43	2.4E-01	A4936316.1	EST_HUMAN	on70d04.s1 Scars_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562023 3'
873	13926	26874	2.48	2.4E-01	BF576124.1	EST_HUMAN	602132442F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271578 5'
1330	14364	27312	12.06	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1330	14364	27313	12.06	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1411	14442	27395	1.04	2.4E-01	Y17293.1	NT	Homo sapiens FLN-1 gene, partial
1873	14896		17.09	2.4E-01	AF267753.1	NT	Mesembryanthemum crystallinum putative potassium channel protein Mkt1p mRNA, complete cds
1918	14839	27916	1.12	2.4E-01	AF251708.1	NT	Zaocys dhurmadia fructose-1,6-bisphosphatase mRNA, complete cds
2152	15164	28168	1.03	2.4E-01	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
2181	15192		1.16	2.4E-01	P45394	SWISSPROT	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGA1 PROTEASE)
2278	15288	28296	1.94	2.4E-01	AE000680.1	NT	Aquifex aeolicus section 12 of 109 of the complete genome
2407	15412	28415	1.44	2.4E-01	BF002171.1	EST_HUMAN	7h23d04.x1 NCJ_CGAP_Cot6 Homo sapiens cDNA clone IMAGE:3316807 3' similar to SW:PRSB_XENLA
2566	15565	28565	1.9	2.4E-01	Z36534.1	NT	O42586 26S PROTEASE REGULATORY SUBUNIT 6A;
2812	15801	28800	2.72	2.4E-01	XT1783.1	NT	D discoideum (AX3-K) pomA gene
2834	15823	28819	4.96	2.4E-01	AF030154.1	NT	S.pombe swi6 gene
						NT	Bovine adenovirus 3 complete genome
3177	18227		3.63	2.4E-01	U72725.1	NT	Oryza longistaminata receptor kinase-like protein, family member D, and retrofl (gag/pol) genes, complete cds
3824	18554	29738	0.87	2.4E-01	AE000312.1	NT	Escherichia coli K-12 MG1655 section 202 of 400 of the complete genome

Page 88 of 545  
Table 4

## Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5049	18048		1.32	2.4E-01	AL161589.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
5205	18198	31038	0.67	2.4E-01	AW078596.1	EST_HUMAN	xb18a02.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:2576618 3'
5205	18198	31039	0.67	2.4E-01	AW078596.1	EST_HUMAN	xb18a02.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:2576618 3'
5648	18722	31627	0.84	2.4E-01	AI025707.1	EST_HUMAN	w033d05.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2467120 3'
5648	18722	31628	0.84	2.4E-01	AI025707.1	EST_HUMAN	w033d05.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2467120 3'
5673	18747	31638	0.66	2.4E-01	D50871.1	NT	Glycine max mRNA for mitotic cyclin b1-type, complete cds
5852	18923	32038	13.04	2.4E-01	AF091216.1	NT	Mus musculus Wrm protein (Wrm) gene, complete cds
5852	18923	32039	13.04	2.4E-01	AF091216.1	NT	Mus musculus Wrm protein (Wrm) gene, complete cds
5880	18949		0.67	2.4E-01	M83377.1	NT	Gallus gallus brain-derived neurotrophic factor (BDNF) gene, 5' end
6106	25639		0.88	2.4E-01	AJ133836.2	NT	Branchiostoma floridae mRNA for calmodulin 2 (calm2 gene)
6113	19173	32305	2.65	2.4E-01	BF592336.1	EST_HUMAN	7154d04.x1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3338503 3' similar to SW:SFR4_HUMAN
6215	19270	32423	2.36	2.4E-01	AF035546.1	NT	Q08170 SPLICING FACTOR, ARGININE/SERINE-RICH 4; contains element TAR1 TAR1 repetitive element
6327	19377	32544	2.06	2.4E-01	7661801	NT	Drosophila melanogaster p38a MAP kinase gene, complete cds
6381	19430	32598	1.07	2.4E-01	AV733787.1	EST_HUMAN	Homo sapiens HSPC142 protein (HSPC142), mRNA
6647	19686	32877	0.56	2.4E-01	AA398672.1	EST_HUMAN	AV733787.cdA Homo sapiens cDNA clone c0AADE11 5'
6814	19847	33058	3.19	2.4E-01	AI688989.1	EST_HUMAN	z170d02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727683 3'
7399	20097	33331	0.47	2.4E-01	AF163863.1	NT	wc62c11.x1 NCI_CGAP_Pant1 Homo sapiens cDNA clone IMAGE:2323220 3' similar to gb:J03464
7729	20661	33959	10.49	2.4E-01	L43001.1	NT	PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN);
7927	20849	34155	0.46	2.4E-01	N48732.1	EST_HUMAN	Muscle vison tyrosine aminotransferase gene, complete cds
8185	21092		0.43	2.4E-01	U05013.1	NT	Bos taurus guanylyl cyclase-activating protein 2 (guca2) mRNA, complete cds
8187	21094	34425	0.96	2.4E-01	AF229644.1	NT	Y056c11.1 Soares_multiple_sclerosis_2NBHMSP Homo sapiens cDNA clone IMAGE:277460 5'
8658	21589	34925	0.56	2.4E-01	X97252.1	NT	Rattus norvegicus Sprague-Dawley heme oxygenase-2 non-reducing isoform gene, complete cds
8658	21589	34926	0.56	2.4E-01	X97252.1	NT	Mus musculus DXImx48e protein (DXImx48e) mRNA, complete cds
8776	21706	35051	0.66	2.4E-01	AJ006397.1	NT	M.musculus path gene and promoter
8776	21706	35052	0.66	2.4E-01	AJ006397.1	NT	M.musculus path gene and promoter
8923	21853	35208	1.8	2.4E-01	AJ012585.1	NT	M.musculus path gene and promoter
9167	22089	35449	1.27	2.4E-01	BF242794.1	EST_HUMAN	Streptococcus pneumoniae r08 and h08 genes; two component system 08
9676	22602	35975	0.59	2.4E-01	AL139077.2	NT	Streptococcus pneumoniae r08 and h08 genes; two component system 08
9676	22602	35976	0.59	2.4E-01	AL139077.2	NT	Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2
							60'-877679F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4109298 5'
							Campylobacter jejuni NCTC11168 complete genome; segment 4/6
							Campylobacter jejuni NCTC11168 complete genome; segment 4/6

Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10092	22885	36269	6.68	2.4E-01	AI093151.1	EST_HUMAN	w443a02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330908 3' similar to contains MER22 b1 TAR1 repetitive element;
10226	23117	36518	0.68	2.4E-01	AF220067.1	NT	Drosophila melanogaster SKPB gene, complete cds
10226	23117	36519	0.68	2.4E-01	AF220067.1	NT	Drosophila melanogaster SKPB gene, complete cds
10919	23804	37231	1.74	2.4E-01	Q03692	SWISSPROT	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR
11206	24132	37360	2.55	2.4E-01	AL161494.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
11275	24197	37660	2.16	2.4E-01	AF030199.1	NT	Mus musculus type 1 sigma receptor gene, complete cds
11615	24523	37991	1.63	2.4E-01	BE296917.1	EST_HUMAN	601176415F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531843 5'
11615	24523	37992	1.63	2.4E-01	BE296917.1	EST_HUMAN	601176415F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531843 5'
11647	24553		2.11	2.4E-01	Z21047.1	NT	P. asiatica mosaic virus genomic RNA
12373	25747		1.94	2.4E-01	AF004213.1	NT	Arabidopsis thaliana ethylene-insensitive3-like1 (EIL1) mRNA, complete cds
13034	25372		5.21	2.4E-01	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
410	13483	26403	1.54	2.3E-01	S75898.1	NT	aromatase [Drosophila guttata=zebra finches, ovary, mRNA, 3188 nt]
660	13722		2.97	2.3E-01	U09713.1	NT	Mycoplasma genitalium section 35 of 51 of the complete genome
690	13751	26666	21.44	2.3E-01	U07596.1	NT	Methanococcus jannaschii section 138 of 150 of the complete genome
982	14012	28954	3.47	2.3E-01	BE311893.1	EST_HUMAN	601142073F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505818 5'
1630	14560	27520	1.07	2.3E-01		NT	Mus musculus vacuolar protein sorting 4b (yeast) (Vps4b), mRNA
1658	14888	27649	2.08	2.3E-01		NT	Mus musculus cdk5 gene, exon 1, partial
2059	15075		1.13	2.3E-01	Y10887.2	NT	Homo sapiens partial intron 3 of the wild type AF-4/FEL gene
2470	15473	28472	1.99	2.3E-01	BE297718.1	EST_HUMAN	601175562F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531015 5'
2700	15894	28688	1.34	2.3E-01	M11319.1	NT	Human erythropoietin gene, complete cds
2872	14445	27399	2.23	2.3E-01	AB015033.1	NT	Martiniabilla agarivorans gyrB gene for DNA gyrase subunit B, partial cds, strain:IFO 14957
3004	16056	28960	1.3	2.3E-01	AA013379.1	EST_HUMAN	no16d06.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:130357 3'
3133	16183		7.86	2.3E-01	R21732.1	EST_HUMAN	yf21b07.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130357 3'
3428	16469	28378	1.45	2.3E-01	H69836.1	EST_HUMAN	y97h10.1.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:213283 5'
3912	16941	29820	0.99	2.3E-01	S82821.1	NT	GSTA5=glutathione S-transferase Yc2 subunit (5' region, intron 1) [rat, Morris hepatoma cell line, Genomic, 2212 nt, segment 1 of 3]
4011	17038		6.59	2.3E-01	7662133	NT	Homo sapiens KIAA0450 gene product (KIAA0450), mRNA
4459	17470	30327	0.91	2.3E-01	R82282.1	EST_HUMAN	y17f01.r1 Soares placenta Nb3HP Homo sapiens cDNA clone IMAGE:149017 5'
4508	17516		2.08	2.3E-01	L78789.1	NT	Mus musculus renin (Ren-1c) gene, promoter region
4561	17669	30431	1.04	2.3E-01	D90899.1	NT	Synechocystis sp. PCC6803 complete genome, 1/27, 1-133659
4601	17609	30467	2.01	2.3E-01	AF092635.1	NT	Homo sapiens mitogen-activated protein kinase p38delta (PRKM13) mRNA, complete cds
4669	17674	30544	8.59	2.3E-01	5031984	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5179	18171	31016	0.8	2.3E-01	AB032400.1	NT	Mus musculus tulip 1 mRNA, complete cds
5209	18283	31134	0.69	2.3E-01	BF574804.1	EST_HUMAN	602132210F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271547 5'
5487	18567	31413	2.37	2.3E-01	AB040945.1	NT	Homo sapiens mRNA for KIAA1612 protein, partial cds
5614	18990	31585	2.08	2.3E-01	BF058381.1	EST_HUMAN	7k30b06.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3476699 3' similar to SW:GAG_SMSAV
6720	18793	31885	4.78	2.3E-01	X96587.1	NT	P03330 GAG POLYPROTEIN[CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE
5846	18917		1.14	2.3E-01	L39112.1	NT	SHELL PROTEIN P30; NUCLEOPROTEIN P10] ;
5958	19025	32145	3.24	2.3E-01	S60371.1	NT	C.familiaris rom1 gene
6166	19223	32366	1.86	2.3E-01	A1708840.1	EST_HUMAN	Vitaforma corneum small subunit ribosomal RNA gene
6166	19223	32367	1.86	2.3E-01	A1708840.1	EST_HUMAN	23S rRNA [Leuconostoc carnesum, Genomic, 2866 nt]
6949	19978	33201	0.75	2.3E-01	AF198089.1	NT	as27e12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238
7204	20204	33449	4.52	2.3E-01	A1718148.1	EST_HUMAN	CYTCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
7470	20410	33688	0.65	2.3E-01	8923323	NT	as27e12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238
7667	20601	33899	0.75	2.3E-01	AF000227.1	NT	CYTCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
7816	20745	34050	2.81	2.3E-01	AF175398.1	NT	Oryctolagus cuniculus cytochrome oxidase subunit VIa (coxVIa2) mRNA, complete cds; nuclear gene for
7819	20748	34052	2.15	2.3E-01	AV719681.1	EST_HUMAN	mitochondrial product
7819	20748	34053	2.15	2.3E-01	AV719681.1	EST_HUMAN	as4212.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318887 3' similar to contains Alu
8052	20965		3.54	2.3E-01	6754779	NT	repetitive element;
8057	20970	34286	1.55	2.3E-01	BE886071.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA
8219	21124		2.68	2.3E-01	N80983.1	EST_HUMAN	Sacale carale omega toxin gene, complete cds
8267	21172	34506	0.64	2.3E-01	11416821	NT	Glycine max resistance protein LM17 precursor RNA, partial cds
8267	21172	34507	0.64	2.3E-01	11416821	NT	AV719681 GLC Homo sapiens cDNA clone GLCDB08 5'
8410	21313	34645	0.55	2.3E-01	AF177946.1	NT	AV719681 GLC Homo sapiens cDNA clone GLCDB08 5'
8434	21366	34706	0.72	2.3E-01	AL161558.2	NT	Mus musculus myosin XV (Myo15), mRNA
8573	21504	34848	1.85	2.3E-01	M69931.1	NT	601511573F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912859 5'
9332	22260	35624	0.57	2.3E-01	AW090541.1	EST_HUMAN	za12e08.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:292366 5'
9445	22373	36738	0.55	2.3E-01	AW954460.1	EST_HUMAN	Homo sapiens protocadherin alpha cluster (LOC63960), mRNA
9683	22809	35882	0.63	2.3E-01	AA372184.1	EST_HUMAN	Homo sapiens protocadherin alpha cluster (LOC63960), mRNA
							Streptomyces coelicolor A3(2) phosphoenolpyruvate carboxylase (ppc) gene, complete cds
							Arabidopsis thaliana DNA chromosome 4, contig fragment No. 58
							Oxytricha nova macronuclear telomere-binding protein alpha subunit (tel-alpha alanine version) gene, complete cds
							xc90e06.x1 NCI_CGAP_Brn35 Homo sapiens cDNA clone IMAGE:2591554 3'
							EST376533 MAGE resequences, MAGH Homo sapiens cDNA
							EST84061 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X63368)



Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9883	22809	35983	0.63	2.3E-01	AA372184.1	EST_HUMAN	EST184061 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X63368)
10110	23001	36397	0.74	2.3E-01	6679318	NT	Mus musculus phosphatidylinositol 3-kinase catalytic subunit delta (PIK3cd), mRNA
10249	23140	36546	0.61	2.3E-01	BE277860.1	EST_HUMAN	601120110F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2986739 5'
10301	23191	36602	0.94	2.3E-01	AW964460.1	EST_HUMAN	EST376533 MAGE sequences, MAGH Homo sapiens cDNA
10347	23236	36654	1.53	2.3E-01	X52124.1	NT	Haemophilus influenzae genes for HincII restriction-modification system (HincII methyltransferase (EC 2.1.1.72) and HincII endonuclease (EC 3.1.21.4))
10380	23269	36691	0.68	2.3E-01	AW964633.1	EST_HUMAN	PM2-DT0038-281299-001-404 DT0038 Homo sapiens cDNA
10443	23332	36749	3.13	2.3E-01	BE173060.1	EST_HUMAN	MRO-HT0559-240400-014-g11 HT0559 Homo sapiens cDNA
10498	23386	36796	2.6	2.3E-01	AJ293281.1	NT	Rhizobium leguminosarum partial genomic DNA for exopolysaccharide biosynthesis genes
10823	23808	37236	0.95	2.3E-01	AF201926.1	EST_HUMAN	Murine hepatitis virus strain 2, complete genome
10933	23818		6.03	2.3E-01	BF133577.1	EST_HUMAN	601646159R2 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4102092 3'
11453	24369	37818	1.7	2.3E-01	AF004833.1	NT	Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds
11453	24369	37810	1.7	2.3E-01	AF004833.1	NT	Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds
11634	24540	38012	2.07	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11834	24540	38013	2.07	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11790	24712	38203	3.1	2.3E-01	AE002187.2	NT	Chlamydia pneumoniae AR39, section 4 of 94 of the complete genome
12206	25041		1.55	2.3E-01	AV709736.1	EST_HUMAN	AV709736 ADG Homo sapiens cDNA clone ADCAGH01 5'
12369	25148		3.95	2.3E-01	U45426.1	NT	Borrelia burgdorferi 2.9-b locus, ORF-A-D genes, complete cds and REP+ gene, partial cds
12436	25194		42.5	2.3E-01	T27231.1	EST_HUMAN	HCOEST144 HT28M8 Homo sapiens cDNA clone HCoE44 5'
12516	25375	31474	3.18	2.3E-01	AW303623.1	EST_HUMAN	x21d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813773 3' similar to TR:Q9Z176
12562	25916	31370	9.63	2.3E-01	BE882464.1	EST_HUMAN	Q9Z175 LYSYL OXIDASE-RELATED PROTEIN 2; contains PTR5.b2 TAR1 repetitive element;
12597	25283		1.91	2.3E-01	BF663319.1	EST_HUMAN	601507202F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908689 5'
12645	25321		1.8	2.3E-01	AJ00519.1	NT	602144459F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297719 5'
12736	25321		1.6	2.3E-01	AJ006519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
12968	25533		1.91	2.3E-01	BF475911.1	EST_HUMAN	Rattus norvegicus mRNA for acid gated ion channel
92	13205	26118	0.78	2.2E-01	AI052190.1	EST_HUMAN	rac39h12.x1 Lupsid_sclaitc_nerve Homo sapiens cDNA clone IMAGE:3395950 3' similar to contains element MER38 repetitive element;
1585	14616	27579	2	2.2E-01	AF187850.1	NT	ox14a10.x1 Soares_fetal_liver_spleen_NFLS_S1 Homo sapiens cDNA clone IMAGE:1676290 3' similar to TR:Q13040 Q13040 ATP-BINDING CASSETTE PROTEIN;
2101	15115	28120	2.24	2.2E-01	M34640.1	NT	Homo sapiens PPAR delta gene, promoter region
2426	15429	28430	5.5	2.2E-01	BF677538.1	EST_HUMAN	Fresh-water sponge Emf1 alpha collagen (COLF1) gene
2627	15625	28618	1.92	2.2E-01	BE18258.1	EST_HUMAN	602085609F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249969 5'
						EST_HUMAN	601462629F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866190 5'

Page 92 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2627	15625	28819	1.92	2.2E-01	BE18258.1	EST_HUMAN	G01462629F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866190 5'
2924	15977	28875	5.61	2.2E-01	BE155625.1	EST_HUMAN	PM2-HT0353-281299-003-a12 HT0353 Homo sapiens cDNA
2924	15977	28876	5.61	2.2E-01	BE155625.1	EST_HUMAN	PM2-HT0353-281299-003-a12 HT0353 Homo sapiens cDNA
2963	16015		2.07	2.2E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
3451	16492		3.7	2.2E-01	AL161562.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 62
3816	16846	28731	0.66	2.2E-01	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
3884	16913		1.11	2.2E-01	AF155728.1	NT	Xiphophorus maculatus truncated Rax1 retrolactonase reverse transcriptase (RT) pseudogene
4308	17322		1.03	2.2E-01	AF119102.1	NT	Drosophila melanogaster UNC-119 (unc-119) gene, complete cds
4316	17330	30194	6.07	2.2E-01	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds
4363	17377	30240	2.9	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase 1 (Mek1) mRNA, complete cds
4363	17377	30241	2.9	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase 1 (Mek1) mRNA, complete cds
4465	17475	30334	1.18	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4465	17475	30335	1.18	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4939	17938		1.66	2.2E-01	D50804.1	NT	Human beta-cytoplasmic actin (ACTBP9) pseudogene
4945	17944	30802	1.72	2.2E-01	AA211216.1	EST_HUMAN	zq87c05.r1 Striatagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648998 5'
5088	18085	30936	1.06	2.2E-01	M86524.1	NT	Human dystrophin gene
5173	18185		1.2	2.2E-01	L13299.1	NT	Mus musculus vinculin gene, exon 3
5283	18259	31117	1.18	2.2E-01	H60548.1	EST_HUMAN	y42h09.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:208001 5' similar to gb:214116.m1 CD69 GLYCOPROTEIN PRECURSOR (HUMAN);
5402	18384	31224	1.59	2.2E-01	5835974	NT	Vidua chalybeata mitochondrion, complete genome
5403	18385	31225	1.32	2.2E-01	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
5951	19018	32138	1.79	2.2E-01	5803002	NT	Homo sapiens diaphanous (Drosophila, homolog 2) (DIAPH2), transcript variant 156, mRNA
5962	19029		3.45	2.2E-01	D64000.1	NT	Synechocystis sp. PCC6803 complete genome, 19/27, 2392729-2538999
6231	19285	32443	0.76	2.2E-01	U67087.1	NT	Gallus gallus T-box containing protein (Ch-TbxT) mRNA, complete cds
6231	19285	32444	0.76	2.2E-01	U67087.1	NT	Gallus gallus T-box containing protein (Ch-TbxT) mRNA, complete cds
7003	20030	33261	0.69	2.2E-01	AB038490.1	NT	Homo sapiens gene for tukulin, complete cds
7105	20311	33572	0.45	2.2E-01	AA490106.1	EST_HUMAN	ab02ae09.s1 Striatagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839656 3'
7105	20311	33573	0.45	2.2E-01	AA490106.1	EST_HUMAN	ab02ae09.s1 Striatagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839656 3'
7372	20366	33636	8.36	2.2E-01	AV766238.1	EST_HUMAN	AV766238 BM Homo sapiens cDNA clone BMF-AHC06 5'
7489	20429	33708	1.58	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphoglycerate kinase (pgkA) and ABC transporter ATP-binding protein (stpA) genes, complete cds; and unknown genes

Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7489	20429	33709	1.58	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphatidylglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (slpA) genes, complete cds; and unknown genes
7671	20605	33903	1.87	2.2E-01	M24136.1	NT	Human glycoprotein B gene, exon 4
7671	20605	33904	1.87	2.2E-01	M24136.1	NT	Human glycoprotein B gene, exon 4
7908	20831	34134	0.68	2.2E-01	AE000035.2	NT	Mycoplasma pneumoniae M129 section 45 of 63 of the complete genome
8155	21062	34993	0.61	2.2E-01	AF287867.1	NT	Homo sapiens homeobox B7 (HOXB7) gene, partial cds; and homeobox B6 (HOXB6), homeobox B5 (HOXB5), homeobox B4 (HOXB4), and homeobox B3 (HOXB3) genes, complete cds
8191	21098	34428	0.62	2.2E-01	AB024553.1	NT	Bacillus halodurans DNA, complete and partial cds, strain C-125
8599	21530		2.43	2.2E-01	AF155143.1	NT	Mus musculus nm23-M1 gene, promoter region
8667	21598	34938	0.76	2.2E-01	Z48933.1	NT	E.coli sepA and sepB genes
9115	22043	35399	0.63	2.2E-01	AJ132918.1	NT	Pen troglodytes MeCP2 gene 3'UTR
9439	22367	35728	0.57	2.2E-01	L23312.1	NT	Mouse HD protein mRNA, complete cds
9439	22367	35729	0.57	2.2E-01	L23312.1	NT	Mouse HD protein mRNA, complete cds
9453	22381	35743	4.62	2.2E-01	AE001713.1	NT	Thermoloba maritima section 25 of 136 of the complete genome
9473	22401	35783	0.8	2.2E-01	U09984.1	NT	Mus musculus ICR/Swiss glyceroldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
9873	22600		2.97	2.2E-01	AW856039.1	EST_HUMAN	PM3-C10263-241289-009-b07 C10263 Homo sapiens cDNA
9859	22585	35956	2.61	2.2E-01	8393247	NT	Mus musculus deformed epidermal autoregulatory factor 1 (Drosophila) (Deaf1), mRNA
9740	22684	36049	1.46	2.2E-01	BF376364.1	EST_HUMAN	MR1-TN0045-110900-006-c02 TN0045 Homo sapiens cDNA
9829	22735	36117	1.49	2.2E-01	W02988.1	EST_HUMAN	zad408.r1 Soares melanocyte 2NBM Homo sapiens cDNA IMAGE:291691 5'
9847	22955	36345	17.3	2.2E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BA72 (HLA-B-ASSOCIATED TRANSCRIPT 2)
9890	22805	36193	0.81	2.2E-01	AJ009839.1	NT	Xenopus laevis mRNA for kinesin-like protein 3 (xklp3)
9901	22889	36273	0.95	2.2E-01	7657428	NT	Mus musculus osteoblast specific factor 2 (OSF-2), mRNA
9915	22903	36290	4.25	2.2E-01	M89643.1	NT	Brachydanio rerio epandymin beta and gamma chains (Epd) gene, complete cds
10147	23038	36437	0.66	2.2E-01	Q90980	SWISSPROT	CYCLIC NUCLEOTIDE GATED CHANNEL, ROD PHOTORECEPTOR, ALPHA SUBUNIT (CNG CHANNEL 3) (CNG-3) (CNG3)
10331	23220	36634	3.89	2.2E-01	AF197941.1	NT	Funaria hygrometrica chloroplast-localized small heat shock protein (CPs-HSP21) mRNA, complete cds; nuclear gene for chloroplast product
10460	23348	36765	2.15	2.2E-01	BF208507.1	EST_HUMAN	G01869724F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100189 5'
10673	23559	36991	1.18	2.2E-01	9625671	NT	Human herpesvirus 5, complete genome
							Pseudomonas aeruginosa quinoxaline elhamol dehydrogenase (exaA) gene, partial cds; cytochrome c550 precursor (exaB), NAD+ dependent acetaldehyde dehydrogenase (exaC), and pyrrodoquinone synthase A (pqqA) genes, complete cds; and pyrroquinol
10857	23743	37166	0.54	2.2E-01	AF068264.1	NT	Mus musculus PHR1 (Phr1) gene, partial cds
10924	23809		0.7	2.2E-01	AF071001.1	NT	

Page 94 of 545  
Table 4

## Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10968	23852	37277	0.59	2.2E-01	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
10968	23852	37278	0.59	2.2E-01	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
11652	24558	38028	1.46	2.2E-01	AB021083.1	NT	TT virus ORF1 gene, isolate TS4-II, partial cds
11854	24704	38195	5.43	2.2E-01	X01918.1	NT	Drosophila 68C glue gene cluster
11893	23893	37432	3.94	2.2E-01	7708215	NT	Homo sapiens H-2K binding factor-2 (LOC51580), mRNA
12293	25104		2.1	2.2E-01	BE870959.1	EST_HUMAN	601446957F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850670.5
12392	26926		4.39	2.2E-01	U82871.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), calreticlin (CALT), NAD(P)-H dehydrogenase-like protein (NSDHL), and LIP
12468	25214		3.94	2.2E-01	AF188843.1	NT	Vitis vinifera cultivar Pinot Noir plasma membrane aquaporin (PIP1a) mRNA, complete cds
12567	18428	31362	3.91	2.2E-01	AW367098.1	EST_HUMAN	RC1-CT0249-141189-021-g04 CT0249 Homo sapiens cDNA
12618	25305	31815	1.89	2.2E-01	11426873	NT	Homo sapiens zinc finger protein 220 (ZNF220), mRNA
13042	25921		2.36	2.2E-01	AV694801.1	EST_HUMAN	AV694801 GKC Homo sapiens cDNA clone GKCAH802.5
997	14047	26881	1.65	2.1E-01	AA569289.1	EST_HUMAN	nm31a11.s1 NCI_CGAP_Lp2 Homo sapiens cDNA clone IMAGE:1061804
1000	14049	26893	1.18	2.1E-01	AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
1151	14192		2.58	2.1E-01	AE002314.2	NT	Chlamydia muridarum, section 45 of 85 of the complete genome
1226	14263	27206	1.16	2.1E-01	6754299	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1228	14263	27206	1.16	2.1E-01	6754299	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1531	14561	27521	1.32	2.1E-01	AJ248965.1	NT	Mus musculus mas proto-oncogene and Igf2r gene for insulin-like growth factor type 2 and L41ps and Au76 pseudogenes
1930	14951	27927	1.7	2.1E-01	AA906824.1	EST_HUMAN	ok73e02.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1519610.3 similar to gb.K02765
2170	15182	28188	2.31	2.1E-01	BF695073.1	EST_HUMAN	COMPLEMENT C3 PRECURSOR (HUMAN);
2503	15925	28505	1.01	2.1E-01	H73968.1	EST_HUMAN	602083129F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247503.5
2503	15925	28506	1.01	2.1E-01	H73968.1	EST_HUMAN	y00407.s1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:232837.3
2586	15584	28578	0.96	2.1E-01	AF022814.1	NT	y00407.s1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:232837.3
2967	16019	28916	2.34	2.1E-01	6912445	NT	Fugu rubripes transcription factor (SLP-1) and heme-oxygenase genes, complete cds
3874	16903		7.46	2.1E-01	9838361	NT	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 4 (KCNH4), mRNA
4139	17160	30036	1.04	2.1E-01	P11675	SWISSPROT	Beta vulgaris mitochondrion, complete genome
4139	17160	30037	1.04	2.1E-01	P11676	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4348	17362		1.11	2.1E-01	AF124526.1	NT	IMMEDIATE-EARLY PROTEIN IE180
4483	17494		1.74	2.1E-01	AB033041.1	NT	Orchestia carymana calcium-binding protein BP23 precursor (BP23) gene, complete cds
4691	17696	30562	2.64	2.1E-01	AB010273.1	NT	Homo sapiens mRNA for KIAA1215 protein, partial cds
						NT	Homo sapiens psnp47 gene, complete cds

Page 95 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4746	17751	30609	0.66	2.1E-01	X93161.1	NT	P.falciparum mRNA for small GTPase rab11
5156	18149	30995	1.7	2.1E-01	D13567.1	NT	Lampetia japonica mRNA for alpha-2-macroglobulin, complete cds
5395	18377	31219	1.12	2.1E-01	4557484	NT	Homo sapiens ceruloplasmin (ferroxidase) (CP) mRNA
5414	18385	31232	0.76	2.1E-01	BE157936.1	EST_HUMAN	MR2-HT0377-070100-011-g08 HT0377 Homo sapiens cDNA
5484	18565	31409	0.2	2.1E-01	BF072395.1	EST_HUMAN	602152001F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293001 5'
7214	20214	33461	1.1	2.1E-01	AJ233392.1	NT	Dodo fragilis mitochondrial 16S rRNA gene, partial
7228	20136	33376	2.05	2.1E-01	U04642.1	NT	Human olfactory receptor (OR17-2) gene, partial cds
7805	20734	34036	0.67	2.1E-01	Q01956	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7805	20734	34037	0.67	2.1E-01	Q01956	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7818	20747		2.13	2.1E-01	AE000972.1	NT	Archaeoglobus fulgidus section 135 of 172 of the complete genome
8169	21072	34402	1.76	2.1E-01	AF000949.1	NT	Canis familiaris keratin (KRT9) gene, complete cds
8218	21123	34455	1.3	2.1E-01	AF068687.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
8218	21123	34456	1.3	2.1E-01	AF068687.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
8285	21188		0.45	2.1E-01	T87354.1	EST_HUMAN	yc83b01.r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:114793 5'
8650	21581		1.26	2.1E-01	7305030	NT	Mus musculus erythrocyte protein band 4.1-like 3 (Epb4.13), mRNA
9069	21998	36352	3.85	2.1E-01	U88389.1	NT	Haemophilus influenzae hmcD, putative haemochrom processing protein (hmcC), putative ABC transporter (hmcB), putative haemochrom structural protein (hmcA), and haemochrom immunity protein (hmcI) genes, complete cds
9355	22283	35944	0.94	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0614_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434H0614 5'
9355	22283	35945	0.94	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0614_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434H0614 5'
9589	22515	35877	6.8	2.1E-01	Z35786.1	NT	S.cerevisiae chromosome II reading frame ORF YBL025w
10035	22935	36323	0.7	2.1E-01	N42536.1	EST_HUMAN	Y711e10.r1 Soares melanocyte 2N1bHM Homo sapiens cDNA clone IMAGE:270954 5'
10035	22935	36324	0.7	2.1E-01	N42536.1	EST_HUMAN	Y711e10.r1 Soares melanocyte 2N1bHM Homo sapiens cDNA clone IMAGE:270954 5'
10044	22960	36348	2.89	2.1E-01	X97378.1	NT	A.thaliana mRNA for ATRAP1b protein
10144	23035	36433	0.97	2.1E-01	AB036529.1	NT	Homo sapiens p53R2 gene for ribonucleotide reductase, exon 8
10818	23704	37132	1.48	2.1E-01	Z97067.1	NT	Beta vulgaris mRNA for elongation factor 1-beta
10846	23732	37155	2.12	2.1E-01	P52824	SWISSPROT	DIACYLGLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DELTA)
10853	23739	37162	0.84	2.1E-01	BF574254.1	EST_HUMAN	(80 KD DIACYLGLYCEROL KINASE)
11918	24763		1.7	2.1E-01	A1141875.1	EST_HUMAN	602131427F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4270831 5'
11996	24838		2.83	2.1E-01	11036647	NT	q65108.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1691751 3'
12011	24853	36354	2.01	2.1E-01	BE180422.1	EST_HUMAN	Homo sapiens pancreatic polypeptide 2 (PPY2), mRNA
							RC3-HT0622-040500-013-b11 HT0622 Homo sapiens cDNA

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12230	25524		2.08	2.1E-01	X57624.1	NT	Drosophila melanogaster ALA-E6 DNA, repeat region
12713	25564		1.45	2.1E-01	AF217400.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
12956	26517		1.97	2.1E-01	BE622149.1	EST_HUMAN	6014407.12F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916676 5'
13097	25593	31725	1.51	2.1E-01	BE672330.1	EST_HUMAN	7a59e02.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3223034 3'
213	13312	26230	1.93	2.0E-01	AB017437.1	NT	Gallus gallus mRNA for avian, complete cds
557	13826		2.34	2.0E-01	7705601	NT	Homo sapiens CGI-18 protein (LOC51008). mRNA
723	13781	26703	0.98	2.0E-01	M77085.1	NT	O cuniculus germline IgH heavy chain V-H pseudogene, allotype VHa2
836	13891	26828	1.97	2.0E-01	AF027885.1	NT	Mus musculus Major Histocompatibility Locus class II region
1039	14085	27024	0.79	2.0E-01	D80905.1	NT	Synochocystis sp. PCC8803 complete genome, 7/27, 781449-920915
1152	14193	27131	2.56	2.0E-01	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
1282	14315	27264	1.45	2.0E-01	AJ132695.5	NT	Homo sapiens rac1 gene
1334	14368	27318	1.4	2.0E-01	AW384937.1	EST_HUMAN	PM1-HT0422-291299-002-c06 HT0422 Homo sapiens cDNA
1479	14510		1.16	2.0E-01	AJ243987.1	NT	Plum pox virus strain M, complete genome, isolate PS
1505	14536	27499	9.31	2.0E-01	4503408	NT	Homo sapiens dystrobrevin, alpha (DTNA), mRNA
1574	14604	27564	1.95	2.0E-01	AB007974.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0505
1579	14609	27670	1.13	2.0E-01	AF260700.1	NT	Homo sapiens sodium/iodide symporter mRNA, partial cds
1723	14751	27719	1.33	2.0E-01	U22346.1	NT	Human bradykinin B1 receptor (bradyb1) gene, complete cds
1746	14773		1.69	2.0E-01	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1782	14808		2.69	2.0E-01	U67625.1	NT	Methanococcus jannaschii section 67 of 150 of the complete genome
2370	15376		1.69	2.0E-01	X82877.1	NT	H. sapiens Na+-D-glucose cotransport regulator gene
2932	15985		1.05	2.0E-01	AF074690.1	NT	Homo sapiens full length insert cDNA YH85A11
3646	16584	29489	0.86	2.0E-01	P46907	SWISSPROT	HOMEBOX PROTEIN GLABRA2 (HOMEBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)
3628	16664		1.19	2.0E-01	AW238005.1	EST_HUMAN	xp15b02.x1 NCL_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2740395 3' similar to contains element
3770	18802	29689	0.84	2.0E-01	P34641	SWISSPROT	MER21 repetitive element;
4038	17085	29955	0.98	2.0E-01	Z46906.1	NT	CEB-11 PROTEIN
4114	17137	30011	0.85	2.0E-01	X83997.1	NT	Sus scrofa
4538	17547	30408	0.66	2.0E-01	AF242431.1	NT	C.parasilica eapC gene
4681	17686		7.99	2.0E-01	BE826165.1	EST_HUMAN	Mus musculus neuronal apoptosis inhibitory protein 6 (Naip6) gene, complete cds; and Naip3 gene, exons 2-9 and 11-16
5154	18147	30992	0.81	2.0E-01	AA861824.1	EST_HUMAN	QV4-EN0032-180500-223-e03 EN0032 Homo sapiens cDNA
5154	18147	30993	0.81	2.0E-01	AA861824.1	EST_HUMAN	ak35h06.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1407995 3'
5154	18147	30993	0.81	2.0E-01	AA861824.1	EST_HUMAN	ak35h06.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1407995 3'
5170	18162	31010	8.09	2.0E-01	8922080	NT	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA

Page 97 of 545  
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Single Exon Probes Expressed in Adult Liver

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5201	16584	29489	0.66	2.0E-01	P46607	SWISSPROT	HOMEOBOX PROTEIN GLABRA2 (HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)
5244	18231	31081	0.95	2.0E-01	Y19216.1	NT	Homo sapiens putative psithbD pseudogene for hair keratin, exons 1 to 9
5358	18341		1.34	2.0E-01	A1274530.1	EST_HUMAN	qv10e02.x1 NCL CGAP_Kid8 Homo sapiens cDNA clone IMAGE:1981178 3' similar to gb:M16967
5630	18706	31605	2.4	2.0E-01	X56600.1	NT	COAGULATION FACTOR V PRECURSOR (HUMAN);
5944	18011	32130	2.06	2.0E-01	11432540	NT	Rat SOD-2 gene for manganese-containing superoxide dismutase
6054	18116	32245	0.78	2.0E-01	X91856.1	NT	Homo sapiens dual oxidase-like domains 2 (DUOX2) mRNA
6296	19348	32514	6.16	2.0E-01	U15300.1	NT	F. rubripes DNA encoding for valyl-tRNA synthetase
6416	19463		0.61	2.0E-01	M75987.1	NT	Saccharomyces cerevisiae Hal5p (HAL5) mRNA, complete cds
6538	19581	32765	0.59	2.0E-01	P02467	SWISSPROT	Human hepatocyte growth factor gene, exon 1
6697	19733	32834	4.07	2.0E-01	X61033.1	NT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
6808	19841	33052	3.82	2.0E-01	AW360885.1	EST_HUMAN	M. auratus mu class glutathione transferase gene
7665	20502	33791	0.54	2.0E-01	U98724.1	NT	PM1-CT0247-141099-001-g06 CT0247 Homo sapiens cDNA
7674	20608	33907	1.19	2.0E-01	AF250371.1	NT	Mycoplasma genitalium section 46 of 61 of the complete genome
7849	20776	34077	0.77	2.0E-01	P84422	SWISSPROT	Mus musculus phosphotransferase-1 C isozyme (Pfkf) gene, exons 3 through 7
8248	21153	34488	0.64	2.0E-01	V00726.1	NT	GAMMA-GLUTAMYL TRANSPEPTIDASE PRECURSOR
8369	21273	34608	5.19	2.0E-01	AK024427.1	NT	Mouse germ line gene coding for beta-globin (Y2)
8531	21462		7.24	2.0E-01	AF028026.1	NT	Homo sapiens mRNA for FLJ00016 protein, partial cds
8779	21709	35055	3.52	2.0E-01	X91151.1	NT	Andes virus strain O123133 glycoprotein G1 and G2 precursor, gene, partial cds
9889	22804	36192	1.26	2.0E-01	U82511.1	NT	M. musculus sep2 gene exon 14
9927	22832	36219	0.69	2.0E-01	U71122.1	NT	Dichostelium discoidium random slug cDNA19 protein (scs19) mRNA, partial cds
10085	22878	36566	5.64	2.0E-01	AE001278.1	NT	Arabidopsis pyruvate decarboxylase-2 (Pdc2) gene, complete cds
10266	23156	36567	0.53	2.0E-01	P11420	SWISSPROT	Chlamydia trachomatis section 5 of 87 of the complete genome
10403	23292		2.26	2.0E-01	AF146692.1	NT	DAUGHTERLESS PROTEIN
10544	23430	36850	2.07	2.0E-01	AF086907.1	NT	Homo sapiens filamin 2 (FLN2) mRNA, complete cds
10544	23430	36851	2.07	2.0E-01	AF086907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
10864	23550	36983	0.8	2.0E-01	AF157814.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
10564	23550	36984	0.6	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10710	23596		0.85	2.0E-01	X78388.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10890	23775	37201	1.03	2.0E-01	X97121.1	NT	D. melanogaster DNA mobile element (hoppe)
11278	24200	37652	2.76	2.0E-01	D99088.1	NT	R. norvegicus mRNA for NTR2 receptor
11278	24200	37653	2.76	2.0E-01	D99088.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds

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12213	25047		1.44	2.0E-01	P24873	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 6
12223	25057	38556	45.65	2.0E-01	AA559191.1	EST_HUMAN	1168c12.s1 NC1_CGAP_P4.1 Homo sapiens cDNA clone IMAGE:1045846 similar to gbM81105 MYOSIN HEAVY CHAIN, NONMUSCLE TYPE A (HUMAN);
12891	26348		1.92	2.0E-01	AF206637.2	NT	Pinephales promelas liver glucose-6-phosphate-1-dehydrogenase mRNA, partial cds
12872	25773		1.89	2.0E-01	AF302773.1	NT	Homo sapiens nilein-Lm isoform (nilein) mRNA, complete cds
12885	25704	31661	2.56	2.0E-01	AW975297.1	EST_HUMAN	EST387405 MAGE resequences, MAGN Homo sapiens cDNA
12920	25530	31748	3.46	2.0E-01	AI023592.1	EST_HUMAN	ov80a10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1643610 3'
12941	25508		15.98	2.0E-01	AF078184.2	NT	Homo sapiens Ku70-binding protein (KUB3) mRNA, partial cds
114	13222		5.83	1.9E-01	7549743	NT	Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Ahr1), mRNA
372	13459	26374	5.8	1.9E-01	AF004353.1	NT	Mus musculus pale ear (ep) gene, wild type allele, 3' region, partial cds
679	13741	26655	1.15	1.9E-01	U32581.2	NT	Homo sapiens lambda1/cia protein kinase C-interacting protein mRNA, complete cds
679	13741	26656	1.15	1.9E-01	U32581.2	NT	Homo sapiens lambda1/cia protein kinase C-interacting protein mRNA, complete cds
686	13748	26663	4.55	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-401 BT0502 Homo sapiens cDNA
687	13748	26663	6.39	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-401 BT0502 Homo sapiens cDNA
1013	14062		3.84	1.9E-01	7305180	NT	Mus musculus interleukin 2 receptor, gamma chain (Il2rg), mRNA
1131	14173	27111	5.97	1.9E-01	AA358813.1	EST_HUMAN	EST67784 Fetal lung II Homo sapiens cDNA 5' end
1397	14428	27382	1.72	1.9E-01	AF081282.1	NT	Sorghum bicolor 22 kDa kafirin cluster
1455	14487		3.57	1.9E-01	AF184623.1	NT	Plasmodium vivax reticulocyte binding protein-2 (rbp-2) gene, complete cds
2404	16409	28412	6.5	1.9E-01	8922533	NT	Homo sapiens hypothetical protein FLJ10581 (FLJ10581), mRNA
2965	16017	28914	4.62	1.9E-01	U66066.1	NT	Sigmoidon hiepidus p53 gene, partial cds
2980	16031		8.17	1.9E-01	J00922.1	NT	Callus gallus ovalbumin (Y) gene, complete cds
3045	16097	29000	0.97	1.9E-01	U25148.1	NT	Rattus norvegicus brush border myosin-1 (BBM1) mRNA, partial cds
3441	16482	29390	0.82	1.8E-01	5803065	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
3455	16496	29400	8.52	1.9E-01	D13197.1	NT	Mouse gene for immunoglobulin diversity region D1
3539	16577	29481	6.95	1.9E-01	R16467.1	EST_HUMAN	y4210.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:129547 5'
3872	16901	29784	0.76	1.9E-01	AF264017.1	NT	Rattus norvegicus arylacetamide deacetylase gene, complete cds
4078	17104	29983	4.85	1.9E-01	AB006784.1	NT	Schizosaccharomyces pombe DNA for cytoplasmic dynein heavy chain, complete cds
4171	17192	30064	2.05	1.9E-01	AW754106.1	EST_HUMAN	CM3-CT0315-271199-045-b11 CT0315 Homo sapiens cDNA
4231	17247		0.98	1.9E-01	AE001912.1	NT	Deinoceratus radiodurans R1 section 49 of 229 of the complete chromosome 1
4331	17345	30210	1.12	1.9E-01	BE834943.1	EST_HUMAN	MR1-FN0010-290700-007-404 FN0010 Homo sapiens cDNA
4581	17589	30450	0.76	1.9E-01	AL181493.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 5
4885	17884	30750	0.84	1.9E-01	Z93780.1	NT	Fugu rubripes genes encoding carboxyl phosphate synthetase III, myosin light chain, MAP2
5134	18130		1.22	1.9E-01	AF223842.1	NT	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds



Page 99 of 545  
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5798	18870		4.81	1.9E-01	AW130149.1	EST_HUMAN	x129a07.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2819444 3' similar to gb.M73779 RETINOIC ACID RECEPTOR ALPHA-1 (HUMAN);
5841	18912	32028	6.81	1.9E-01	AF127037.1	NT	Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a
6053	19115	32244	0.63	1.9E-01	AF091216.1	NT	Mus musculus Wrm protein (Wrm) gene, complete cds
6102	19163		2.78	1.9E-01	AU133116.1	EST_HUMAN	AU133116 NT2RP4 Homo sapiens cDNA clone NT2RP4001328 5'
6187	19244		0.54	1.9E-01	AE001289.1	NT	Chlamydia trachomatis section 26 of 87 of the complete genome
6584	19625	32809	0.94	1.9E-01	AI762391.1	EST_HUMAN	w64h02.x1 NCL_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2394099 3'
6651	19693	32883	0.88	1.9E-01	AW149452.1	EST_HUMAN	x14c08.x1 NCL_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2618030 3' similar to gb.X03559 ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR (HUMAN);
7311	18479	31302	1.77	1.9E-01	IR43212.1	EST_HUMAN	y909a12.c1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:31683 3' similar to contains MER13 repetitive element;
7315	18483	31307	0.57	1.9E-01	X68216.1	NT	P. sativum PS-IAA4/5 gene
7341	20337	33602	0.83	1.9E-01	AF034920.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7341	20337	33603	0.83	1.9E-01	AF034920.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7633	20568	33863	0.59	1.9E-01	U73946.1	NT	Drosophila melanogaster testis-specific RNA-binding protein (bruno) mRNA, complete cds
7888	20814	34120	0.64	1.9E-01	U93688.1	NT	Staphylococcus aureus toxic shock syndrome toxin-1 (tsst), enterotoxin (ent), and integrase (int) genes, complete cds
7913	20837	34140	1.13	1.9E-01	U80922.1	NT	Arabidopsis thaliana serine/threonine protein phosphatase type one (TOPP8) gene, complete cds
7966	20888	34199	2.71	1.9E-01	AF072724.1	NT	Zea mays starch branching enzyme I (sbe1) gene, complete cds
8665	21496	34839	1.72	1.9E-01	AL161657.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57
9244	22172	35529	13.68	1.9E-01	AB033024.1	NT	Homo sapiens mRNA for KIAA1198 protein, partial cds
9500	22428	35790	1.56	1.9E-01	M14568.1	NT	Marsupial cat beta-globin gene mRNA, partial cds
9500	22428	35791	1.56	1.9E-01	M14568.1	NT	Marsupial cat beta-globin gene mRNA, partial cds
10387	23276	36697	0.93	1.9E-01	AA912486.1	EST_HUMAN	o93g10.s1 NCL_CGAP_PNS1 Homo sapiens cDNA clone IMAGE:1537506 3' similar to contains Alu repetitive element;
10736	23622	37053	0.91	1.9E-01	BE830353.1	EST_HUMAN	RC5-E10082-060700-022-A02 E10082 Homo sapiens cDNA
10736	23622	37054	0.91	1.9E-01	BE830353.1	EST_HUMAN	RC5-E10082-060700-022-A02 E10082 Homo sapiens cDNA
11088	24020	37481	2	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
11088	24020	37462	2	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
11196	24121	37567	2.99	1.9E-01	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11936	24780	38276	1.55	1.9E-01	M22253.1	NT	Rattus norvegicus sodium channel 1 mRNA, complete cds
12147	24987	38488	2.14	1.9E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
12169	25005	38508	1.58	1.9E-01	U07344.1	NT	Influenza A/Guangdong/243/72 nucleoprotein (seg 6) gene, 5' end

Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
33	13149	28038	2.65	1.8E-01	U73200.1	NT	Mus musculus p16Rip mRNA, complete cds
278	15871	26288	1.29	1.8E-01	AB022090.1	NT	Mus musculus Ccig gene for chaperonin containing TCP-1 gamma subunit, partial cds
391	13475	26395	1.58	1.8E-01	4502532	NT	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products
770	13827	28768	0.81	1.8E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
1009	14058	27000	0.8	1.8E-01	AF121212.1	EST_HUMAN	wd7102.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337051 3'
1118	14159	27097	1.46	1.8E-01	AF000580.1	NT	Dicotyledon discolorum plasmid Ddp5, complete genome
1315	14348	27295	7.91	1.8E-01	AL117189.1	NT	Yersinia pestis plasmid pOD1
1889	14910		1.15	1.8E-01	AF13708.1	EST_HUMAN	qg22d10.x5 NCL CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1761811 3' similar to TR:O75936 O75936 GAMMA BUTYROBETAINE HYDROXYLASE ;
1931	14952	27928	1.64	1.8E-01	AB051897.1	NT	Mus musculus Scya6, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
2742	15735		2.61	1.8E-01	AW935728.1	EST_HUMAN	QV3-DT0018-081299-038-g04 DT0018 Homo sapiens cDNA
2940	15993		1.86	1.8E-01	AF184589.1	NT	Jonopsidium acule LEAFY protein (LEAFY2) gene, partial cds
2947	15999	28901	1.18	1.8E-01	AW182300.1	EST_HUMAN	X41a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659756 3'
3169	16219	29109	1.07	1.8E-01	AW995178.1	EST_HUMAN	QV0-BN0041-070300-147-c04 BN0041 Homo sapiens cDNA
3423	16484	28371	0.99	1.8E-01	BF183682.1	EST_HUMAN	BD1809723R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040821 3'
3687	16720	29612	0.86	1.8E-01	H03369.1	EST_HUMAN	y45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:161704 3' similar to contains Alu repetitive element;
3687	16720	29613	0.86	1.8E-01	H03369.1	EST_HUMAN	y45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:161704 3' similar to contains Alu repetitive element;
4345	17359	30224	1.01	1.8E-01	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
4441	17452		0.99	1.8E-01	D37954.1	NT	Bovine NB25 mRNA for MHC class II (BoLA-DQB), complete cds
4671	17675	30545	6.57	1.8E-01	AL161598.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 56
4886	17885	30751	2.43	1.8E-01	AB051897.1	NT	Mus musculus Scya6, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
5177	18169	31014	1.77	1.8E-01	AW814270.1	EST_HUMAN	MR3-ST0203-151299-112-g06 ST0203 Homo sapiens cDNA
5230	18213	31065	1.04	1.8E-01	AF181250.1	NT	Mesocricetus auratus Na-taurocholate cotransporting polypeptide mRNA, partial cds
5259	18245	31096	1.16	1.8E-01	AF143981.1	EST_HUMAN	if57e04.x1 NCL CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2134590 3'
5324	18308	31158	0.71	1.8E-01	AL161559.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
5481	18562	31406	0.56	1.8E-01	BE082626.1	EST_HUMAN	RC6-BT0841-300300-011-H03 BT0841 Homo sapiens cDNA
8019	19081	32207	1.05	1.8E-01	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6149	19203	32347	0.88	1.8E-01	N28629.1	EST_HUMAN	yx38h08.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:264063 5'
6368	19417	32582	1.05	1.8E-01	6678428	NT	Mus musculus Tnf receptor-associated factor 6 (Traf6), mRNA
6368	19417	32583	1.05	1.8E-01	6678428	NT	Mus musculus Tnf receptor-associated factor 6 (Traf6), mRNA
6790	19823	33035	1.39	1.8E-01	Q9QY14	SWISSPROT	FORKHEAD BOX PROTEIN E3
6839	19871		2.26	1.8E-01	N94853.1	EST_HUMAN	yy62h02.r1 Soares, multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:278163 5'
7186	20188		0.48	1.8E-01	11430167	NT	Homo sapiens KIAA0173 gene product (KIAA0173), mRNA
7350	20346	33613	1.04	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wvus, complete cds
7350	20346	33614	1.04	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wvus, complete cds
7410	20109	33343	0.67	1.8E-01	BE961353.1	EST_HUMAN	601648361R2 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:3932247 3'
7850	20777	34078	0.67	1.8E-01	AP001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
8881	22793	36182	1.18	1.8E-01	M73258.1	NT	Human cellular DNA/Human papillomavirus proviral DNA
9913	22901	36288	1.76	1.8E-01	9626232	NT	Bacteriophage like, complete genome
10024	22924		0.63	1.8E-01	AA493751.1	EST_HUMAN	rh02a05.s1 NC1_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943088 similar to contains L1.13 L1 repetitive element;
10103	22994	36389	1.07	1.8E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
10103	22994	36390	1.07	1.8E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
10141	23032	36428	0.96	1.8E-01	M26019.1	NT	S.commune orotidine-5'-phosphate decarboxylase (URA1) gene, complete cds
10141	23032	36429	0.96	1.8E-01	M26019.1	NT	S.commune orotidine-5'-phosphate decarboxylase (URA1) gene, complete cds
10298	23185	36599	0.76	1.8E-01	P08123	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
10302	23192	36603	0.76	1.8E-01	U67546.1	NT	Methanococcus jannaschii section 90 of 150 of the complete genome
10632	23519		0.84	1.8E-01	AF200252.1	NT	Aquarius amplius cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial gene for mitochondrial product
10655	23741	37184	1.52	1.8E-01	X63440.1	NT	M.musculus mRNA for P19-protein tyrosine phosphatase
11082	24014	37456	3.41	1.8E-01	X77336.1	NT	A.italiana mRNA for ribonucleotide reductase R2
11121	24051	37496	5.92	1.8E-01	U38906.1	NT	Bacteriophage r11 integrase, repressor protein (ro), dUTPase, holin and lysis genes, complete cds
11177	20346	33613	3.11	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wvus, complete cds
11177	20346	33614	3.11	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wvus, complete cds
11178	24104	37551	5.51	1.8E-01	AF019107.1	NT	Dictyostelium discoideum unknown (DG1041) gene, complete cds
11457	24372	37820	3.47	1.8E-01	M59257.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 4
11894	23994	37433	3.87	1.8E-01	X57033.1	NT	B.laurus mRNA for potassium channel
12178	25014	38519	2.19	1.8E-01	8394421	NT	Rattus norvegicus Thromboxane receptor (Tbx2r), mRNA
12322	25123		2.08	1.8E-01	10086561	NT	Bovine ephemeral fever virus, complete genome
12804	25423		4.9	1.8E-01	Q96982	SWISSPROT	DNA TERMINAL PROTEIN (BELLETTI PROTEIN) (PTP PROTEIN)

Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12912	25495		20.38	1.8E-01	R24494.1	EST_HUMAN	Yr48h10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133027 5'
12951	25514		2.7	1.8E-01	Y1114.1	NT	E. dispar mRNA for hexokinase (hxt1)
599	13663	26566	2.03	1.7E-01	BE385164.1	EST_HUMAN	601274604F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615788 5'
831	13885	26824	2.18	1.7E-01	X53350.1	NT	P. clumerillii histone gene cluster for core histones H2A, H2B, H3 and H4
987	14038		1.61	1.7E-01	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
1085	14129	27066	0.82	1.7E-01	AF081810.1	NT	Lymantria dispar nucleopolydnavirus, complete genome
1085	14129	27067	0.82	1.7E-01	AF081810.1	NT	Lymantria dispar nucleopolydnavirus, complete genome
1839	14862	27844	0.92	1.7E-01	AL161673.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
1998	15016		2.77	1.7E-01	AF255051.1	NT	Homo sapiens BNIP3H (BNIP3H) gene, complete cds; nuclear gene for mitochondrial product
2902	15956	28855	2.06	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
2902	15956	28856	2.06	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
2969	16021	28919	1.83	1.7E-01	AA336909.1	EST_HUMAN	EST41651 Endometrial tumor Homo sapiens cDNA 5' end
3040	16092	28994	1.2	1.7E-01	AJ238736.1	NT	Naja naja atra cdx-1 gene, exons 1-3
3040	16092	28995	1.2	1.7E-01	AJ238736.1	NT	Naja naja atra cdx-1 gene, exons 1-3
3152	16202	29093	2.18	1.7E-01	AF081614.1	NT	Taxus canadensis geranylgeranyl diphosphate synthase mRNA, complete cds
3422	16463	29370	0.78	1.7E-01	N55763.1	EST_HUMAN	J2346F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2346 5'
3507	16545	29445	2.08	1.7E-01	AJ269505.1	NT	Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene
3672	16705	29597	1.11	1.7E-01	AJ224877.1	NT	Homo sapiens hap1 gene, complete CDS
3692	16725		1.11	1.7E-01	5031886	NT	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA
4015	17042	29932	6.66	1.7E-01	AJ235377.1	NT	Homo sapiens derivative 11 breakpoint fragment; partial intron 10 of the ALL-1/MLL/HRX gene fused to intron 5 of the AF-4/FEL gene
4675	17680		1.86	1.7E-01	X52936.1	NT	Schistosoma gregaria alpha repetitive DNA
4653	17851	30809	1.75	1.7E-01	AJ247635.1	EST_HUMAN	qH57c09.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848808 3' similar to contains ORF.b1 ORF repetitive element;
5298	18282	31132	1.57	1.7E-01	X17012.1	NT	Rat IGfII gene for insulin-like growth factor II
5298	18282	31133	1.57	1.7E-01	X17012.1	NT	Rat IGfII gene for insulin-like growth factor II
5313	18287	31150	0.7	1.7E-01	BF030010.1	EST_HUMAN	601557256F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827197 5'
5593	18659	31547	1.9	1.7E-01	AA470886.1	EST_HUMAN	net3a02.st NCI CGAP_C03 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);

Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5593	18669	31548	1.9	1.7E-01	AA470886.1	EST_HUMAN	ne13a02.s1 NCL CGAP_Co3 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5787	18859	31967	0.75	1.7E-01	U43599.1	NT	Brugia pahangi microfilarial sheath protein SHP3 (shp3) gene, complete cds
6698	19827	32810	15.24	1.7E-01	H72118.1	EST_HUMAN	y502g05.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213658 3'
6815	19858		0.49	1.7E-01	AJ235270.1	NT	Rickettsia prowazekii strain Madrid E, complete genome, segment 1/4
6630	19889	32881	0.69	1.7E-01	AJ370876.1	EST_HUMAN	1a29c11.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
6650	19889	32882	0.69	1.7E-01	AJ370876.1	EST_HUMAN	1a29c11.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
7172	18444	31313	0.61	1.7E-01	BE300286.1	EST_HUMAN	600944067T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860248 3'
7206	20206		2.1	1.7E-01	AF026552.3	NT	Mesocricetus auratus oviductin precursor (OVI) gene, complete cds
7344	20340		0.63	1.7E-01	Z92910.1	NT	Homo sapiens HFE gene
7599	20525	33814	1.46	1.7E-01	AP000422.1	NT	Escherichia coli O157:H7 genomic DNA, Sakai-VT2 prophage inserted region
7877	20611	33910	10.98	1.7E-01	BE734179.1	EST_HUMAN	601589022F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843904 5'
7900	20826	34130	1.25	1.7E-01	P18724	SWISSPROT	PROBABE PROCESSING AND TRANSPORT PROTEIN UL56 (HFLFO PROTEIN)
7918	25679	34144	0.88	1.7E-01	Q01955	SWISSPROT	COLLAGEN ALPHA 3(IV) CHAIN PRECURSOR
8341	21246	34581	0.41	1.7E-01	BF326962.1	EST_HUMAN	QV3-BN0047-020800-284-d08 BN0047 Homo sapiens cDNA
8367	21271	34605	0.44	1.7E-01	AL114566.1	NT	QV3-BN0047-020800-284-d08 BN0047 Homo sapiens cDNA
8443	21375	34715	1.47	1.7E-01	AF000573.1	NT	Bethylis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
8541	21472	34813	0.84	1.7E-01	AF150669.1	NT	Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds
8853	21783	35130	6.01	1.7E-01	7708428	NT	Pseudomonas putida long-chain-fatty-acid-CoA ligase (fcd) gene, complete cds
8853	21783	35131	6.01	1.7E-01	7708428	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
9235	22183	35538	0.54	1.7E-01	AW992873.1	EST_HUMAN	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
9287	22215	35573	2.31	1.7E-01	D00384.1	NT	RC2-BN0032-120200-011-a10 BN0032 Homo sapiens cDNA
9403	22331	35693	1	1.7E-01	AF217413.1	NT	Rat (SHR strain) SX1 gene
9403	22331	35694	1	1.7E-01	AF217413.1	NT	Homo sapiens neuroigin 3 isoform gene, complete cds, alternatively spliced
9549	22478	35834	0.56	1.7E-01	R77002.1	EST_HUMAN	Homo sapiens neuroigin 3 isoform gene, complete cds, alternatively spliced
10118	23009	36405	10.51	1.7E-01	AP001508.1	NT	y86g02.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:144242 5'
10220	23111	36512	0.54	1.7E-01	AW977455.1	EST_HUMAN	Bacillus halodurans genomic DNA, section 2/14
10237	23128	36531	2.6	1.7E-01	U18288.1	NT	EST1389584 MAGe resequences, MAGO Homo sapiens cDNA
10324	23213	36625	0.92	1.7E-01	AJ251749.1	NT	EST1389584 MAGe resequences, MAGO Homo sapiens cDNA
10728	23814		2.47	1.7E-01	AL163284.2	NT	Human class IV alcohol dehydrogenase (ADH7) gene, exon 3
						NT	Drosophila melanogaster mRNA for serine protease inhibitor (serpin-6), (sp6 gene)
						NT	Homo sapiens chromosome 21 segment HS21C084
						NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 2 (SLC7A2), mRNA
10880	23765	37190	1.28	1.7E-01	11427203	NT	

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10881	23766	37191	1.66	1.7E-01	AA627972.1	EST_HUMAN	nq60e07.s1 NCI_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1148292 3' similar to gb:L25081 TRANSFORMING PROTEIN RHOC (HUMAN);
11123	24053	37499	7.92	1.7E-01	BE390835.1	EST_HUMAN	601286547F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613258 5'
11245	24199	37616	2.42	1.7E-01	AA814617.1	EST_HUMAN	af43a03.s1 NCI_CGAP_CNS1 Homo sapiens cDNA clone IMAGE:1428924 3'
11552	24461	37924	9.7	1.7E-01	7106300	NT	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
11552	24461	37925	9.7	1.7E-01	7106300	NT	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
11636	24542	38016	2.25	1.7E-01	Y08391.1	NT	S.pombe pop1+ gene
11814	24735	38226	2.11	1.7E-01	AA883375.1	EST_HUMAN	ak4509.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460297 3'
12134	24975		1.42	1.7E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
12166	25002	38503	1.49	1.7E-01	P55899	SWISSPROT	IGG RECEPTOR FCRL LARGE SUBUNIT P51 PRECURSOR (FCRL) (NEONATAL FC RECEPTOR)
12166	25002	38504	1.49	1.7E-01	P55899	SWISSPROT	IGG FC FRAGMENT RECEPTOR TRANSPORTER, ALPHA CHAIN
12235	25094	38566	3.57	1.7E-01	11418167	NT	IGG RECEPTOR FCRL LARGE SUBUNIT P51 PRECURSOR (FCRL) (NEONATAL FC RECEPTOR)
12607	25737		1.47	1.7E-01	A1824404.1	EST_HUMAN	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
12880	25477	31763	8.17	1.7E-01	U01317.1	NT	ACID RECEPTOR ALPHA-1 (HUMAN);
13097	25850		1.48	1.7E-01	AJ011763.1	NT	Human beta globin region on chromosome 11
130	13234	26151	1.48	1.6E-01	AF217632.1	NT	Bos taurus prostacyclin receptor gene, 5'UTR
703	15946	26679	1.14	1.6E-01	R31497.1	EST_HUMAN	Homo sapiens mevalonate kinase gene, exon 6 and 7
1523	14554	27515	1.52	1.6E-01	AA548863.1	EST_HUMAN	yh75f12.1 Soares placenta Nb2-IP Homo sapiens cDNA clone IMAGE:135569 5'
1544	14574	27534	3.98	1.6E-01	AF298117.1	NT	nk28d12.s1 NCI_CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014839 3'
1939	14960	27938	1.56	1.6E-01	P22063	SWISSPROT	Homo sapiens homeobox protein OTX2 gene, complete cds
2001	15019		1.11	1.6E-01	U10334.1	NT	AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
2408	15923	28416	1.13	1.6E-01	X94232.1	NT	Crassostrea gigas RNA polymerase II largest subunit mRNA, partial cds
2516	15517	28521	1.85	1.6E-01	AB037729.1	NT	H. sapiens mRNA for novel T-cell activation protein
2934	15987	28886	16.49	1.6E-01	AF185589.1	NT	Homo sapiens mRNA for KIAA1308 protein, partial cds
2934	15987	28887	16.49	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3409	16450	29357	0.98	1.6E-01	AF062843.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3657	15019		1.22	1.6E-01	U10334.1	NT	Danio rerio Pim1 mRNA, complete cds
3700	16732	29622	1.11	1.6E-01	AJ003165.1	NT	Crassostrea gigas RNA polymerase II largest subunit mRNA, partial cds
3700	16732	29623	1.11	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
3840	16869	29763	1.5	1.6E-01	AE000962.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
4086	17111		2.69	1.6E-01	AE004413.1	NT	Archaeoglobus fulgidus section 145 of 172 of the complete genome
							Vibrio cholerae chromosome II, section 70 of 93 of the complete chromosome

Page 105 of 545  
Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4117	17140	30073	0.98	1.6E-01	AF084466.1	NT	Citridia fasciculata hyaluronidase 1 (bnl) gene, complete cds
4398	17409		1.11	1.6E-01	U62771.1	NT	Lymnaea stagnalis octopamine receptor type 1 (Lym oar1) mRNA, complete cds
4436	17447	30307	15.13	1.6E-01	AF179690.1	NT	Homo sapiens apelin gene, complete cds
4567	17575		3.62	1.6E-01	AW968601.1	EST_HUMAN	EST380677 IMAGE resequences, MAGJ Homo sapiens cDNA
4575	17593		5.22	1.6E-01	6753319	NT	Mus musculus chaperonin subunit 3 (gamma) (Cct3), mRNA
4816	17817	30684	0.74	1.6E-01	AF100154.1	NT	Rattus norvegicus kynurenine aminotransferase/glutamine transaminase K (Kat) gene, complete cds
4816	17817	30685	0.74	1.6E-01	AF100154.1	NT	Rattus norvegicus kynurenine aminotransferase/glutamine transaminase K (Kat) gene, complete cds
5035	18032	30889	0.74	1.6E-01	P40631	SWISSPROT	MIKRONUCLEAR LINKER HISTONE POLYPROTEIN (MIC LH) [CONTAINS: LINKER HISTONE PROTEINS ALPHA, BETA, DELTA AND GAMMA]
5059	18056	30908	1.69	1.6E-01	AA088343.1	EST_HUMAN	Z84h09.s1 Stratagene cdon (#937204) Homo sapiens cDNA clone IMAGE:511361 3' similar to TR:E221955
5086	18083	30933	1.39	1.6E-01	AJ006356.1	NT	E221955 38,855 BP SEGMENT OF CHROMOSOME XIV ;
5086	18083	30934	1.39	1.6E-01	AJ006356.1	NT	Lycopodium obscurum RsaI fragment 2, satellite region
5161	18154	31001	0.95	1.6E-01	BE018707.1	EST_HUMAN	b583h08.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048023 5' similar to gb:M61715
5192	18184	31027	1.02	1.6E-01	AI017141.1	EST_HUMAN	TRYPTOPHANYL-TRNA SYNTHETASE (HUMAN); gb:X69657 M. musculus (MOUSE);
5572	18850	31528	0.86	1.6E-01	L40608.1	NT	ov34c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1639208 3'
6896	18785	31715	2.52	1.6E-01	AW197498.1	EST_HUMAN	Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
5712	18785	31715	2.52	1.6E-01	AW197498.1	EST_HUMAN	xm43f01.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2686969 3' similar to TR:O75984 O75984
5712	18785	31716	2.52	1.6E-01	AW197498.1	EST_HUMAN	HYPOTHETICAL 127.6 KD PROTEIN ;
5724	18797	31889	2.17	1.6E-01	AF034716.1	NT	HYPOTHETICAL 127.6 KD PROTEIN ;
6261	19312	32477	0.86	1.6E-01	BE925803.1	EST_HUMAN	Rattus norvegicus CCAAT/enhancer binding protein epsilon (cebpe) gene, complete cds
6505	19549	32728	0.55	1.6E-01	BF183584.1	EST_HUMAN	RC3-BN0034-310800-113-h01 BN0034 Homo sapiens cDNA
6505	19549	32729	0.55	1.6E-01	BF183584.1	EST_HUMAN	601809725R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040335 3'
6896	19732	32932	1.77	1.6E-01	AL161588.2	NT	601809725R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040335 3'
6896	19732	32933	1.77	1.6E-01	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
7090	20286	33556	0.57	1.6E-01	AA388047.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
7110	20314	33577	0.7	1.6E-01	AB046786.1	NT	z880404.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:729511 5'
7162	20289		0.54	1.6E-01	BF683630.1	EST_HUMAN	Homo sapiens mRNA for KIAA1566 protein, partial cds
7300	18469	31291	4.25	1.6E-01	AW291215.1	EST_HUMAN	602139855F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301004 5'
7680	20614	33913	0.57	1.6E-01	Z49632.1	NT	UJ-H-B12-agi-b-06-0-UJ.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724418 3'
							S.cerevisiae chromosome X reading frame ORF YJR132w

Page 106 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8250	21155	34489	1.28	1.6E-01	AW246359.1	EST_HUMAN	2822248.9prime NIH_MGC. 7 Homo sapiens cDNA clone IMAGE:2822248 5'
8296	21200	34538	0.55	1.6E-01	6753237	NT	Mus musculus Ca <sup>2+</sup> -dependent activator protein for secretion (Cadps), mRNA
8311	21215		0.48	1.6E-01	AU136525.1	EST_HUMAN	AU136525 PLACE1 Homo sapiens cDNA clone PLACE1004466 5'
8450	21382	34724	1.68	1.6E-01	L49349.1	NT	Gorilla gorilla androgen receptor gene, partial exon
8603	21534		0.75	1.6E-01	BE244087.1	EST_HUMAN	TCBAP1E0607 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0607
8695	21627	34971	0.75	1.6E-01	U38243.1	NT	Bacteroides vulgatus beta-lactamase (cfxA) gene, complete cds and mobilization protein (mobA) gene, complete cds
9191	22119	35475	1.12	1.6E-01	Z99119.1	NT	Bacillus subtilis complete genome (section 16 of 21): from 2987771 to 3213410
9365	22313	35875	1.03	1.6E-01	R13973.1	EST_HUMAN	y60h08.t1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:28879 5'
9488	22416		0.78	1.6E-01	L36861.1	NT	Homo sapiens guanylate cyclase activating protein (GCAP) gene exons 1-4, complete cds
9523	22450	35813	2.14	1.6E-01	Z49501.1	NT	S.cerevisiae chromosome X reading frame ORF YJR001W
9655	22581		0.77	1.6E-01	AF111107.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
10177	23068		2.24	1.6E-01	BF375171.1	EST_HUMAN	RC3-ST0200-041199-011-H01 ST0200 Homo sapiens cDNA
10179	23070	36459	2.26	1.6E-01	Z49501.1	NT	S.cerevisiae chromosome X reading frame ORF YJR001W
10213	23104		1.17	1.6E-01	BE155664.1	EST_HUMAN	PM2-HT0353-270100-004-f11 HT0353 Homo sapiens cDNA
11100	24031	37476	3.05	1.6E-01	AW850863.1	EST_HUMAN	IL3-CT0220-111199-028-G01 CT0220 Homo sapiens cDNA
11434	24350	37799	8.89	1.6E-01	O14847	SWISSPROT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
11434	24350	37797	8.89	1.6E-01	O14847	SWISSPROT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
11439	24355	37803	1.52	1.6E-01	BE259649.1	EST_HUMAN	60'145793F1 NIH_MGC. 19 Homo sapiens cDNA clone IMAGE:3161183 5'
11555	24464		3.89	1.6E-01	AF106064.1	NT	Plasmodium falciparum calcium-dependent protein kinase-3 (cdpk3) gene, complete cds
11847	24697	38198	8.03	1.6E-01	6871652	NT	Mus musculus adaptor-related protein complex AP-1, beta 1 subunit (Ap1b1), mRNA
12086	24927	38431	2.17	1.6E-01	X07471.1	NT	Human small polydisperse circular DNA (Hspc-64)
12086	24927	38432	2.17	1.6E-01	X07471.1	NT	Human small polydisperse circular DNA (Hspc-64)
12130	24971		1.56	1.6E-01	BF527237.1	EST_HUMAN	602039465F2 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4177073 5'
12355	25145	38169	5.34	1.6E-01	AV716585.1	EST_HUMAN	AV719585 GLC Homo sapiens cDNA clone GLCEMF07 5'
12634	25315	31818	1.58	1.6E-01	L14935.1	NT	Rat convertase PC5 mRNA, 5' end
12661	26332		1.97	1.6E-01	AW839711.1	EST_HUMAN	RC1-LT0074-120200-014-h01_1 LT0074 Homo sapiens cDNA
12784	25718		9.25	1.6E-01	AB045310.1	NT	Cuonius cethus KS mRNA for anti-leucoto synthase, complete cds
12903	25480		2.43	1.6E-01	AK024496.1	NT	Homo sapiens mRNA for FLJ00104 protein, partial cds
12984	25543		4.75	1.6E-01	AF287344.1	NT	Fuchsia hybrid cultivar Qlu 94208 ribosomal protein S10 gene, partial cds; nuclear gene for mitochondrial product
13000	26552	31766	2.07	1.6E-01	8508522	NT	Rattus norvegicus chondroitin sulfate proteoglycan 5 (neuroglycan C) (Cspg5), mRNA



Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
267	13362	26277	1.36	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0819-040700-197-E05 HT0819 Homo sapiens cDNA
267	13362	26278	1.36	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0819-040700-197-E05 HT0819 Homo sapiens cDNA
608	15845		2.06	1.5E-01	AV711696.1	EST_HUMAN	AV711696 DCA Homo sapiens cDNA clone DCAADH06 5'
809	13805	26800	1.13	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1119	14161	27099	2.41	1.5E-01	AJ009735.1	NT	Cyprinus carpio mRNA for EGG522 myosin heavy chain, 3'UTR
1124	14166	27103	1.83	1.5E-01	AJ251885.1	NT	Homo sapiens partial SLC22A2 gene for organic cation transporter (OCT2), exon 1
1140	14182		1.54	1.5E-01	L36126.1	NT	Rattus norvegicus Insulin-responsive glucose transporter (GLUT4) gene, 5' end
1244	14280	27222	0.68	1.5E-01	AW185516.1	EST_HUMAN	xn39d11.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2696085 3'
1302	14335	27281	2.86	1.5E-01	D26835.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
1302	14335	27282	2.86	1.5E-01	D26835.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
1500	14531	27496	1.54	1.5E-01	AF117340.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds
2856	16008		1.21	1.5E-01	AW572516.1	EST_HUMAN	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
3092	16133	28029	4.75	1.5E-01	M81441.1	NT	xw36a02.x2 NCI CGAP_Pant1 Homo sapiens cDNA clone IMAGE:2831978 3' similar to gb.X55072_rna1
3100	16151	28047	0.68	1.5E-01	O78687	SWISSPROT	THYROID HORMONE RECEPTOR ALPHA-1 (HUMAN); Bos taurus factor V variant 2 (factor V) mRNA, complete cds
3401	16443	29350	5.96	1.5E-01	AA935049.1	EST_HUMAN	NADH:UBIQUINONE OXIDOREDUCTASE CHAIN 4
3426	16487	29375	0.79	1.5E-01	Z23104.1	NT	oe68d05.s1 NCI CGAP_GC4 Homo sapiens cDNA clone IMAGE:1571337 3' similar to gb.M11433
3426	16487	29376	0.79	1.5E-01	Z23104.1	NT	RETINOL-BINDING PROTEIN 1, CELLULAR (HUMAN); L. stagnalis mRNA for G protein-coupled receptor
3488	16527	29426	1.01	1.5E-01	AW612237.1	EST_HUMAN	L. stagnalis mRNA for G protein-coupled receptor
3819	16849	29733	2.52	1.5E-01	U08964.1	NT	hh29f02.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2956539 3' similar to contains element MER16 repetitive element;
3835	16864	29747	0.77	1.5E-01	7108368	NT	Mus musculus ICR/Swiss glycerate dehydro 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
3935	16963	29848	2.77	1.5E-01	AW665983.1	EST_HUMAN	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA
4134	17156	30033	0.95	1.5E-01	AW36659.1	EST_HUMAN	h10106.x1 Soares_NFL_T_GEC_S1 Homo sapiens cDNA clone IMAGE:2981411 3'
4188	17208	30073	0.72	1.5E-01	Z12628.1	NT	RC2-HT0149-191099-012-c09 HT0149 Homo sapiens cDNA
4279	17293	30159	12.39	1.5E-01	AL163284.2	NT	B. napus mitochondrion DNA for ORF168
4838	17839	30709	1.6	1.5E-01	BF687665.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
4864	15752	29748	2.4	1.5E-01	BF695391.1	EST_HUMAN	602067192F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4065223 5'
4903	17902	30770	1.13	1.5E-01	BE173796.1	EST_HUMAN	602083266F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
4903	17902	30771	1.13	1.5E-01	BE173796.1	EST_HUMAN	CN0-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA
5120	18117	30959	2.4	1.5E-01	AL161560.2	NT	CN0-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60

Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5437	18519	31244	2.14	1.5E-01	P07996	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5467	18543	31388	0.72	1.5E-01	AF256652.1	NT	Calman crocodilus MHC class II beta chain (hollbeta) gene, complete cds
5511	18590		5.58	1.5E-01	P15196	SWISSPROT	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN)
5728	18801	31894	4.9	1.5E-01	AW850734.1	EST_HUMAN	(SBP) (TESTIS-SPECIFIC ANDROGEN-BINDING PROTEIN) (ABP)
5771	18844	31948	6.93	1.5E-01	U65016.1	NT	IL3-CT0219-180200-064-F10 CT0219 Homo sapiens cDNA
5771	18844	31947	6.93	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGFa) mRNA, complete cds
6127	19183	32321	0.57	1.5E-01	4506810	NT	Mus musculus transforming growth factor alpha (TGFa) mRNA, complete cds
6237	19291	32450	1.69	1.5E-01	6753659	NT	Homo sapiens sodium channel, voltage-gated, type VI, alpha polypeptide (SCN6A) mRNA
6237	19291	32451	1.69	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
6278	19329	32495	2.15	1.5E-01	AJ276505.1	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
6436	19483	32658	3.09	1.5E-01	BE727658.1	EST_HUMAN	Mus musculus genomic fragment, 279 Kb, chromosome 7
6495	19539		2.03	1.5E-01	4506396	NT	601564322F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833981 5'
6601	19842	32824	1.74	1.5E-01	AF134907.1	NT	Homo sapiens RAD54 (S.cerevisiae)-like (RAD54L) mRNA
6779	25654	33024	1.7	1.5E-01	AE001039.1	NT	Influenza B virus (B/Nanchang/480/94) NB protein gene, complete cds; and neuraminidase gene, partial cds
6810	19843	33053	5.41	1.5E-01	11417236	NT	Archaeoglobus fulgidus section 68 of 172 of the complete genome
6821	19854	33066	1.87	1.5E-01	P48508	SWISSPROT	Homo sapiens chromosome 5 open reading frame 3 (C5ORF3), mRNA
6871	19902	33117	2.03	1.5E-01	Q28462	SWISSPROT	GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN)
6981	20008	33239	1	1.5E-01	AA714760.1	EST_HUMAN	AMELOGENIN
7010	20037	33270	1.67	1.5E-01	P30143	SWISSPROT	nw30d10.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241971 3'
7319	18487	31310	6.54	1.5E-01	AW970295.1	EST_HUMAN	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
7363	25669		0.71	1.5E-01	AA811545.1	EST_HUMAN	EST382376 IMAGE resequence, MAGK Homo sapiens cDNA
7583	20519		2.21	1.5E-01	AF210842.1	NT	ob73f02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1337019 3' similar to contains element LTR2 repetitive element
7743	20674	33972	0.51	1.5E-01	AF210842.1	NT	LTR2 repetitive element
7788	20717	34020	1.69	1.5E-01	A1973157.1	EST_HUMAN	Homo sapiens HARP (HARP) gene, exon 17 and complete cds
8030	20846	34262	1	1.5E-01	AF299073.1	NT	Leucophaea maderae mRNA for lipocalin, Lma-P22
8030	20846	34263	1	1.5E-01	AF299073.1	NT	wf52cd8.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2491310 3'
8042	20956	34271	1.48	1.5E-01	AW500611.1	EST_HUMAN	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
8042	20956	34271	1.48	1.5E-01	AW500611.1	EST_HUMAN	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
8205	21111	34442	0.64	1.5E-01	U46560.1	NT	U1-HF-BN0-akk-d-05-0-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
8638	21567	34904	1.1	1.5E-01	P21303	SWISSPROT	U1-HF-BN0-akk-d-05-0-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
							Saccharomyces cerevisiae weak multicopy suppressor of lost1-1 (SOL3) gene, complete cds
							MEROZOITE RECEPTOR PK63 PRECURSOR (66 KD PROTECTIVE MINOR SURFACE ANTIGEN)

Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8768	21728	35077	1.24	1.5E-01	AA970317.1	EST_HUMAN	cc85g12.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573030 3' similar to gb:M26062 INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
8887	21817		0.97	1.5E-01	BE884789.1	EST_HUMAN	601510523F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912004 5'
8970	21903		16.06	1.5E-01	C16900.1	EST_HUMAN	C16800 Clontech human acta polyA+ mRNA (#6672) Homo sapiens cDNA clone GEN:620H09 5'
9002	21931	35287	1.58	1.5E-01	L27835.1	NT	Pargastarodon gigas growth hormone (GH) mRNA, complete cds
9155	22083	35441	1.73	1.5E-01	D84476.1	NT	Homo sapiens mRNA for ASK1, complete cds
9174	22102		0.75	1.5E-01	P43446	SWISSPROT	WNT-10A PROTEIN PRECURSOR
9396	22324	35687	1.62	1.5E-01	4501972	NT	Homo sapiens adaptor-related protein complex 1, beta 1 subunit (ADTB1), mRNA
9649	22575	35946	2.57	1.5E-01	N74226.1	EST_HUMAN	za89e06.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:296866 3' similar to PIR:S44443 S44443 RAD23 protein homolog2 - human ;
9735	22650	36043	1.82	1.5E-01	BF585485.1	EST_HUMAN	GVO000404 Human Psoriasis Differential Display Homo sapiens cDNA
9742	22665		2.45	1.5E-01	AV754819.1	EST_HUMAN	AV754819 TP Homo sapiens cDNA clone TPAAHB12 5'
9885	21343	34678	7.35	1.5E-01	U00455.1	NT	Acipenser transmontano vitellogenin mRNA, partial cds
10332	23221	36635	0.76	1.5E-01	M77144.1	NT	Human type II 3-beta hydroxysteroid dehydrogenase/ 5-delta - 4-delta isomerase gene, complete cds
10432	23321	36738	7.83	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10432	23321	36739	7.83	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10689	23585	37014	2.61	1.5E-01	X98852.1	NT	P. leniusculus mRNA for Integrin beta subunit
10798	23684	37113	3.32	1.5E-01	AI814046.1	EST_HUMAN	wk53h12.x1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10798	23684	37114	3.32	1.5E-01	AI814046.1	EST_HUMAN	GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10875	23761	37188	1.92	1.5E-01	U40932.1	NT	GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
11018	23902	37340	1.48	1.5E-01	AJ011964.1	NT	Danio rerio transcription factor Pax9b (Pax9) mRNA, complete cds
11018	23902	37341	1.49	1.5E-01	AJ011964.1	NT	Claviceps purpurea ps1 gene
11139	24088	37513	1.84	1.5E-01	BE088492.1	EST_HUMAN	Claviceps purpurea ps1 gene
11139	24088	37514	1.84	1.5E-01	BE088492.1	EST_HUMAN	CM2-BT0688-210300-122-111 BT0688 Homo sapiens cDNA
11263	24186	37634	5.36	1.5E-01	AL163280.2	NT	CM2-BT0688-210300-122-111 BT0688 Homo sapiens cDNA
11263	24186	37635	5.36	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
11515	24425	37883	1.58	1.5E-01	AW841916.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
11607	20717	34020	1.49	1.5E-01	AI973157.1	EST_HUMAN	IL5-CN0024-030300-025-D04 CN0024 Homo sapiens cDNA
12050	24891		1.57	1.5E-01	AI193704.1	EST_HUMAN	wr52c08.x1 NCI_CGAP_U01 Homo sapiens cDNA clone IMAGE:2491310 3'
12315	25766		41.76	1.5E-01	BF700582.1	EST_HUMAN	qr72e01.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1744536 3' similar to gb:M17887 60S ACIDIC RIBOSOMAL PROTEIN P2 (HUMAN);
							602128763F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285549 5'

Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12660	25331		2.53	1.5E-01	AF030358.2	NT	Rattus norvegicus chemokine CX3C mRNA, complete cds
12702	25357		1.67	1.5E-01	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
12721	25793		3.93	1.5E-01	R93077.1	EST_HUMAN	yp87e04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194430 5'
12801	26803		3.37	1.5E-01	AV741272.1	EST_HUMAN	AV741272 CB Homo sapiens cDNA clone CBDA04 5'
12802	26722	31667	7.76	1.5E-01	AL139074.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 1/6
13082	26603	31732	6.57	1.5E-01	AJ276242.1	NT	Sus scrofa mRNA for sodium iodide symporter
319	13411		1.38	1.4E-01	AF009663.1	NT	Homo sapiens T cell receptor beta locus, TORBV855P to TORBV21S2A2 region
935	13997		3.3	1.4E-01	ID78638.1	EST	Xenopus laevis mRNA for DNA (cytosine-5-)-methyltransferase, complete cds
1286	14319		1.33	1.4E-01	T91864.1	EST_HUMAN	Y54c01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:112032 3'
1774	14800		1.35	1.4E-01	6679980	NT	Mus musculus growth differentiation factor 5 (Gdrf5), mRNA
1778	14802	27770	1.31	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
1923	14044		1.06	1.4E-01	AW135741.1	EST_HUMAN	UI-H-B11-acf-a-06-0-UJ.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2714009 3'
2002	15020		11.07	1.4E-01	AA720615.1	EST_HUMAN	ny72d07.s1 NCI CGAP_GGB1 Homo sapiens cDNA clone IMAGE:1289821 3'
2496	15498	29498	1.35	1.4E-01	P30706	SWISSPROT	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT)
2840	15829	28828	3.98	1.4E-01	A1933498.1	EST_HUMAN	wm74d01.x1 NCI CGAP_U12 Homo sapiens cDNA clone IMAGE:2441865 3'
3349	16395	29296	1.03	1.4E-01	R56395.1	EST_HUMAN	yp90a10.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:40648 5'
3966	16996	29880	1.25	1.4E-01	R59232.1	EST_HUMAN	yp97a03.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:41467 5'
4269	17286	30192	1.25	1.4E-01	R59232.1	EST_HUMAN	yp97a03.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:41467 5'
4269	17285	30153	10.37	1.4E-01	A1699094.1	EST_HUMAN	b56e02.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4337	17351	30214	4.49	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
4518	17527		0.96	1.4E-01	AA776287.1	EST_HUMAN	z50b01.s1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:453873 3' similar to gb:X01057_maf1 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN); contains Alu repetitive element
4980	17878	30838	0.98	1.4E-01	AV69659.1	EST_HUMAN	AV69659 GK0 Homo sapiens cDNA clone GK0DUG09 5'
5489	18559	31416	4.8	1.4E-01	T90677.1	EST_HUMAN	ye15c11.1 Stralagene lung (#937210) Homo sapiens cDNA clone IMAGE:117812 3'
5512	18591	31438	4.32	1.4E-01	AB004558.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5512	18591	31439	4.32	1.4E-01	AB004558.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
6562	19504	32782	3.04	1.4E-01	BE326801.1	EST_HUMAN	h67e02.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133538 3'
6757	19791	33004	4.3	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
6757	19791	33005	4.3	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
6853	19855	33099	4.04	1.4E-01	AW082796.1	EST_HUMAN	x671d12.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2581761 3'
6867	19899		1.6	1.4E-01	BE266538.1	EST_HUMAN	601193523F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537581 5'

Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6891	19921	33138	2.17	1.4E-01	BF378533.1	EST_HUMAN	QV1-UM0036-080300-103-409 UM0036 Homo sapiens cDNA
7486	20426		1.03	1.4E-01	AL118568.1	EST_HUMAN	DKFZp761A0910_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A0910 5'
7782	20711		1.6	1.4E-01	AW015373.1	EST_HUMAN	U1-H-B10-eak-c-09-0-U1.s1 NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
7810	20739	34042	0.62	1.4E-01	F08745.1	EST_HUMAN	HSC1DB011 normalized infant brain cDNA Homo sapiens cDNA clone c-1db01
7865	20793		0.68	1.4E-01	AI782827.1	EST_HUMAN	w04r12.x1 NCL_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2389295 3' similar to SW:ICE4_HUMAN P49662 CASPASE-4 PRECURSOR ;
7869	20796		0.43	1.4E-01	T53770.1	EST_HUMAN	ye90f11.2 Strategene placenta (#837225) Homo sapiens cDNA clone IMAGE:68973 5' similar to contains Alu repetitive element
8089	20982	34099	1.21	1.4E-01	U85645.1	NT	Cryptolagus cuniculus fructose 1,6, biphosphate aldolase (AldB) gene, complete cds
8220	21126	34457	1.89	1.4E-01	AI305192.1	EST_HUMAN	q190b12.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1879583 3'
8553	21484		0.85	1.4E-01	BF310258.1	EST_HUMAN	601894760F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124189 5'
9044	21973		1.55	1.4E-01	AV659047.1	EST_HUMAN	AV659047 GLC Homo sapiens cDNA clone GLCFSH06 3'
9343	22271		0.57	1.4E-01	AI436093.1	EST_HUMAN	th92b12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126111 3' similar to TR:Q02710 Q02710 GAG POLYPROTEIN. ;
9470	22398	35761	5.31	1.4E-01	AA307073.1	EST_HUMAN	EST178192 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
9545	22472	35830	0.76	1.4E-01	AW023636.1	EST_HUMAN	df58b03.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487485 5'
9687	22593	35967	1.2	1.4E-01	R62746.1	EST_HUMAN	y10h05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5'
9687	22593	35968	1.2	1.4E-01	R62746.1	EST_HUMAN	y10h05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5'
9728	22653	36036	8.78	1.4E-01	BF310959.1	EST_HUMAN	601895465F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124824 5'
9813	22721	36104	1.39	1.4E-01	W93411.1	EST_HUMAN	zd94a04.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:357102 5' similar to contains element KER repetitive element ;
9885	22800	36186	0.51	1.4E-01	X73293.1	NT	M.vannielii genes rpoH, rpoB and rpoA
9885	22800	36187	0.51	1.4E-01	X73293.1	NT	M.vannielii genes rpoH, rpoB and rpoA
9896	22811	36200	1.26	1.4E-01	Y10196.1	NT	Homo sapiens PHEX gene
9896	22811	36201	1.26	1.4E-01	Y10196.1	NT	Homo sapiens PHEX gene
9982	21340	34676	1.58	1.4E-01	AF121361.1	NT	Drosophila melanogaster signal transducing adaptor protein (STAM), sarlike threonine kinase 1a (IAL), and zinc finger protein (DNZ1) genes, complete cds
10321	23210	36622	0.74	1.4E-01	X65092.1	NT	C.perfringens ORF for putative membrane transport protein
10493	23381	36794	1.11	1.4E-01	AF023813.1	NT	Macromitrium levatum small ribosomal protein 4 (rps4) gene, chloroplast gene encoding chloroplast protein, partial cds
10590	23476	36903	0.73	1.4E-01	AW021908.1	EST_HUMAN	df29h03.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
10590	23476	36904	0.73	1.4E-01	AW021908.1	EST_HUMAN	df29h03.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
10750	23636	37068	0.7	1.4E-01	BF375285.1	EST_HUMAN	MR3-ST0218-211299-013-e08 ST0218 Homo sapiens cDNA
10750	23636	37069	0.7	1.4E-01	BF375285.1	EST_HUMAN	MR3-ST0218-211299-013-e09 ST0218 Homo sapiens cDNA

Page 112 of 545  
Table 4  
Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11151	24080		1.76	1.4E-01	AA811480.1	EST_HUMAN	oa89a03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1320364 3'
11280	24202	37654	3.28	1.4E-01	R53400.1	EST_HUMAN	y70c05.17 Soares breast 2NdtHst Homo sapiens cDNA clone IMAGE:154088 5'
11469	24382	37829	1.52	1.4E-01	AW104982.1	EST_HUMAN	x473e10.x1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2603274 3'
11537	24447	37908	1.51	1.4E-01	T96102.1	EST_HUMAN	ye47g10.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:120930 5'
11537	24447	37909	1.51	1.4E-01	T96102.1	EST_HUMAN	ye47g10.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:120930 5'
11639	24449	37912	1.6	1.4E-01	P08648	SWISSPROT	INTEGRIN ALPHA-5 PRECURSOR (FIBRONECTIN RECEPTOR ALPHA SUBUNIT) (INTEGRIN ALPHA-F) (VLA-5) (CD49E)
11738	24640	38120	1.77	1.4E-01	X68092.1	NT	C-perfringens ORF for putative membrane transport protein
11773	20711		1.65	1.4E-01	AW015373.1	EST_HUMAN	UI-H-B10-aal-c-09-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
11901	24001	37440	2.06	1.4E-01	U28760.1	NT	Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds
11937	24800		1.44	1.4E-01	X52102.1	NT	M.musculus p16K gene for 16 kDa protein
12180	24998	38499	1.51	1.4E-01	AF146793.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; PHLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFTZ7 (Pftz7) gene, complete cds; and H5AR (H5ar) gene, complete cds
12602	25298	31873	4.54	1.4E-01	X74773.1	NT	P.salina plastid gene secY
12614	25305		2.27	1.4E-01	11968117	NT	Rattus norvegicus desmin (Des), mRNA
12659	25943		2.04	1.4E-01	BE513902.1	EST_HUMAN	601315638F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634329 5'
12747	25386		6.48	1.4E-01	AF083221.1	NT	Fugu rubripes putative neurotransmitter receptors, YDR140w homolog, and glycylamide ribonucleotide transferase (GART) genes, complete cds
12825	25961		5.22	1.4E-01	P10447	SWISSPROT	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL
13019	25784		3.23	1.4E-01	D82983.1	NT	Mus musculus mRNA for prolidase, complete cds
13108	25622		3.39	1.4E-01	U01337.1	NT	Human Ser/Thr protein kinase (A-RAF-1) gene, complete cds
342	13432	26346	2.17	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
342	13432	26347	2.17	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
552	13621	26529	1.89	1.3E-01	AB013139.1	NT	Homo sapiens gene for NBS1, complete cds
659	13721	26632	1.24	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
659	13721	26633	1.24	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
869	13922	26869	0.84	1.3E-01	X53330.1	NT	P.dumerilli histone gene cluster for core histones H2A, H2B, H3 and H4
919	13971	26918	1.37	1.3E-01	AF139518.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds
1053	14097	27035	1.24	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1154	14195		2.28	1.3E-01	AL115265.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation

Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1243	14279	27221	1.32	1.3E-01	AV712467.1	EST_HUMAN	AV712467 DCA Homo sapiens cDNA clone DCAAFF05 5'
1462	14493		0.95	1.3E-01	AF146277.1	NT	Homo sapiens adapter protein CMS mRNA, complete cds
1882	14903	27887	1.13	1.3E-01	6680057	NT	Mus musculus procollagen, type XI, alpha 1 (Col11a1), mRNA
1973	14991	27974	2.21	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2183	15194		0.93	1.3E-01	AJ243578.1	NT	Rhodospseudomonas acidophila pucB5, pucA5, pucB6, pucA7, pucB8, pucA8 and pucC genes and ORF151
2309	18317		1.15	1.3E-01	AW812104.1	EST_HUMAN	RC4-ST0173-191099-032-d12 ST0173 Homo sapiens cDNA
2403	15409		2.79	1.3E-01	AE001016.1	NT	Archaeoglobus fulgidus section 91 of 172 of the complete genome
2925	15623	28616	2.66	1.3E-01	M86918.1	NT	Cerastius auratus keratin type I mRNA, complete cds
3410	16452	29358	0.66	1.3E-01	AF196779.1	NT	Homo sapiens transcription factor IGEM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel $\alpha_2$
3512	16550	29450	1.1	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds
3786	16817	29704	0.78	1.3E-01	AF000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7)
3786	16817	29705	0.78	1.3E-01	AF000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7)
3870	16899	29783	0.67	1.3E-01	6978840	NT	Rattus norvegicus Fibrinogen, gamma polypeptide (Fgg), mRNA
4074	17100		1.57	1.3E-01	AL161881.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
4135	13721	26632	0.77	1.3E-01	AJ277606.1	NT	Human calicivirus HU/NLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK
4135	13721	26633	0.77	1.3E-01	AJ277606.1	NT	Human calicivirus HU/NLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK
4236	17292		1.13	1.3E-01	AF020713.1	NT	Bacteriophage SPBc2 complete genome
4255	17271	30148	4.13	1.3E-01	AF036434.1	EST_HUMAN	QV3-DT0018-081299-036-a03 DT0018 Homo sapiens cDNA
4263	17279	30148	2.18	1.3E-01	AF026805.1	NT	Schistosoma mansoni fructose biphosphate aldolase mRNA, complete cds
4282	17298	30182	26.88	1.3E-01	AW273741.1	EST_HUMAN	x23f10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813995 3'
4387	17401	30269	1.05	1.3E-01	AV752279.1	EST_HUMAN	AV752279 NP0 Homo sapiens cDNA clone NPDAZE02 5'
4387	17401	30270	1.05	1.3E-01	AV752279.1	EST_HUMAN	AV752279 NP0 Homo sapiens cDNA clone NPDAZE02 5'
4419	17430		1.93	1.3E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4592	17600	30457	0.88	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds
4650	17656	30522	2.2	1.3E-01	BE272339.1	EST_HUMAN	60126096F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2690063 5'
6099	18096		1.01	1.3E-01	AU136619.1	EST_HUMAN	AU136619 PLACET1 Homo sapiens cDNA clone PLACE1004693 5'
5152	18145		0.74	1.3E-01	BF091980.1	EST_HUMAN	RC4-TN0077-180900-012-c05 TN0077 Homo sapiens cDNA
5255	18241	31093	1.2	1.3E-01	AI432531.1	EST_HUMAN	It38c10.x1 NCI_OGAP_Pan1 Homo sapiens cDNA clone IMAGE:2120562 3'
5268	18254	31103	0.66	1.3E-01	L76979.1	NT	Schizosaccharomyces pombe HMG-CoA reductase (hmg1+) gene, complete cds

Page 114 of 545  
Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5377	18359	31198	0.92	1.3E-01	8922935	NT	Homo sapiens hypothetical protein FLJ11198 (FLJ11198), mRNA
5608	18587	31436	0.76	1.3E-01	AW469888.1	EST_HUMAN	ha07b06.x1 NCL_CGAP_K1d12 Homo sapiens cDNA clone IMAGE:2872978 3' similar to contains L1.b1 L1
5547	18625	31500	1.89	1.3E-01	AW604417.1	EST_HUMAN	L1 repetitive element;
5691	18764		0.81	1.3E-01	AF107793.1	NT	QV0-UM00093-100400-189-a06 UMO0093 Homo sapiens cDNA
5778	18850		22.2	1.3E-01	AF056880.1	NT	Emericella nidulans DNA-dependent RNA polymerase II RPB140 (RPB2) gene, partial cds
5926	18993	32112	0.88	1.3E-01	BF210920.1	EST_HUMAN	Hepatitis C virus 68_CL10 genome polyprotein gene, partial cds
6216	19271	32424	0.68	1.3E-01	BF527281.1	EST_HUMAN	601874591F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101119 5'
6216	19271	32425	0.68	1.3E-01	BF527281.1	EST_HUMAN	602039337F2 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4177233 5'
6758	19792	33006	17.04	1.3E-01	AB031326.1	NT	602039337F2 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4177233 5'
6850	19882	33096	1.91	1.3E-01	X88891.1	NT	Schizosaccharomyces pombe gene for Alp41, complete cds
7096	20302		0.74	1.3E-01	W26367.1	EST_HUMAN	C jacchus intron 4 of visual pigment gene (red allele)
7148	20255	33508	0.55	1.3E-01	BE782926.1	EST_HUMAN	26f3 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
7148	20255	33508	0.55	1.3E-01	BE782926.1	EST_HUMAN	601465957F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3869079 5'
7359	20354		0.73	1.3E-01	BF529560.1	EST_HUMAN	601465957F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3869079 5'
7637	20572		1.85	1.3E-01	H48664.1	EST_HUMAN	602044345F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4181866 5'
8262	21167		0.45	1.3E-01	BF681615.1	EST_HUMAN	Yr33d02.r1 Soares fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:207075 5'
8537	21468		0.87	1.3E-01	BE272339.1	EST_HUMAN	602156643F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297384 5'
8551	21482	34823	1.67	1.3E-01	11423294	NT	601126096F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990063 5'
8592	21613	34857	1.28	1.3E-01	BF690522.1	EST_HUMAN	Homo sapiens PRO0811 protein (PRO0811), mRNA
8850	21780	35127	0.7	1.3E-01	11421556	NT	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4289074 3'
8919	21849		4.33	1.3E-01	Z74102.1	NT	Homo sapiens TED protein (TED), mRNA
8957	21887		5.17	1.3E-01	8923919	NT	S.cerevisiae chromosome IV reading frame ORF YDL064c
8992	22021	35378	2.2	1.3E-01	BF690522.1	EST_HUMAN	Homo sapiens core histone macroH2A2.2 (MACROH2A2), mRNA
9503	22430	35792	0.88	1.3E-01	R11172.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4289074 3'
9503	22430	35793	0.88	1.3E-01	R11172.1	EST_HUMAN	Y39q11.r1 Soares fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:129284 5' similar to
9760	22684	36070	0.78	1.3E-01	11068003	NT	SP:RL2B_RAT P29316 60S RIBOSOMAL PROTEIN ;
9760	22684	36071	0.78	1.3E-01	11068003	NT	SP:RL2B_RAT P29316 60S RIBOSOMAL PROTEIN ;
10005	22822	36210	4.26	1.3E-01	AF023129.1	NT	Plutella xylostella granulovirus, complete genome
10554	23440		1.09	1.3E-01	8393940	NT	Plutella xylostella granulovirus, complete genome
10629	23515	36948	1.21	1.3E-01	AW851599.1	EST_HUMAN	Orctolagus cuniculus H+K+ATPase alpha 2s subunit mRNA, complete cds
10879	25695	37189	1.15	1.3E-01	AL193246.2	NT	Rattus norvegicus peptidyl arginine deiminase, type IV (Pdi4), mRNA
							MR2-CT0222-201099-001-401 CT0222 Homo sapiens cDNA
							Homo sapiens chromosome 21 segment HS21C046



Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11078	24010		2.71	1.3E-01	BF330999.1	EST_HUMAN	MR4-BT0358-130700-010-H08 BT0358 Homo sapiens cDNA
11301	24220	37669	1.62	1.3E-01	H01883.1	EST_HUMAN	y32d09.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150449 5'
11540	24450	37913	1.66	1.3E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
11624	24531		1.66	1.3E-01	BF092708.1	EST_HUMAN	MR4-TN0112-120900-102-e08 TN0112 Homo sapiens cDNA
11697	24599		4.27	1.3E-01	6871749	NT	Mus musculus cofilin 2, muscle (Cif2), mRNA
11776	24675	38163	1.54	1.3E-01	BF677328.1	EST_HUMAN	602087045F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4261346 5'
11778	24875	38194	1.54	1.3E-01	BF677328.1	EST_HUMAN	602087045F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4261346 5'
12025	24867	38369	3.34	1.3E-01	BE279449.1	EST_HUMAN	601158052F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504804 5'
12145	24985	38485	1.51	1.3E-01	BE619394.1	EST_HUMAN	601473369F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876208 5'
12461	25208	31852	1.75	1.3E-01	BE618346.1	EST_HUMAN	601462741F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866003 5'
12587	25285		3.46	1.3E-01	AJ242780.1	NT	Gallus gallus scyc1 gene for lymphotactin, exons 1-3
12657	25518		1.79	1.3E-01	AW001114.1	EST_HUMAN	wu24d09.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2520977 3' similar to TR:O60287 O60287 KIAA0539 PROTEIN. ;
404	13517	26438	6.66	1.2E-01	AI421744.1	EST_HUMAN	tf39b02.x1 NCJ_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2098539 3' similar to gb:U05760_rna1
447	13114		1.08	1.2E-01	U66912.1	NT	ANNEXIN V (HUMAN);
569	13637		2.5	1.2E-01	AF039442.1	NT	Dichytellium discoideum ORF DG1018 gene, partial cds
1403	14434	27389	2.23	1.2E-01	AU149146.1	EST_HUMAN	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
1403	14434	27390	2.23	1.2E-01	AU149146.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1410	14441		2.04	1.2E-01	AV735249.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1526	14557		1.23	1.2E-01	AA867474.1	EST_HUMAN	AV735249 cdA Homo sapiens cDNA clone cdaAJB11 5'
1655	14665	27648	1.2	1.2E-01	Q14934	SWISSPROT	al48a09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460584 3' similar to TR:Q16671
1677	14707	27670	3.09	1.2E-01	AI285402.1	EST_HUMAN	Q16671 ANTI-MULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR. ;
1793	14819		14.19	1.2E-01	X89211.1	NT	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR NFAT3) (NF-ATC4) (NF-AT3)
2196	15207	28211	1.22	1.2E-01	BF248490.1	EST_HUMAN	q6909.x1 NCJ_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1960563 3'
2305	15313	28317	0.98	1.2E-01	AL163213.2	NT	H sapiens DNA for endogenous retroviral like element
2630	15628	28621	1.96	1.2E-01	AW696556.1	EST_HUMAN	601821567F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4046224 5'
							Homo sapiens chromosome 21 segment HS21C013
							QV3-BN0046-220300-129-f10 BN0046 Homo sapiens cDNA
							Is18y07.x1 NCJ_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2228988 3' similar to TR:Q14048 Q14048
2776	15767	28762	1.09	1.2E-01	AI623388.1	EST_HUMAN	COLLAGEN VI ALPHA-2 ALTERNATIVE C-TERMINAL DOMAIN. [1] ;contains element PTR5 repetitive
2898	15942	28844	1.24	1.2E-01	U18018.1	NT	Human E1A enhancer binding protein (E1A-F) mRNA, partial cds

Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2046	15998	28900	6.32	1.2E-01	AI720470.1	EST_HUMAN	as80c09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb:L05095
2977	16029	28931	6.06	1.2E-01	M16364.1	NT	60S RIBOSOMAL PROTEIN L30 (HUMAN);
3048	16100	29003	0.87	1.2E-01	X59882.1	NT	Human creatine kinase-B mRNA, complete cds
3277	16325	29231	3	1.2E-01	AW370668.1	EST_HUMAN	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3302	16349		1.05	1.2E-01	U67600.1	NT	QV1-B70259-261059-021-c05 B10259 Homo sapiens cDNA
3404	16446	29354	1.03	1.2E-01	AW503374.1	EST_HUMAN	Melanococcus jannaschii section 142 of 160 of the complete genome
3538	16576		0.66	1.2E-01	Z99118.1	NT	UI-IF-BN0-ekw-a-10-Q-UJr1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078427 5'
3582	16619	29522	0.95	1.2E-01	X58882.1	NT	Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540
3582	16619	29523	0.95	1.2E-01	X58882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3669	16576		1.11	1.2E-01	Z99118.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3833	15862		1.19	1.2E-01	BF128551.1	EST_HUMAN	Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540
4278	17262	30167	2.81	1.2E-01	Z64255.1	NT	601810786R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053688 3'
4278	17292	30158	2.81	1.2E-01	Z54255.1	NT	P. clarkii mRNA; repeat region (ID 2MRT7)
4417	17428	30290	0.74	1.2E-01	M15861.1	NT	P. clarkii mRNA; repeat region (ID 2MRT7)
4834	17835	30705	1.1	1.2E-01	Z48183.1	NT	Chicken neutral cell-adhesion molecule (N-CAM) gene, exon 19
4887	17886		0.73	1.2E-01	L32873.1	NT	L. esculentum mRNA for glyoxalase-I
4989	17988	30846	1.03	1.2E-01	BF311914.1	EST_HUMAN	Arabidopsis thaliana homeodomain protein (GLABRA2) gene, complete cds
5033	18030	30887	1.04	1.2E-01	AF134904.1	NT	601897754F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4127004 5'
5214	18204		0.97	1.2E-01	P16466	SWISSPROT	Schistocerca gregaria semaphorin 2a mRNA, complete cds
5251	18237	31087	1.02	1.2E-01	AL163227.2	NT	HEMOLYSIN PRECURSOR
5251	18237	31088	1.02	1.2E-01	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
5415	18396	31233	0.86	1.2E-01	L31380.1	NT	Homo sapiens chromosome 21 segment HS21C027
5431	18513	31236	0.87	1.2E-01	AA744369.1	EST_HUMAN	Macaca mulatta vitamin K dependent protein S (PROS) mRNA, complete cds
5483	18584	31408	0.89	1.2E-01	AF223391.1	NT	ny63c04.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1282950 3'
5493	18573	31418	2.48	1.2E-01	W33035.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5583	18631	31510	2.87	1.2E-01	Z98286.1	NT	z06d02.r1 Soares_papillary tumor NbrHPA Homo sapiens cDNA clone IMAGE:321699 5'
5695	18768	31693	0.93	1.2E-01	Z48234.1	NT	Homo sapiens gene encoding plakophilin (exons 1-13)
0441	19487	32054	1.9	1.2E-01	BE620945.1	EST_HUMAN	M. domestica Borkh. Granny Smith adh mRNA for alcohol dehydrogenase
6496	19540	32717	0.73	1.2E-01	P10842	SWISSPROT	601493518F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895613 5'
6553	19595	32783	2.24	1.2E-01	AW845275.1	EST_HUMAN	MATING-TYPE P-SPECIFIC POLYPEPTIDE P1
6623	19663	32848	1.56	1.2E-01	M26925.1	NT	ILD-CT0031-221099-113-e04 CT0031 Homo sapiens cDNA
6699	19735	32937	0.88	1.2E-01	AA747635.1	EST_HUMAN	Mouse galactosyltransferase mRNA, complete cds
							nx85c01.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1269024 3'

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6939	19968	33191	1.13	1.2E-01	BF347985.1	EST_HUMAN	802023112F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158386 5'
7107	20312	33575	0.43	1.2E-01	AF295739.1	NT	JC virus agnoprotein, VP2, VP3, VP1, large T antigen, and small t antigen genes, complete cds
7358	20363	33622	0.71	1.2E-01	H47798.1	EST_HUMAN	yp80f04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:193759 5'
7358	20363	33623	0.71	1.2E-01	H47799.1	EST_HUMAN	yp80f04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:193759 5'
8039	20953	34268	0.64	1.2E-01	AJ271741.1	NT	Homo sapiens partial ILF3 gene for interleukin enhancer binding factor 3 (alternative transcripts drbp76, drbp76 gamma, drbp76 alpha and ILF3)
8306	21210	34546	0.5	1.2E-01	D87458.1	NT	Human mRNA for KIAA0282 gene, partial cds
8306	21210	34547	0.5	1.2E-01	D87458.1	NT	Human mRNA for KIAA0282 gene, partial cds
8472	21403		1.62	1.2E-01	BE007072.1	EST_HUMAN	PM3-BN0137-290300-002-f09 BN0137 Homo sapiens cDNA
8540	21471	34812	3.35	1.2E-01	AJ913753.1	EST_HUMAN	wc98g03.x1 NCL_CGAP_C63 Homo sapiens cDNA clone IMAGE:2328804 3' similar to SW:GST2_HUMAN
8586	21517	34861	0.66	1.2E-01	O02359	SWISSPROT	Q99735 MICROSOMAL GLUTATHIONE S-TRANSFERASE II:
8884	21814	35165	0.74	1.2E-01	AJ832681.1	EST_HUMAN	NADH-UBIQUINONE OXIDOREDUCTASE B22 SUBUNIT [COMPLEX I-B22]
8967	21897		10.92	1.2E-01	AW083652.1	EST_HUMAN	at7b10.x1 Barslead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2317435 3'
8967	21897		10.92	1.2E-01	AW083652.1	EST_HUMAN	xc49d07.x1 NCL_CGAP_Es02 Homo sapiens cDNA clone IMAGE:2587597 3' similar to gb:M13452 LAMIN A (HUMAN);
8987	21916		4.31	1.2E-01	AF053772.1	NT	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (ein) gene, partial cds; and transcriptional regulator QacR (qacR) and multidrug efflux protein QacB (qacB) genes, complete cds
9023	21952	35308	1.07	1.2E-01	J03956.1	NT	N.crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
9023	21952	35309	1.07	1.2E-01	J03956.1	NT	N.crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
9163	22091		0.92	1.2E-01	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region, segment 22
9247	22175		1.72	1.2E-01	U32714.1	NT	Haemophilus influenzae Rd section 29 of 163 of the complete genome
9282	22210		0.85	1.2E-01	X15191.1	NT	M.musculus DNA fragment of Apolipoprotein B gene
10100	22949	36338	2.16	1.2E-01	X77961.1	NT	S.cerevisiae HXT5 gene
10510	23397	36809	1.47	1.2E-01	AV710857.1	EST_HUMAN	AV710857 Cu Homo sapiens cDNA clone CuAAKE08 5'
11323	24242		2.68	1.2E-01	D26184.1	NT	Yeast MPT5 gene for suppressor protein, complete cds
11604	24414		3.06	1.2E-01	BE962324.2	EST_HUMAN	601655578T1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3840283 3'
11587	24498		1.63	1.2E-01	BF314481.1	EST_HUMAN	601800763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
11702	24604	38079	2.65	1.2E-01	AF190493.1	NT	Homo sapiens dynein intermediate chain DNAL1 (DNAL1) gene, exon 17
11768	24659	38143	1.76	1.2E-01	R40249.1	EST_HUMAN	yp80c02.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:28880 3'
11845	24695	38185	1.43	1.2E-01	9994174	NT	Homo sapiens UDP-Gal-beta-GlcNAc beta 1,4-galactosyltransferase, polypeptide 4 (B4GALT4), mRNA
11940	24784		1.41	1.2E-01	M65109.1	NT	Rabbit glycogen-associated protein phosphatase regulatory subunit (RG1) mRNA, complete cds
12221	25055	38554	1.51	1.2E-01	BF368735.1	EST_HUMAN	CM2-E70016-310500-206-b11 E70016 Homo sapiens cDNA

Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12250	25072		1.82	1.2E-01	AV658033.1	EST_HUMAN	AV658033 GLC Homo sapiens cDNA clone GLCFIB12 3'
12570	25275		3.58	1.2E-01	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
12647	25903	31363	2.74	1.2E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW136) (CD136 ANTIGEN)
12753	25399		1.79	1.2E-01	AF188992.1	NT	Drosophila melanogaster strain Oregon R potential RNA-binding protein gene, complete cds; and syntaxin gene, partial cds
12755	13637		22.79	1.2E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
12846	25458		2.72	1.2E-01	X53981.1	NT	R. norvegicus NF68 gene for 68kDa neurofilament
12833	25502	31771	5.48	1.2E-01	AI289903.1	EST_HUMAN	qn20g05.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1888840 3'
12954	25515		3.58	1.2E-01	L10187.1	NT	Xenopus laevis integrin alpha 3 subunit mRNA, partial cds
12959	25845		6.55	1.2E-01	O98433	SWISSPROT	CYCLIN T
12985	25544	31752	1.63	1.2E-01	AE004428.1	NT	Vibrio cholerae chromosome II, section 85 of 93 of the complete chromosome
596	13654	25559	0.78	1.1E-01	AI561003.1	EST_HUMAN	in1808.x1 NCI_CGAP_Bir25 Homo sapiens cDNA clone IMAGE:2187983 3'
638	13699	26605	2.48	1.1E-01	AA569006.1	EST_HUMAN	hmo3g11.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1059620 3' similar to gb-X06985_mn1
1081	14125	27063	1.8	1.1E-01	BF697308.1	EST_HUMAN	602129847F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286771 5'
1112	14154		1.47	1.1E-01	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
1186	15894	27184	4.18	1.1E-01	AW972158.1	EST_HUMAN	EST384142 IMAGE resequences, MAGI Homo sapiens cDNA
1277	14311	27261	1.96	1.1E-01	D64004.1	NT	Synechocystis sp. PCC6803 complete genome, 23/27, 2663767-3002965
1542	14572	27531	2.28	1.1E-01	AU140383.1	EST_HUMAN	AU140383 PLACE2 Homo sapiens cDNA clone PLACE2000403 5'
2188	15209		0.99	1.1E-01	AJ006701.1	NT	Homo sapiens mRNA for putative serine/threonine protein kinase, partial
2335	15343		3.96	1.1E-01	6755215	NT	Mus musculus pre T-cell antigen receptor alpha (Ptcra), mRNA
2567	15860		0.91	1.1E-01	6078676	NT	Rattus norvegicus Procollagen II alpha 1 (Col2a1), mRNA
2602	16600		1.2	1.1E-01	AW821809.1	EST_HUMAN	RCO-ST0379-210100-032-g04 ST0379 Homo sapiens cDNA
3080	16131	29027	0.67	1.1E-01	F03265.1	EST_HUMAN	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1f02 3'
3390	16433		2.14	1.1E-01	6753231	NT	Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Cacna1g), mRNA
3482	16522	29421	3	1.1E-01	BE393186.1	EST_HUMAN	601308679F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3627066 5'
3513	16551	29451	1.39	1.1E-01	X62135.1	NT	C. reinhardtii nuclear gene on linkage group XIX
3550	16598	29494	0.82	1.1E-01	R96946.1	EST_HUMAN	yq62g08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:200414 3' similar to contains
3644	16680	29577	0.99	1.1E-01	Y07695.1	NT	Alu repetitive element
3765	16797		1.08	1.1E-01	P97384	SWISSPROT	Alimerae gene for transposase
3772	16804	29691	1.8	1.1E-01	X52708.1	NT	ANNEXIN XI (CALCYCLIN-ASSOCIATED ANNEXIN 50) (CAP-50)
4204	17222	30086	1.03	1.1E-01	AW819412.1	EST_HUMAN	G.gallus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5

Page 119 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4204	17222	30087	1.03	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0290-290100-025-g07 ST0290 Homo sapiens cDNA
							Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds;
4210	17227		0.65	1.1E-01	AF030001.1	NT	Noch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2),
4351	17365		11.07	1.1E-01	AF157068.1	NT	CREB-RP, and tenascin X (TNX) genes, complete>
4384	17398	30266	0.69	1.1E-01	AW802056.1	EST_HUMAN	Drosophila melanogaster Kirsicht protein (Klar) mRNA, complete cds
							IL5-UM0070-020500-068-a08 UM0070 Homo sapiens cDNA
							Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and
4683	17688	30555	0.8	1.1E-01	AF064594.2	NT	WSB1 protein (WSB1) genes, complete cds
4946	17945	30803	1.28	1.1E-01	Y07695.1	NT	A.immersus gene for transposase
5143	18138		0.69	1.1E-01	AW028547.1	EST_HUMAN	ww14102.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:262655 3'
							Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds;
5148	17227		0.82	1.1E-01	AF030001.1	NT	Noch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2),
5241	18228	31076	0.76	1.1E-01	AW819412.1	EST_HUMAN	CREB-RP, and tenascin X (TNX) genes, complete>
5241	18228	31077	0.76	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0290-290100-025-g07 ST0290 Homo sapiens cDNA
5303	18287	31140	1.02	1.1E-01	P70281	SWISSPROT	MR3-ST0290-290100-025-g07 ST0290 Homo sapiens cDNA
							SYNAPTONEMAL COMPLEX PROTEIN 3 (SCP-3) PROTEIN
							nt76a03.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1268140 similar to contains Alu repetitive
							element; contains element MER35 repetitive element;
5867	18938		1.53	1.1E-01	AA747216.1	EST_HUMAN	6 Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 6
5942	19009	32128	1.26	1.1E-01	AF020927.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
5982	19047	32171	0.81	1.1E-01	AL110885.1	NT	602035176F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4186818 5'
6017	19079	32204	0.76	1.1E-01	BF339519.1	EST_HUMAN	602035176F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4186818 5'
6017	19079	32205	0.76	1.1E-01	BF339519.1	EST_HUMAN	S.pombe sta8 gene encoding protein kinase
6049	19111	32240	1.96	1.1E-01	X88851.1	NT	Providencia rettgeri penicillin G amidase gene
6086	19147	32282	4.55	1.1E-01	M85533.1	NT	Homo sapiens LGMD2B gene
6259	19310	32474	1.59	1.1E-01	AJ007973.1	NT	PM3-FT0024-130600-004-f12 FT0024 Homo sapiens cDNA
6281	19332	32498	1.8	1.1E-01	BE769152.1	EST_HUMAN	RC3-CT0254-280999-011-a01 CT0254 Homo sapiens cDNA
6301	19352	32521	8.23	1.1E-01	AW853699.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
6692	19728	32928	0.61	1.1E-01	AL163282.2	NT	AF035746 Human salivary gland cell line HSG Homo sapiens cDNA clone RL43
6700	19736	32938	1.43	1.1E-01	AF035746.1	EST_HUMAN	9q76d05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841099 3'
6746	19780	32993	0.81	1.1E-01	AI219307.1	EST_HUMAN	ACETYL-COENZYM A SYNTHETASE (ACETATE--COA LIGASE) (ACYL-ACTIVATING ENZYME)
6894	19924	33139	4.03	1.1E-01	O69635	SWISSPROT	Homo sapiens syn14n 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds
7001	20028		3.2	1.1E-01	AF032922.1	NT	Homo sapiens phosphatidylinositol glycan, class B (PIGB), mRNA
7103	20309	33570	2.17	1.1E-01	11432372	NT	Ureaplasma urealyticum section 59 of 59 of the complete genome
7400	20099	33333	0.61	1.1E-01	AE002155.1	NT	

Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7400	20099	33334	0.61	1.1E-01	AE002165.1	NT	Ureaplasma urealyticum section 58 of 59 of the complete genome
7551	25981		0.89	1.1E-01	BF382758.1	EST_HUMAN	601816524F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050653 5'
7685	25974	33919	0.98	1.1E-01	AP000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1486000 nt. position (6/7)
7963	20885	34195	8.05	1.1E-01	BF684628.1	EST_HUMAN	602140976F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4302019 5'
7963	20885	34196	8.05	1.1E-01	BF684628.1	EST_HUMAN	602140976F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4302019 5'
8023	20939	34254	0.62	1.1E-01	AA095908.1	EST_HUMAN	ou44g03.s1 Soarea_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1629172 3'
8104	21016	34343	1.87	1.1E-01	P41067	SWISSPROT	TRAB PROTEIN
8149	21058		0.72	1.1E-01	Z14098.1	NT	B. subtilis gene encoding hypothetical polyketide synthase
8150	21059	34390	3.26	1.1E-01	AA788784.1	EST_HUMAN	eh31b06.s1 Soarea_perathyroid_tumor_NBHPA Homo sapiens cDNA clone 1240403 3' similar to gb.J03483
8327	21232	34567	0.63	1.1E-01	BE782280.1	EST_HUMAN	CHROMOGGRANIN A PRECURSOR (HUMAN);
8546	21477	34819	0.8	1.1E-01	U67492.1	NT	601470055F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873229 5'
8786	21716	35083	1.64	1.1E-01	AA493574.1	EST_HUMAN	Methanococcus jannaschii section 34 of 150 of the complete genome
8786	21716	35084	1.64	1.1E-01	AA493574.1	EST_HUMAN	nh04g10.s1 NCI_CGAP_Tiny1 Homo sapiens cDNA clone IMAGE:943362
8830	21760	35106	1.42	1.1E-01	X91233.1	NT	nh04g10.s1 NCI_CGAP_Tiny1 Homo sapiens cDNA clone IMAGE:943362
8870	21800		1.1	1.1E-01	AW817918.1	EST_HUMAN	H.sapiens LI15 gene
8925	21855	35211	1.96	1.1E-01	AL134349.1	EST_HUMAN	PM1-ST0270-080200-001-f09 ST0270 Homo sapiens cDNA
9377	22305	35666	1.95	1.1E-01	U02482.1	NT	DKFZp547P194_r1 547 (synonym: nfor1) Homo sapiens cDNA clone DKFZp547P194 5'
9469	22397	35760	1.28	1.1E-01	AI807474.1	EST_HUMAN	Pedococcus acidilactici H plasmid pSMB74 pediocin ACh production (pap) gene cluster papA, papB, papC and papD genes, complete cds
9560	22487	35848	0.6	1.1E-01	AF050081.1	NT	wf48c01.x1 Soarea_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359816 3' similar to contains Alu repetitive element;
9595	22521	35894	2.84	1.1E-01	AA192153.1	EST_HUMAN	Homo sapiens C16orf3 large protein mRNA, complete cds
9595	22521	35885	2.84	1.1E-01	AA192153.1	EST_HUMAN	zp93b12.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
9678	22604	35977	0.62	1.1E-01	Y12727.1	NT	zp93b12.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
9708	22633	36013	4.43	1.1E-01	T72675.1	EST_HUMAN	P. furiosus partial dph5 gene and argF gene
9733	22658		0.73	1.1E-01	BE893280.1	EST_HUMAN	yd19h03.s1 Soarea fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:108725 3' similar to gb.M81181 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN);
9956	22861		0.88	1.1E-01	BE142305.1	EST_HUMAN	601436972F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922048 5'
10029	22929		2.47	1.1E-01	BF085149.1	EST_HUMAN	CK3-HT0142-271099-026-g11 HT0142 Homo sapiens cDNA
10421	23310		0.64	1.1E-01	AL161543.2	NT	MR2-GN0027-040900-005-a08 GN0027 Homo sapiens cDNA
10702	23588		1.49	1.1E-01	R80590.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 43
10825	23711	37138	1.14	1.1E-01	U60529.1	NT	y96a09.s1 Soarea placenta NbZHP Homo sapiens cDNA clone IMAGE:147064 3'
11244	16131	29027	2.09	1.1E-01	F03265.1	EST_HUMAN	Ceratitis capitata yoyo retrotransposon gag-like, pol-like and env-like genes, complete cds
							HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1f02 3'

Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11359	24277		2.21	1.1E-01	AF169032.1	NT	Caressius auratus activin beta A precursor, mRNA, complete cds
11481	24384	37844	3.66	1.1E-01	R23708.1	EST_HUMAN	yh35f12.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131759 5' similar to contains Alu repetitive element; contains TAR1 repetitive element ;
11490	24402	37853	1.78	1.1E-01	6981351	NT	Rattus norvegicus Phosphofructokinase, liver, B-type (Pfkf), mRNA
11656	24562	38033	2.69	1.1E-01	Z11910.1	NT	Z.mobilis lgt and lig genes encoding RNA guanine transglycosylase and DNA ligase
11656	24562	38034	2.68	1.1E-01	Z11910.1	NT	Z.mobilis lgt and lig genes encoding RNA guanine transglycosylase and DNA ligase
11751	24652	38133	2.81	1.1E-01	P17437	SWISSPROT	SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)
12059	24940		1.53	1.1E-01	AL161511.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
12343	25136		1.64	1.1E-01	AA192153.1	EST_HUMAN	zpe3b12.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
12444	25199		1.89	1.1E-01	BE767023.1	EST_HUMAN	RC2.NT0112-120600-014-603 NT0112 Homo sapiens cDNA
12676	25731		1.99	1.1E-01	BE974956.1	EST_HUMAN	601680551R2 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:3950604 3'
1229	14266		2.23	1.0E-01	O62855	SWISSPROT	DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)
1299	14332	27278	2.06	1.0E-01	A1985469.1	EST_HUMAN	ws08401.x1 NCL CGAP Kld11 Homo sapiens cDNA clone IMAGE:2496577 3' similar to contains MER7.k3
1419	14450	27404	2.07	1.0E-01	AL161504.2	NT	MER7 repetitive element ;
2512	15513	28516	1.08	1.0E-01	AW451385.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
3572	16609	29512	1.46	1.0E-01	BF033991.1	EST_HUMAN	UI-H-B18-alc-4-07-0-UI.s1 NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736420 3'
3783	16814	29701	0.98	1.0E-01	BF239818.1	EST_HUMAN	601456301F1 NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3859849 5'
4036	17063	29852	3.36	1.0E-01	BF365703.1	EST_HUMAN	601908489F1 NIH_MGC 54 Homo sapiens cDNA clone IMAGE:4134071 5'
4513	17522	30387	1.05	1.0E-01	AE002266.2	NT	QV2.NT0048-160800-316-ed5 NT0048 Homo sapiens cDNA
4870	17675		0.76	1.0E-01	A1792349.1	EST_HUMAN	Chlamydomonas reinhardtii AR39, section 91 of 94 of the complete genome
4825	17826	30694	1.33	1.0E-01	U50450.1	NT	an32x04.y6 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700359 5'
5030	18027	30885	2.62	1.0E-01	AW062344.1	EST_HUMAN	Drosophila melanogaster tyrosine kinase p45 isoform (ter) mRNA, complete cds
5300	18284	31135	0.68	1.0E-01	BE389100.1	EST_HUMAN	EST1364414 IMAGE sequences, MAG8 Homo sapiens cDNA
5504	18583		8.68	1.0E-01	W86490.1	EST_HUMAN	601286969F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3613662 5'
5603	18678		0.64	1.0E-01	X54015.1	NT	zh62h04.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416695 3'
5685	18758		0.43	1.0E-01	Q36960	SWISSPROT	X.campestris genes for sensor and regulator protein
6095	19156		0.99	1.0E-01	AK024472.1	NT	CYTCHROME C OXIDASE POLYPEPTIDE III
6257	19309	32473	12.02	1.0E-01	AF274875.1	NT	Homo sapiens mRNA for FUJ00065 protein, partial cds
6592	19633	32815	0.84	1.0E-01	AA481879.1	EST_HUMAN	Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds
6606	19647	32830	0.68	1.0E-01	AA406039.1	EST_HUMAN	z441g10.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:766268 3' similar to contains L1.13 L1 repetitive element ;
7369	20363		1.63	1.0E-01	R23821.1	EST_HUMAN	z467c12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:743062 3'
							yh34h06.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131675 5' similar to contains Alu repetitive element;

Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8200	21106		2.05	1.0E-01	Y12488.1	NT	M.musculus wlm gene
8324	21229	34593	0.51	1.0E-01	AJ011400.1	NT	Bos taurus mRNA for b17.2 subunit of NADH:ubiquinone oxidoreductase complex (complex I)
8324	21229	34584	0.51	1.0E-01	AJ011400.1	NT	Bos taurus mRNA for b17.2 subunit of NADH:ubiquinone oxidoreductase complex (complex I)
8420	21333	34666	0.41	1.0E-01	BF128224.1	EST_HUMAN	601810459RT NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053494 3'
8512	21443	34785	0.69	1.0E-01	AA861091.1	EST_HUMAN	ak32901.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1407898 3' similar to gb:M34182 CAMP-DEPENDENT PROTEIN KINASE, GAMMA-CATALYTIC SUBUNIT (HUMAN);
8744	21674		0.6	1.0E-01	4758365	NT	Homo sapiens fibroblast growth factor 13 (FGF13) mRNA
9061	21990		1.28	1.0E-01	AW189797.1	EST_HUMAN	x109501.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2875689 3' similar to gb:X17206 40S
9727	22652	36036	1.23	1.0E-01	AF102855.2	NT	RIBOSOMAL PROTEIN S4 (HUMAN); contains TAR1.13 TAR1 repetitive element ;
10028	22928	36316	0.57	1.0E-01	R44993.1	EST_HUMAN	Rattus norvegicus synaptic SAPAP-interacting protein Synapmon mRNA, complete cds
10038	22938		2.14	1.0E-01	M76729.1	NT	Yg33h04.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34549 3'
10079	22872		2.71	1.0E-01	AE001501.1	NT	Human pro-alpha-1(V) collagen mRNA, complete cds
10093	22943	36331	0.77	1.0E-01	W01955.1	EST_HUMAN	Helicobacter pylori, strain J99 section 02 of 132 of the complete genome
10336	23225	36640	2.03	1.0E-01	BF210754.1	EST_HUMAN	z66610 s1 Soares_fetal heart_NbHH19W Homo sapiens cDNA clone IMAGE:327282 3'
10444	23333	36780	9.79	1.0E-01	AB046799.1	NT	6018056631F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133487 5'
10444	23333	36751	9.79	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
10641	23527		1.21	1.0E-01	AW957425.1	EST_HUMAN	Homo sapiens mRNA for KIAA1579 protein, partial cds
10646	23532	36984	0.56	1.0E-01	T51952.1	EST_HUMAN	EST369815 IMAGE resequences, IMAGE Homo sapiens cDNA
10820	23706	37133	1.27	1.0E-01	BE792760.1	EST_HUMAN	y629a06.s1 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:72562 3' similar to contains Alu repetitive element
11101	24032		1.86	1.0E-01	AU159127.1	EST_HUMAN	601581604F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939066 5'
11472	24385	37834	2.34	1.0E-01	BF242946.1	EST_HUMAN	AU159127 THYRO1 Homo sapiens cDNA clone THYRO1000895 3'
11472	24386	37835	2.34	1.0E-01	BF242946.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
11837	24688	38177	4.8	1.0E-01	BE780543.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
12430	25505		3	1.0E-01	BE537719.1	EST_HUMAN	601582558F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936734 5'
12658	25330		1.89	1.0E-01	X00854.1	NT	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
12909	25896		4	1.0E-01	U52691.1	NT	Drosophila melanogaster ftz gene
12937	25505		2.82	1.0E-01	BE537719.1	EST_HUMAN	Gonyaulax polyedra putative type-1 serine/threonine phosphatase (PP1) mRNA, complete cds
12996	25874		30.18	1.0E-01	U66834.1	NT	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
13043	25578		8.63	1.0E-01	AP001607.1	NT	Saccharomyces cerevisiae suppressor of ABF1 (SAB2) gene, complete cds
2829	15818	28813	1.39	9.9E-02	AF274008.1	NT	Bacillus halodurans genomic DNA, section 1/14
2835	15824	28820	1.29	9.9E-02	BE545554.1	EST_HUMAN	Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pka-R11) mRNA, complete cds



Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2835	18824	28821	1.29	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
3311	16359	29259	1.23	9.9E-02	AF099810.1	NT	Homo sapiens neurxin III-alpha gene, partial cds
4032	17059	29948	0.9	9.9E-02	AB21637.1	EST_HUMAN	zu45c03.x5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740932 3'
7185	20185	33429	0.49	9.9E-02	BE613498.1	EST_HUMAN	601604252F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906084 5'
7309	18477	31299	8.22	9.9E-02	D83710.1	NT	Aspergillus terreus BSD mRNA for blestidin S deaminase, complete cds
8494	21425	34765	0.52	9.9E-02	AW103088.1	EST_HUMAN	xd43c08.x1 NCL_CGAP_OV23 Homo sapiens cDNA clone IMAGE:2596528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element ;
8494	21425	34766	0.52	9.9E-02	AW103088.1	EST_HUMAN	xd43c08.x1 NCL_CGAP_OV23 Homo sapiens cDNA clone IMAGE:2596528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element ;
9799	22763	36148	1.86	9.9E-02	6755111	NT	Mus musculus phospholipid transfer protein (Plip), mRNA
585	13653		1.16	9.8E-02	X58338.1	NT	O. sativa RAmY3C gene for alpha-amylase
3188	16237	29131	4.99	9.8E-02	AF184274.1	NT	Daucus carota leucoanthocyanidin dioxygenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds
4323	17337	30201	9.42	9.8E-02	AF257329.1	NT	Leptospira meculans beta-tubulin mRNA, complete cds
4323	17337	30202	9.42	9.8E-02	AF257329.1	NT	Leptospira meculans beta-tubulin mRNA, complete cds
7902	20827		0.93	9.8E-02	X54133.1	NT	Human HPTP delta mRNA for protein tyrosine phosphatase delta
9798	22780		1.08	9.8E-02	M81943.1	NT	Human laminin B1 chain gene, exon 26
11892	23992	37431	2.03	9.8E-02	BF037421.1	EST_HUMAN	601460793F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3864287 5'
12402	25174		1.7	9.8E-02	8393751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
1379	14411	27366	1.33	9.7E-02	AB005808.1	NT	Alcea arborescens mRNA for NADP-malic enzyme, complete cds
1608	14638		0.99	9.7E-02	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
2278	15287	28295	2.33	9.7E-02	BE168660.1	EST_HUMAN	QV1-HT0516-070300-095-404 HT0516 Homo sapiens cDNA
4068	17094		4.76	9.7E-02	Q89795	SWISSPROT	CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
5529	18608	31456	0.93	9.7E-02	AF099189.1	NT	Caulobacter crescentus thymidylate kinase (tnk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
5529	18608	31457	0.93	9.7E-02	AF099189.1	NT	Caulobacter crescentus thymidylate kinase (tnk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
8247	18303	32460	1.38	9.7E-02	AW954476.1	EST_HUMAN	EST336546 IMAGE resequences, MAGC Homo sapiens cDNA
7679	20613	33912	3.3	9.7E-02	Z69119.1	NT	Bacillus subtilis complete genome (section 16 of 21): from 2997771 to 3213410
8562	21403	34835	1.62	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
8562	21493	34836	1.62	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
9408	22336	35700	1.25	9.7E-02	AI953984.1	EST_HUMAN	wx78b06.x1 NCL_CGAP_OV38 Homo sapiens cDNA clone IMAGE:2549747 3' similar to gb:X52851_mn1 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN);
11642	24548		2.11	9.7E-02	U58337.1	NT	Mus musculus ligatin (Lgt) mRNA, partial cds

Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2029	16046	28041	1.01	9.6E-02	A080721.1	EST_HUMAN	oz47d11.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
2029	15046	28042	1.01	9.6E-02	A080721.1	EST_HUMAN	oz47d11.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
4454	17464	30321	8.84	9.6E-02	Z32866.2	NT	Proteus mirabilis fimbrial operon, strain H4320
5122	16118	30960	1.47	9.6E-02	AW966230.1	EST_HUMAN	EST378303 MAGE resequencing, MAGI Homo sapiens cDNA
5296	18281	31131	0.74	9.6E-02	BE061728.1	EST_HUMAN	RC5-BT0254-031099-011-a03 BT0254 Homo sapiens cDNA
8343	19393		2.9	9.6E-02	BE910039.1	EST_HUMAN	501498088F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900165 5'
8402	21303		0.48	9.6E-02	66578753	NT	Mus musculus lymphocyte antigen 78 (Ly78), mRNA
8947	21877		0.8	9.6E-02	AU137084.1	EST_HUMAN	AU137084 PLACE1 Homo sapiens cDNA clone PLACE1005740 5'
10073	22988	36383	2.18	9.6E-02	AV687898.1	EST_HUMAN	AV687898 GKC Homo sapiens cDNA clone GKCAAH02 5'
10384	23273		1.71	9.6E-02	BE894895.1	EST_HUMAN	801434060F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919363 5'
10542	23428	36848	1.69	9.6E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10542	23428	36849	1.69	9.6E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10620	23506	36940	0.64	9.6E-02	BF677270.1	EST_HUMAN	602086769F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250969 5'
10648	23534	36966	2	9.6E-02	AB013985.1	NT	Anthrax toxin major transposon Tam3 pseudogene for transposase (in S-5 copy)
10648	23534	36967	2	9.6E-02	AB013985.1	NT	Anthrax toxin major transposon Tam3 pseudogene for transposase (in S-5 copy)
10751	23637	37070	4.05	9.6E-02	P08174	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR (CD55)
11183	24109	37556	6.87	9.6E-02	Z79702.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 102/162
12141	24981	38481	1.43	9.6E-02	AA625755.1	EST_HUMAN	zu91g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
12974	25536		1.87	9.6E-02	H14569.1	EST_HUMAN	ym19h03.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:48553 3'
13103	25618		3.56	9.6E-02	AJ300197.1	NT	Xenopus laevis mRNA for dickkopf2 (dkk2 gene)
4192	17212	30079	2.37	9.5E-02	AV992395.1	EST_HUMAN	CM2-BN0023-050200-087-f12 BN0023 Homo sapiens cDNA
5862	18933	32052	0.88	9.5E-02	P51854	SWISSPROT	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
7684	20618	33918	4.96	9.5E-02	AB003473.1	NT	Trimeresurus flavoviridis DNA for phospholipase A2 inhibitor, complete cds
8001	20919	34236	7.96	9.5E-02	AL161638.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
8152	18933	32052	0.88	9.5E-02	P51854	SWISSPROT	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
8460	21391	34732	2.46	9.5E-02	BF035881.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
8460	21391	34733	2.46	9.5E-02	BF035881.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
11122	24052	37497	2.86	9.5E-02	BF035881.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
11222	24052	37498	2.86	9.5E-02	BF035881.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
12226	25060	38558	1.83	9.5E-02	U37070.1	NT	Human transforming growth factor-beta type II receptor (TGF-beta RI), promoter region
13031	25570		1.79	9.5E-02	AF272732.1	NT	Arabidopsis thaliana putative transcription factor (MYB110) mRNA, complete cds
1857	14879	27856	3.42	9.4E-02	BF671063.1	EST_HUMAN	502150882F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291817 5'
3949	16977	29861	6.79	9.4E-02	Z33059.1	NT	M. capricolum DNA for CONTIG MC073
5182	18174	31019	0.71	9.4E-02	6753517	NT	Mus musculus coding region determinant-binding protein (Crbp), mRNA

Page 125 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6572	19513	32799	0.82	9.4E-02	AF097363.1	NT	Triticum aestivum heat shock protein 101 (Hsp101e) mRNA, complete cds
8036	20951	34266	0.62	9.4E-02	L78833.1	NT	Human BRCA1, Rho7 and vatl genes, complete cds, and ipf35 gene, partial cds
9162	22090		1.8	9.4E-02	Z46963.1	NT	Acinetobacter sp. cyaD, cobQ, sodM, lysB, rubA, rubB, eaeB, oxyR, ptkA, mtgA, ORF2 and ORF3 genes
11372	20951	34266	2.5	9.4E-02	L78833.1	NT	Human BRCA1, Rho7 and vatl genes, complete cds, and ipf35 gene, partial cds
12298	25814		7.24	9.4E-02	U31815.1	NT	Rattus norvegicus calcium channel alpha-1C subunit (ROB2) mRNA, partial cds
13095	25612	31735	2.36	9.4E-02	U27699.1	NT	Human pepBGT-1 beta1ne-GABA transporter mRNA, complete cds
3031	16083		2.22	9.3E-02	4809280	NT	Homo sapiens BAI1-associated protein 3 (BAIAP3) mRNA
3075	16127		7.87	9.3E-02	6912525	NT	Homo sapiens nasopharyngeal epithelium specific protein 1 (NESG1), mRNA
3301	16348	29263	1.91	9.3E-02	BF676511.1	EST_HUMAN	602133086F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288269 5'
4245	17261	30127	1.3	9.3E-02	BE543175.1	EST_HUMAN	601065147F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3455435 5'
4250	17265	30133	3.6	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4260	17263	30134	3.6	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4848	17849		2.35	9.3E-02	AV732224.1	EST_HUMAN	AV732224 HTF Homo sapiens cDNA clone HTFAUA06 5'
5136	18132	30974	1	9.3E-02	AF115443.1	NT	HIV-1 isolate Br112 from Brazil gag protein (gag) gene, partial cds
5859	18930		1.09	9.3E-02	AP001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
8374	21278	34610	0.4	9.3E-02	M75984.1	NT	Human hepatocyte growth factor gene exon 18, 3' end
8391	21295	34628	0.61	9.3E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
8823	21763	35099	0.67	9.3E-02	AW586007.1	EST_HUMAN	EST69 Human Fetal Brain MATCHMAKER cDNA Library Homo sapiens cDNA
9669	22595		0.52	9.3E-02	AL113179.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
10232	23123	36525	2.62	9.3E-02	BE92631.2	EST_HUMAN	601655989F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855981 3'
10688	23574	37003	4.48	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
10689	23574	37004	4.48	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
10809	23695		4.05	9.3E-02	AW206117.1	EST_HUMAN	U1-H-B1-afx-h-05-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723553 3'
12637	25748		2.76	9.3E-02	AJ248850.1	NT	Phlebotomus damela subsp. damela partial gyrB gene for DNA gyrase B subunit
12878	25772		22.87	9.3E-02	AW468850.1	EST_HUMAN	hd28h12.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2910887 3'
							Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bing1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1, 3-galactosyl tr>
13059	25813		3.15	9.3E-02	AF100956.1	NT	galactosyl transferase (beta1, 3-galactosyl tr>
247	13345	26255	5.64	9.2E-02	U60316.1	NT	Molluscum contagiosum virus subtype 1, complete genome
247	13345	26256	5.64	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
247	13345	26257	5.64	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
2240	15250		2.02	9.2E-02	R54186.1	EST_HUMAN	yg98107.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:41618 5'
3222	16270	29169	4.67	9.2E-02	Q28631	SWISSPROT	MAJOR EPIDIDYMISS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)

Page 126 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3351	16397	29297	1.11	9.2E-02	AA534354.1	EST_HUMAN	nt79e01.st NCL CGAP Co3 Homo sapiens cDNA clone IMAGE:926136 3'
3647	16683		1.21	9.2E-02	6755215	NT	Mus musculus pre T-cell antigen receptor alpha (P1cra), mRNA
4338	17352		1.5	9.2E-02	U92048.1	NT	Human herpesvirus 1 strain KOS-63, latency-associated transcript, promoter region
4412	17423		0.67	9.2E-02	BE299722.1	EST_HUMAN	600944365F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960176 5'
4750	17755	30615	1.81	9.2E-02	X66402.1	NT	G.gallus Mla-OK gene
8587	21518	34862	2.03	9.2E-02	T49920.1	EST_HUMAN	y99c09.r1 Stratagene placenta (#937225) Homo sapiens cDNA clone IMAGE:66808 5' similar to similar to
8755	21885	35028	2.03	9.2E-02	X65256.1	NT	gb:568009 GUANINE NUCLEOTIDE-BINDING PROTEIN G(S), ALPHA SUBUNIT (HUMAN)
13045	25966		1.57	9.2E-02	11458872	NT	H.vulgaris xylose isomerase gene
446	13113	26000	3	9.1E-02	X77665.1	NT	O. cuticulus K12 keratin gene
2440	15444	28444	1.27	9.1E-02	P78985	SWISSPROT	5-PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE)
3737	16769		1.41	9.1E-02	AW372569.1	EST_HUMAN	PM2-BT0349-161299-001-402 BT0349 Homo sapiens cDNA
4698	17606	30463	2.1	9.1E-02	AL161654.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 54
6932	18999	32119	1.65	9.1E-02	AF129756.1	NT	Homo sapiens MSH55 gene, partial cds; and GLIC1, DDAH, G6b, G6c, G5b, G8d, G8e, G6f, BAT5, G5b, CSK2B, BAT14, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
7690	25982		0.45	9.1E-02	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
7783	20712	34014	11.62	9.1E-02	AW160658.1	EST_HUMAN	au74e05.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781068 5'
8128	21039	34397	0.87	9.1E-02	AP000061.1	NT	Aeropyrum pernix genomic DNA, section 47
8169	21076	34406	0.79	9.1E-02	U39073.1	NT	Mus musculus thymopentin zeia mRNA, complete cds
8372	21276	34608	0.42	9.1E-02	AJ286667.1	NT	Welwitschia mirabilis partial phyN gene for phytochrome
9480	22408	35769	1.08	9.1E-02	Y14379.1	NT	Homo sapiens gamma adducin gene, exon 9
10810	23795		1.58	9.1E-02	T02984.1	EST_HUMAN	FB19F10 Fetal brain, Stratagene Homo sapiens cDNA clone FB19F10 3' end
10936	23821	37248	0.93	9.1E-02	S74059.1	NT	Tg616=CyI actin [Tripteneustes gratillae=sea urchins, embryos, Genomic, 5275 nt]
10964	23948	37274	0.88	9.1E-02	Y11187.1	NT	A.thaliana RH1, TC1, G14587-5, G14587-6, and PRL1 genes
11608	24517	37987	3.26	9.1E-02	AF037625.1	NT	Rana catesbeiana dihydropyridine receptor mRNA, complete cds
12525	25249		2.31	9.1E-02	AF032695.1	NT	Rattus norvegicus cell cycle protein p55GDC gene, complete cds
12888	25767		10.65	9.1E-02	AJ291360.1	NT	Homo sapiens partial MUC3B gene for MUC3B mucin, exons 1-11
							FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED RECEPTOR MOV18) (KB CELLS FBP)
768	13625	26755	2.93	9.0E-02	P15328	SWISSPROT	ANTIGEN MOV18 (KB CELLS FBP)
1680	14690	27650	5.44	9.0E-02	BE220482.1	EST_HUMAN	h39g10.x1 NCL CGAP Lu24 Homo sapiens cDNA clone IMAGE:3175842 3' similar to contains Alu repetitive element

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2850	15839	28837	5.76	9.0E-02	AF138522.1	NT	HIV-1 p8c085-06 from USA envelope glycoprotein (env) gene, partial cds
2850	15839	28838	5.76	9.0E-02	AF138522.1	NT	HIV-1 p8c085-06 from USA envelope glycoprotein (env) gene, partial cds
3385	16428	20333	0.73	9.0E-02	AF279135.1	NT	Dicystelium discoideum spore coat structural protein SP65 (colE) gene, complete cds
4779	17784	30654	2.36	9.0E-02	X65740.2	NT	Plasmodium falciparum P-type ATPase 3 gene
6227	19282	32437	13.23	9.0E-02	W56037.1	EST_HUMAN	zab8a12.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:297694 5' similar to PIR:S52171 S52171 small G protein - human :
7019	20045		0.93	9.0E-02	BF062651.1	EST_HUMAN	7h63d03.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3320645 3' similar to contains Alu repetitive element
7072	20278	33632	0.61	9.0E-02	R62805.1	EST_HUMAN	y11508.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138903 3'
12811	25433		1.71	9.0E-02	AF022236.1	NT	Escherichia coli strain E2348/69 pathogenicity island, rOrf1 (rOrf1), rOrf2 (rOrf2), EscR (escR), EscS (escS), EscT (escT), EscU (escU), CesD (cesD), EscC (escC), EscJ (escJ), SepZ (sepZ), EscV (escV), EscN (escN), SepQ (sepQ), Tir (tir), OrfU (orfU), >
1457	14489	27449	1.46	8.9E-02	BF701593.1	EST_HUMAN	602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
1457	14489	27460	1.46	8.9E-02	BF701593.1	EST_HUMAN	602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
2410	15414	29417	0.91	8.9E-02	BE153572.1	EST_HUMAN	PMO-HT0339-251199-003-d01 HT0339 Homo sapiens cDNA
4285	17309		2.07	8.9E-02	AF286055.1	NT	Atrichum angustatum AtranFic2 protein (AtranFic2) gene, partial cds
6064	19123	32255	3.18	8.9E-02	AW452122.1	EST_HUMAN	UI-H-B13-alc-f-08-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'
6064	19123	32256	3.18	8.9E-02	AW452122.1	EST_HUMAN	UI-H-B13-alc-f-08-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'
6081	19142	32278	3.36	8.9E-02	11433478	NT	Homo sapiens similar to endoglycan (H. sapiens) (LOC63107), mRNA
7557	20494	33784	1.49	8.9E-02	P47259	SWISSPROT	FOLD BIFUNCTIONAL PROTEIN [INCLUDES: METHYLENETETRAHYDROFOLATE DEHYDROGENASE; METHENYL-TETRAHYDROFOLATE CYCLOHYDROLASE]
7990	20909		1.78	8.9E-02	Z79021.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA20F8
8628	21559	34897	1.01	8.9E-02	P29475	SWISSPROT	NITRIC-OXIDE SYNTHASE, BRAIN (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS) (CONSTITUTIVE NOS) (NC-NOS) (BNOS)
8707	21638	34985	0.85	8.9E-02	BF701685.1	EST_HUMAN	602129111F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5'
8707	21638	34986	0.85	8.9E-02	BF701685.1	EST_HUMAN	602129111F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5'
9160	22088	35447	5.72	8.9E-02	AA309319.1	EST_HUMAN	EST180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
10146	23037	36435	1.02	8.9E-02	AI285627.1	EST_HUMAN	qu65c05.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1968680 3' similar to contains MER10.b1 MER10 repetitive element ;
10146	23037	36436	1.02	8.9E-02	AI285627.1	EST_HUMAN	qu65c05.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1968680 3' similar to contains MER10.b1 MER10 repetitive element ;
10253	23143	36552	0.64	8.9E-02	AA333356.1	EST_HUMAN	EST144454 Fetal brain Homo sapiens cDNA 5' end
12432	25192		3.76	8.9E-02	BF696918.1	EST_HUMAN	602129882F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286180 5'
12582	26283		2.97	8.9E-02	5680220	NT	Mus musculus hippocampus abundant gene transcript 1 (Hiat1), mRNA

Page 128 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12660	25903		1.58	8.9E-02	AE001514.1	NT	Helicobacter pylori, strain J99 section 75 of 132 of the complete genome
1400	14431	27386	0.99	8.8E-02	Q27474	SWISSPROT	PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])
3975	17003	29890	1.24	8.8E-02	AA299128.1	EST_HUMAN	EST11595 Uterus Homo sapiens cDNA 5' end
4118	17141		6.33	8.8E-02	O00268	SWISSPROT	TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT (TAFII135) (TAFII130)
4405	17417		0.8	8.8E-02	4580423	NT	Homo sapiens paired box gene 8 (airlidia, keratins) (PAX6), isoform b, mRNA
7974	20895		0.7	8.8E-02	D17520.1	NT	Sheep mRNA for angiotensinogen, complete cds
9539	22463	35927	2.38	8.8E-02	AA151872.1	EST_HUMAN	zn99a05.s1 Stralagene colon (#937204) Homo sapiens cDNA clone IMAGE:568288 3'
11558	24467	37931	2.78	8.8E-02	BE264455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
11558	24467	37932	2.78	8.8E-02	BE264455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
11709	24611	38088	6.42	8.8E-02	AL040129.1	EST_HUMAN	DKFZp434D1313.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D1313.5'
3769	16791	29681	4.71	8.7E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
3769	16791	29682	4.71	8.7E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
4820	17821	30690	1.35	8.7E-02	AF178636.1	NT	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
5155	18148	30994	0.66	8.7E-02	AI818839.1	EST_HUMAN	wk92a02.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2422826 3'
5497	18576	31422	5.51	8.7E-02	AA286875.1	EST_HUMAN	ze55g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
5497	18576	31423	5.51	8.7E-02	AA286875.1	EST_HUMAN	ze55g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
7161	20268	33524	0.7	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
7161	20268	33525	0.7	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
7394	20093	33327	0.69	8.7E-02	AF281342.1	NT	Oncorhynchus mykiss TAT-binding protein 1 mRNA, partial cds
9081	22010	35366	0.71	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PAO1, section 348 of 529 of the complete genome
9081	22010	35367	0.71	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PAO1, section 348 of 529 of the complete genome
11154	24083		2.6	8.7E-02	L04758.1	NT	Oryctolagus cuniculus cyclochrome P-450 (CYP4A4) gene, 5' end
11756	24957	38140	1.73	8.7E-02	AJ007763.1	NT	Glucobacter oxydans IRNA-1e and IRNA-Ala genes
12487	25230		2.04	8.7E-02	X17116.1	NT	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease
12676	25330		2.57	8.7E-02	6679057	NT	Mus musculus nidogen 2 (Nid2), mRNA
12676	25330		2.57	8.7E-02	6679057	NT	Mus musculus Xq pseudocentromere region; segment 2/2
1280	14313	27262	4.96	8.6E-02	AJ271736.1	NT	Homo sapiens Xq pseudocentromere region; segment 2/2
2259	15269	28275	2.28	8.6E-02	BE408667.1	EST_HUMAN	601304016F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638843 5'
3231	16279	29179	3.01	8.6E-02	L05468.1	NT	Trichomonas vaginalis beta-tubulin (tubt1) gene, complete cds
3713	16745		5.42	8.6E-02	AF153382.1	NT	Dictyostelium discoideum adenylyl cyclase (acrA) gene, complete cds

Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5306	18280	31143	1.83	8.6E-02	AF060174.1	NT	Rattus norvegicus synaptic vesicle protein 2C (SV2C) mRNA, complete cds
6331	18381	32549	4.7	8.6E-02	Y10826.1	NT	Homo sapiens LON1b gene
6634	19674	32861	1.63	8.6E-02	J00440.1	NT	Mus musculus IgM chain gene, D region; D-q82, mu switch region (part a)
6634	19674	32862	1.53	8.6E-02	J00440.1	NT	Mus musculus IgM chain gene, D region; D-q82, mu switch region (part a)
8017	20533	34251	1.04	8.6E-02	P14616	SWISSPROT	INSULIN RECEPTOR-RELATED PROTEIN PRECURSOR (IRR) (IR-RELATED RECEPTOR)
8509	21440	34780	1.23	8.6E-02	5730066	NT	Homo sapiens Sfr2-related CBP activator protein (SRCAP) mRNA
8509	21440	34781	1.23	8.6E-02	5730066	NT	Homo sapiens Sfr2-related CBP activator protein (SRCAP) mRNA
8648	21579	34916	0.59	8.6E-02	11427428	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA
8708	21639	35555	0.89	8.6E-02	U60168.1	NT	Dicotyledon discoid protein subunit C2 homolog PnC (pnc) gene, complete cds
10257	23147	35555	1.3	8.6E-02	AF111170.3	NT	Homo sapiens 14q32 Jaggad2 gene, complete cds; and unknown gene
10292	23182	35555	0.67	8.6E-02	AW662153.1	EST_HUMAN	h20c08.x1 NCL CGAP GU1 Homo sapiens cDNA clone IMAGE:2972846 3'
10650	23536	36969	0.71	8.6E-02	AF028504.1	NT	Rattus norvegicus SPA-1 like protein p1284 mRNA, complete cds
11385	24301	37747	1.89	8.6E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
11385	24301	37748	1.89	8.6E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
11605	24597	38074	2.74	8.6E-02	BF305606.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11695	24597	38075	2.74	8.6E-02	BF305606.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11872	23972	37409	6.04	8.6E-02	AE001073.1	NT	Archaeoglobus fulgidus section 34 of 172 of the complete genome
12007	24849	38348	1.83	8.6E-02	AF283660.1	NT	Bacillus stearothermophilus BsrFI methylase (FIM) and BsrFI restriction endonuclease (FIR) genes, complete cds
2419	15423	28424	3.2	8.5E-02	AE000652.1	NT	Helicobacter pylori 26695 section 130 of 134 of the complete genome
5866	18937	32055	0.7	8.5E-02	AA985491.1	EST_HUMAN	q43b07.s1 NCL CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1592917 3' similar to gb-K01144 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, GAMMA CHAIN PRECURSOR (HUMAN);
5907	18978	32055	1.89	8.5E-02	P08089	SWISSPROT	M PROTEIN, SEROTYPE 8 PRECURSOR
8244	19298	32456	5.44	8.5E-02	AF233885.1	NT	Mus musculus phospholipase C-like protein mRNA, partial cds
9167	22095	35454	2.4	8.5E-02	6754779	NT	Mus musculus myosin XV (Myo15), mRNA
10351	23240	36659	3.24	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
10351	23240	36660	3.24	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
10849	23735	37168	0.67	8.5E-02	X76731.1	NT	V. ammodontes gene for ammodontin C
10963	23847	37273	0.89	8.5E-02	11418108	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
11596	24505	37990	10.13	8.5E-02	AF155510.1	NT	Homo sapiens heparanase precursor, mRNA, complete cds
11614	24522	37990	3.62	8.5E-02	AB001562.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
12856	25713		2.03	8.5E-02	AJ005585.1	NT	Anthrithum majus mRNA for MYB-related transcription factor

Page 130 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12875	25871		2.65	8.5E-02	AF110403.1	NT	Bactrocera tryoni transposon Homer putative transposase gene, complete cds
13012	25559		2.28	8.5E-02	AA362834.1	EST_HUMAN	EST72736 Ovary II Homo sapiens cDNA 5' end
2716	15931	28708	3.67	8.4E-02	W69330.1	EST_HUMAN	z444a11.1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:343532 5'
5400	18382	31222	1.1	8.4E-02	AB042555.1	NT	Homo sapiens mRNA, similar to rat myomegalin, complete cds
5495	18574	31420	9.5	8.4E-02	BE267153.1	EST_HUMAN	601190436F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3534393 5'
6986	20013	33244	1.74	8.4E-02	AK024458.1	NT	Homo sapiens mRNA for FLJ00050 protein, partial cds
8607	21538	34880	5.84	8.4E-02	BE065074.1	EST_HUMAN	CM3-B70790-260400-182-d05 BT0790 Homo sapiens cDNA
9401	22329	35691	0.81	8.4E-02	AF218890.1	NT	Homo sapiens attractin precursor (ATRN) gene, exon 2
10848	23734	37157	1.86	8.4E-02	A1735184.1	EST_HUMAN	as88g10.x1 Barestead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335842 3' similar to TR:O88312
3653	16689	29584	8.44	8.3E-02	P75334	SWISSPROT	O88312 GOB-4 ;
3685	16718	29609	0.82	8.3E-02	A1436797.1	EST_HUMAN	HYPOTHETICAL LIPOPROTEIN MG309 HOMOLOG PRECURSOR
3686	16718	29610	0.82	8.3E-02	A1436797.1	EST_HUMAN	th82g06.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
4404	17416		0.67	8.3E-02	M54984.1	NT	th82g06.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
6510	19564	32734	0.87	8.3E-02	A1942338.1	EST_HUMAN	C.hummi A2b region open reading frame, complete cds
6626	19666	32851	3.45	8.3E-02	AF052883.1	NT	w078f11.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2461581 3'
8580	21491	34832	3.01	8.3E-02	AF195787.1	NT	Homo sapiens protocadherin 43 gene, exon 1
8591	21522		1.29	8.3E-02	AA865285.1	EST_HUMAN	Rattus norvegicus dystrophin-related protein 2 A-form splice variant (Dip2) mRNA, complete cds
8874	21804		1.57	8.3E-02	AA987873.1	EST_HUMAN	0988g08.s1 NCL CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1455422 3' similar to contains L1.11 L1 L1
10067	22983	36374	1.33	8.3E-02	AW593503.1	EST_HUMAN	0981f10.s1 NCL CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1692779 3'
10080	22873		1.54	8.3E-02	AL161595.2	NT	Subunit of SODIUM POTASSIUM ATPASE LIKE ;
10829	23715		1.16	8.3E-02	AF020409.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
1406	14437		7.8	8.2E-02	Y08170.2	NT	Dicotyledon discoidium Doca (doca) mRNA, complete cds
1514	14545	27507	1.48	8.2E-02	AF167077.2	NT	Gallus gallus mRNA for for OBCAM protein gamma isoform
3122	16173		2.45	8.2E-02	AL163206.2	NT	Cantis familiaris glutamate transporter (EAT4) mRNA, complete cds
3868	16898		2.09	8.2E-02	AL161498.2	NT	Homo sapiens chromosome 21 segment HS21C006
4382	17396	30261	7.87	8.2E-02	P49960	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4382	17396	30262	7.87	8.2E-02	P49960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
5202	18193	31035	0.65	8.2E-02	AF240776.1	NT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
5216	18206	31051	3.24	8.2E-02	U76009.1	NT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
5518	18597	31446	1.73	8.2E-02	BE897030.1	EST_HUMAN	Mus musculus pepsinogen F (Pepf) mRNA, complete cds
						NT	Mus musculus zinc transporter (ZnT-3) gene, complete cds
						EST_HUMAN	601439576F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924523 5'



Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7370	20364	33633	2.85	8.2E-02	AF309555.1	NT	Bos taurus connective tissue growth factor precursor (CTGF) gene, complete cds
8196	21103		0.62	8.2E-02	AV743341.1	EST_HUMAN	AV743341 CB Homo sapiens cDNA clone CBLANF07 5'
9266	22194		0.55	8.2E-02	U29397.1	NT	Rattus norvegicus plasma membrane Ca2+ ATPase isoform 3 (PMCA3) gene, 5' flanking region
9331	22259	35923	3.87	8.2E-02	AW875126.1	EST_HUMAN	RC2-PT0004-031299-011-d05 P T0004 Homo sapiens cDNA
10128	23017	36412	6.21	8.2E-02	X04197.1	NT	Beet necrotic yellow vein virus RNA-2
10283	23173	36585	2.27	8.2E-02	BE254318.1	EST_HUMAN	601115055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355596 5'
11648	24554	38024	1.63	8.2E-02	9509428	NT	Rattus norvegicus B-cell translocation gene 3 (Big3), mRNA
12507	25241	31865	4.43	8.2E-02	AE002246.2	NT	Chlamydomonas reinhardtii AR39, section 73 of 94 of the complete genome
12711	25363	31799	1.46	8.2E-02	AW862195.1	EST_HUMAN	QV4-C10361-021299-049-b01 C10361 Homo sapiens cDNA
12882	25703		3.61	8.2E-02	AF276366.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
1513	14544	27506	1.22	8.1E-02	AB017138.1	NT	Pseudomonas putida malonate decarboxylase gene cluster (mdcA, mdcB, mdcC, mdcD, mdcE, mdcG, mdcH, mdcI, and mdcM genes), complete cds
5961	19028	32149	1.02	8.1E-02	AE004008.1	NT	Xylella fastidiosa, section 152 of 229 of the complete genome
6640	19679	32869	0.87	8.1E-02	T11532.1	EST_HUMAN	A1484F Heart Homo sapiens cDNA clone A1484
7561	20498		0.8	8.1E-02	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
8016	20834		1.45	8.1E-02	AI692681.1	EST_HUMAN	wd86108.x1 NCJ_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338503 3'
8914	21844	35197	0.69	8.1E-02	11426974	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
8914	21844	35198	0.69	8.1E-02	11426974	NT	Homo sapiens extracellular glycoprotein lacritin precursor, gene, complete cds
10423	23312		1.79	8.1E-02	AY005150.1	NT	Homo sapiens chromosome 21 segment HS21C002
11929	24774	38272	1.67	8.1E-02	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
6	15864	26009	4.67	8.0E-02	AW954653.1	EST_HUMAN	EST366723 MAGE resequences, MAGEC Homo sapiens cDNA
963	14013	26955	1.84	8.0E-02	U60315.1	NT	Mollusca contigiosum virus subtype 1, complete genome
1726	15908	27721	10.85	8.0E-02	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1726	15908	27722	10.85	8.0E-02	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1921	14942	27919	2.65	8.0E-02	BE067219.1	EST_HUMAN	PM3-BT0347-170200-001-b08 BT0347 Homo sapiens cDNA
2493	15495		3.37	8.0E-02	BF246744.1	EST_HUMAN	601855548F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075619 5'
2868	14160	27098	2.15	8.0E-02	M23449.1	NT	Dicyosellum discoidum cyclic nucleotide phosphodiesterase gene, complete cds
2944	15996	28897	0.79	8.0E-02	AL445067.1	NT	Thermoplasma acidophilum complete genome; segment 5/5
3887	10910	29794	0.65	8.0E-02	AW900118.1	EST_HUMAN	EST376191 MAGE resequences, MAGO Homo sapiens cDNA
4159	17180		0.69	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
4928	17927		7.91	8.0E-02	X72794.1	NT	M. musculus gene for gelatinase B
5404	14013	26955	0.94	8.0E-02	U60315.1	NT	Mollusca contigiosum virus subtype 1, complete genome
6946	19012	32131	0.49	8.0E-02	AW951139.1	EST_HUMAN	EST363209 MAGE resequences, MAGEC Homo sapiens cDNA

Page 132 of 545  
Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6108	19168	32300	3.19	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
7544	19168	32300	1.49	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
8704	21035	34981	2.53	8.0E-02	AL114993.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9926	22831	36217	0.9	8.0E-02	X74208.1	NT	H. sapiens AGT gene, intron 4
9926	22831	36218	0.9	8.0E-02	X74208.1	NT	H. sapiens AGT gene, intron 4
10654	23540		0.51	8.0E-02	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
11232	24158	37607	2.52	8.0E-02	AF217786.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M58, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
12638	25260	31835	4.67	8.0E-02	AJ005375.1	NT	Drosophila arena hunchback region
13056	17180		1.9	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
2187	15198	28203	3.62	7.9E-02	BE250008.1	EST_HUMAN	60C943191F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959510 5'
3020	16072	28974	15.46	7.9E-02	AI692029.1	EST_HUMAN	ar98c08.x1 Barstead colon HPLR87 Homo sapiens cDNA clone IMAGE:2173646 3' similar to gb:Z26876
3917	16945	29824	3.25	7.9E-02	6681044	NT	60S RIBOSOMAL PROTEIN L38 (HUMAN);
3917	16945	29825	3.25	7.9E-02	6681044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
4926	17925		1.21	7.9E-02	AB008019.1	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
5024	18021		0.99	7.9E-02	AW081738.1	EST_HUMAN	Arabidopsis thaliana RXW24L mRNA, partial cds
6994	20021		1.11	7.9E-02	BF368016.1	EST_HUMAN	xb70a10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2581626 3'
8610	21541	34883	3.74	7.9E-02	U27832.1	NT	RC3-GN0042-310800-024-d11 GN0042 Homo sapiens cDNA
10531	23417	36831	6.09	7.9E-02	AI081644.1	EST_HUMAN	Saccharomyces cerevisiae suppressor of MIF2 Smt4p (SMT4) gene, complete cds
10531	23417	36832	6.09	7.9E-02	AI081644.1	EST_HUMAN	au63b05.s1 NCL_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2
12967	25532		1.54	7.9E-02	AI761639.1	EST_HUMAN	CE088111
1238	14274	27216	1.32	7.8E-02	AI793275.1	EST_HUMAN	ou63b05.s1 NCL_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2
1238	14274	27217	1.32	7.8E-02	AI793275.1	EST_HUMAN	CE088111
3812	16942		1	7.8E-02	BE250048.1	EST_HUMAN	wg66h01.x1 Soares_NSF_FB_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370097 3'
4910	17909	30779	0.71	7.8E-02	BE836331.1	EST_HUMAN	oo59c02.y5 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1
5221	16842		3.56	7.8E-02	BE250048.1	EST_HUMAN	oo59c02.y5 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1
7431	20129	33370	1.19	7.9E-02	U82695.2	NT	repetitive element; repetitive element; repetitive element; 60C943055F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959693 5' PM3-FN0058-140700-005-f09 FN0058 Homo sapiens cDNA 60C943055F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959693 5'

Page 133 of 545  
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7431	20129	33371	1.19	7.8E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
9437	22365	35725	0.87	7.8E-02	X78344.1	NT	S.cerevisiae CAT8 gene
9605	22531	35898	0.84	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
9605	22531	35899	0.84	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
9899	22887	36271	1.13	7.8E-02	AA469354.1	EST_HUMAN	nc68b06.r1 NCI_CGAP_Prl Homo sapiens cDNA clone IMAGE:771731
10318	23207	36618	0.51	7.8E-02	Z99124.1	NT	Bacillus subtilis complete genome (section 21 of 21); from 3899281 to 4214814
11108	24039	37483	1.92	7.8E-02	U32323.1	NT	Human interleukin-11 receptor alpha chain gene, complete cds
12883	25479	31764	1.95	7.8E-02	U72847.1	NT	Homo sapiens enoplaikin (EVPL) gene, exons 15 through 18
3648	16684		2.13	7.7E-02	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
6734	18807	31901	0.43	7.7E-02	AF062636.1	NT	Gallus gallus collagen type XI alpha-1 (COL12A1) gene, promoter region and partial cds
8413	21315	34647	0.61	7.7E-02	BE674473.1	EST_HUMAN	7e04f03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3281501 3' similar to TR:O95415 O95415 I3 PROTEIN.;
8488	21419	34756	4.99	7.7E-02	AA402949.1	EST_HUMAN	zu53d11.1 Scores ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:741717 5' similar to TR:G1173905 G1173905 SPLICEOSOME ASSOCIATED PROTEIN.;
10350	23239	36658	5.01	7.7E-02	P38080	SWISSPROT	PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR059C
10630	23516	36949	1.09	7.7E-02	AJ318682.1	EST_HUMAN	ta80x08.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2060359 3' similar to gb:Z26876 50S RIBOSOMAL PROTEIN L38 (HUMAN);
10630	23516	36950	1.09	7.7E-02	AJ318682.1	EST_HUMAN	ta80x08.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2060359 3' similar to gb:Z26876 50S RIBOSOMAL PROTEIN L38 (HUMAN);
11449	24366	37814	5.97	7.7E-02	11422757	NT	Homo sapiens KIAA0628 gene product (KIAA0628), mRNA
12724	25780	29394	1.61	7.7E-02	11438553	NT	Homo sapiens interferon regulatory factor 7 (IRF7), mRNA
3446	16487	29394	3.15	7.6E-02	BE514432.1	EST_HUMAN	601316426F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634903 5'
3468	16506	29409	1.18	7.6E-02	AA286447.1	EST_HUMAN	EST112214 Cerebellum II Homo sapiens cDNA 5' end similar to protocadherin 43
6334	19384	32552	0.7	7.6E-02	AJ061275.1	EST_HUMAN	an25a02.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1699730 3'
5614	19655	32839	0.86	7.6E-02	BE379328.1	EST_HUMAN	601236402F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608401 5'
9908	22897	36284	1.49	7.6E-02	AJ131016.1	NT	Homo sapiens SCL gene locus
10409	23298		1.74	7.6E-02	AL19078.2	NT	Campylobacter jejuni NCTC11168 complete genome, segment 5/6
10715	23601	37028	0.58	7.6E-02	BE709002.1	EST_HUMAN	RC1-HT0545-020800-017-d08 HT0545 Homo sapiens cDNA
10836	23722		0.6	7.6E-02	BE959638.2	EST_HUMAN	601654915R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839810 3'
11060	23944	37350	0.98	7.6E-02	X92656.1	NT	L.esculentum mRNA for triose phosphate translocator

### Table 4 Fluorescent Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (BLAST E Value)	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11060	23942	37381	0.98	7.6E-02	X92656.1	NT	L.esculentum mRNA for thio phosphate translocator
12102	24943	38446	2.23	7.6E-02	AW996645.1	EST_HUMAN	QV3-BN0046:150400-151-e04 BN0046 Homo sapiens cDNA
811	13667	26802	1.05	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
811	13667	26803	1.05	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
4630	17636	30500	0.84	7.5E-02	AB015981.1	NT	Homo sapiens IL-18 gene for interleukin-18, intron 1 and exon 2
6066	19127	32258	1.45	7.5E-02	AB48714.1	EST_HUMAN	wq24H09.x1 NCL_CGAP_K1411 Homo sapiens cDNA clone IMAGE:2472267 3'
							w152b02.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2428491 3' similar to gb:M14328 ALPHA
							ENOLASE (HUMAN);
8913	21843	35196	1.49	7.5E-02	AB64367.1	EST_HUMAN	AU116913 HEMBA1 Homo sapiens cDNA clone HEMBA1000294 5'
9074	22003	35357	1.4	7.5E-02	AU116913.1	EST_HUMAN	AU116913 HEMBA1 Homo sapiens cDNA clone IMAGE:3578504 3' similar to contains element
							7661c05.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:3578504 3' similar to contains element
							MER27 repetitive element;
10595	23421		0.59	7.5E-02	BF221730.1	EST_HUMAN	601670205F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100449 6'
10971	23855	37282	0.87	7.5E-02	BF206809.1	EST_HUMAN	G.fiml DSM 20113 16S rDNA
11061	23945	37382	0.93	7.5E-02	X79460.1	NT	RC5-LT0054+260100-011-H09 LT0054 Homo sapiens cDNA
500	13570	26498	1.17	7.4E-02	AW838547.1	EST_HUMAN	Mus musculus paired-like homeodomain transcription factor 1 (Pitx1), mRNA
2618	13616		0.98	7.4E-02	6755069	NT	wf43h01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358385 3'
3655	16691	29587	0.81	7.4E-02	AB07895.1	EST_HUMAN	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4917	17818	30688	1.15	7.4E-02	L78810.1	NT	Rattus norvegicus Acylin receptor like kinase 1 (Acylt1), mRNA
4909	17908	30778	3.04	7.4E-02	6978442	NT	Mus musculus ADP/ATP carrier protein (ANT-2) gene, complete cds
5054	18051	30904	1.65	7.4E-02	AJ012169.1	NT	Rattus norvegicus Acylin receptor like kinase 1 (Acylt1), mRNA
5366	18348	31191	1.05	7.4E-02	AJ012169.1	EST_HUMAN	Mus musculus ubiquitin C-terminal hydrolase related polypeptide (Uchpr), mRNA
6771	19805		1.56	7.4E-02	AF30422.1	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial
6869	19901	33116	0.41	7.4E-02	AF30422.1	EST_HUMAN	Yg14g06.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:32359 5'
7885	20811	34117	0.65	7.4E-02	AA605132.1	EST_HUMAN	Electrophorus electricus acetylcholinesterase catalytic subunit precursor gene, complete cds
8481	21412	34749	1.33	7.4E-02	BE880112.1	EST_HUMAN	601493366F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:1112269 3'
9068	21997	35351	0.93	7.4E-02	U56089.1	NT	no71d02.x1 NCL_CGAP_AA1 Homo sapiens cDNA clone IMAGE:3895264 5'
							Human periodic tyrosinase protein 2 (PWP2) gene, exons 15 to 21, and complete cds
							601493366F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:2967861 5' similar to SW:SCA2_HUMAN
							hh67d11.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2967861 5' similar to SW:SCA2_HUMAN
							O1527 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2.;
9709	22634	36014	1.1	7.4E-02	AW629605.1	EST_HUMAN	hh67d11.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2967861 5' similar to SW:SCA2_HUMAN
9709	22634	36015	1.1	7.4E-02	AW629605.1	EST_HUMAN	O1527 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2.;
10330	23219	36633	1.02	7.4E-02	U62293.1	NT	Human LIM-kinase1 and alternatively spliced LIM-kinase1 (LIMK1) gene, complete cds
12179	25015		1.49	7.4E-02	U89282.1	NT	Rattus norvegicus telomerase protein component 1 (TLP1) mRNA, complete cds
12717	25884		3.75	7.4E-02	AW379431.1	EST_HUMAN	GM4-HT0243-081199-037-d11 HT0243 Homo sapiens cDNA

Page 135 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12854	25484	31781	2.43	7.4E-02	BF035099.1	EST_HUMAN	601453813F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3857738 5'
461	13562	26478	1.08	7.3E-02	BE964961.2	EST_HUMAN	601668738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
491	13562	26479	1.08	7.3E-02	BE964961.2	EST_HUMAN	601668738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
708	13767	26683	2.8	7.3E-02	AE001789.1	NT	Thermococcus maritima section 101 of 136 of the complete genome
1499	15902	27495	2.95	7.3E-02	AW900281.1	EST_HUMAN	CMD-NN1004-130300-284-q08 NN1004 Homo sapiens cDNA
1870	15912		16.74	7.3E-02	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
4180	17200	30070	1.02	7.3E-02	AJ245944.1	NT	Homo sapiens NGB gene for neuroglobin, exons 1-4
5118	18115		1.64	7.3E-02	U12283.1	NT	Mus musculus transcription factor USE2 (USF2) gene, exons 8-10 and complete cds
6723	19759	32968	2.08	7.3E-02	AA778977.1	EST_HUMAN	z124a02.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:461178 3' similar to
7882	20808	34113	3.2	7.3E-02	P05143	SWISSPROT	gb:L02426 26S PROTEASE SUBUNIT 4 (HUMAN);
7882	20808	34114	3.2	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8293	21197		0.45	7.3E-02	BF316067.1	EST_HUMAN	PROLINE-RICH PROTEIN MP-3
8746	21676		1.48	7.3E-02	7662107	NT	601866047F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126615 5'
8972	21902	35257	0.55	7.3E-02	Y10887.2	NT	Homo sapiens KIAA0424 protein (KIAA0424), mRNA
9761	22675		1.34	7.3E-02	AB011090.1	NT	Mus musculus cdk5 gene, exon 1, partial
11686	19759	32966	2.1	7.3E-02	AA778977.1	EST_HUMAN	Homo sapiens mRNA for KIAA0518 protein, partial cds
124	13230	26145	2.42	7.2E-02	AE000882.1	NT	z124a02.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:461178 3' similar to
124	13230	26146	2.42	7.2E-02	AE000882.1	NT	gb:L02426 26S PROTEASE SUBUNIT 4 (HUMAN);
1494	14525	27486	2.25	7.2E-02	AL163301.2	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
1494	14525	27487	2.25	7.2E-02	AL163301.2	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
2581	15580		3.58	7.2E-02	U14794.1	NT	Human immunodeficiency virus type 1 isolate 2B reverse transcriptase (pol) gene, internal fragment, partial cds
3954	16992	29866	0.72	7.2E-02	AW298322.1	EST_HUMAN	UT-H-BWO-ajl-a-05-0-U1.s1 NCL CGAP_Sub66 Homo sapiens cDNA clone IMAGE:2732049 3'
4455	17465	30322	3.42	7.2E-02	BF572307.1	EST_HUMAN	602077757F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4251950 5'
4806	17807	30673	0.71	7.2E-02	11468563	NT	Rhodomonas salina mitochondrion, complete genome
5470	18551	31393	2.77	7.2E-02	U67531.1	NT	Methanococcus jannaschii section 73 of 160 of the complete genome
5471	18552	31394	8.49	7.2E-02	P11120	SWISSPROT	CALMODULIN
6366	19405		0.55	7.2E-02	BF217598.1	EST_HUMAN	601863905F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096224 5'
7531	20470	33759	1.26	7.2E-02	BF216086.1	EST_HUMAN	601863558F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095710 5'

Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7549	20487	33776	0.63	7.2E-02	AF221126.1	NT	Streptococcus pneumoniae putative response regulator (zmpR), putative histidine kinase (zmpS), and putative zinc metalloprotease (zmpB) genes, complete cds
7576	20512		1.44	7.2E-02	5834897	NT	Strongylocentrotus purpuratus mitochondrion, complete genome
8766	21696	35039	0.69	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8766	21699	35040	0.69	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
9616	22542		0.63	7.2E-02	Y17217.1	NT	Lactococcus lactis cspE gene
10104	22996		0.67	7.2E-02	X16349.1	NT	Human gene for sex hormone-binding globulin (SHBG)
10138	23029	36426	2.37	7.2E-02	AV712452.1	EST_HUMAN	AV712452 DCA Homo sapiens cDNA clone DCAAU301 5'
10279	23169	36582	4.17	7.2E-02	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
10425	23314	36731	1.25	7.2E-02	BF125399.1	EST_HUMAN	601763523F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4028438 5'
10508	23395	36807	2.45	7.2E-02	AW873187.1	EST_HUMAN	hq24f1.x1 NCI_CGAP_Adr1 Homo sapiens cDNA clone IMAGE:3120333 3' similar to TR:Q9Z340 Q9Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN ;
10689	23575	37005	0.82	7.2E-02	AA768204.1	EST_HUMAN	ca62c07.s1 NCI_CGAP_G081 Homo sapiens cDNA clone IMAGE:1316844 3'
10839	23725	37148	2.26	7.2E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
10953	23837	37264	4.92	7.2E-02	BE595003.1	EST_HUMAN	601343928F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685951 5'
10976	23860		3.94	7.2E-02	BE59214.1	EST_HUMAN	601065194F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451559 5'
11351	24269	37711	3.94	7.2E-02	AF049874.1	NT	Rafus norvegicus bHLH transcription factor Mist1 (Mist1) gene, complete cds
12387	25165	31672	1.82	7.2E-02	AA773696.1	EST_HUMAN	af81a04.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1048398 5'
12471	25217		1.81	7.2E-02	AA594465.1	EST_HUMAN	nc05h08.s1 NCI_CGAP_Phet1 Homo sapiens cDNA clone IMAGE:1098639 3'
12526	25250		4.57	7.2E-02	U82628.1	NT	Homo sapiens axidia telangiectasia (ATM) gene, complete cds
12540	25752		5.89	7.2E-02	AW500962.1	EST_HUMAN	CM4-NIN1006-200300-116-c11 NN1009 Homo sapiens cDNA
1922	14943	27920	2.31	7.1E-02	L02290.1	NT	Human Immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds
2311	15319	28320	4.11	7.1E-02	BF208802.1	EST_HUMAN	601872281F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4092981 5'
8486	21417	34753	1.08	7.1E-02	AI123264.1	EST_HUMAN	q492a10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736922 3'
12280	25094		4.11	7.1E-02	BE304764.1	EST_HUMAN	601143974F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051234 5'
551	13620	26528	1.22	7.0E-02	Q07092	SWISSPROT	COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR
1617	14648		1.24	7.0E-02	X96677.1	NT	Martellia Micut-1 gene
1766	14812	27761	1.18	7.0E-02	AA055343.1	EST_HUMAN	z166f04.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:509599 3'
3076	16128	29025	2.02	7.0E-02	AW138152.1	EST_HUMAN	UI-H-B11-acyc-07-o-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716020 3'

Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3867	16995	29879	1.54	7.0E-02	AA815438.1	EST_HUMAN	al85a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375678 3' similar to gb:K03002 60S
4128	17161	30026	1.29	7.0E-02	BE070264.1	EST_HUMAN	RIBOSOMAL PROTEIN L32 (HUMAN);
4237	17253		1.13	7.0E-02	AW792962.1	EST_HUMAN	QV4-BT0407-280100-090-910 BT0407 Homo sapiens cDNA
4310	17324	30191	1.21	7.0E-02	AF077621.1	NT	CMO-UM0001-060300-270-912 UM0001 Homo sapiens cDNA
5041	18038	30894	9.37	7.0E-02	BF381987.1	EST_HUMAN	Canis familiaris inducible nitric oxide synthase mRNA, complete cds
5592	18640		0.82	7.0E-02	Y03143.2	NT	601816291F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050071 5'
7799	20728	34030	0.88	7.0E-02	AV689285.1	EST_HUMAN	Lumbricus rubellus mRNA for cyclophilin B
8050	20963	34279	0.74	7.0E-02	Y19187.1	NT	AY689285 GKG Homo sapiens cDNA clone GKCCAE06 5'
9643	22569	35940	1.23	7.0E-02	9928113	NT	Gallus gallus mRNA for partial ezrin, XL spliced variant (ecz gene)
10124	23015	36411	1.57	7.0E-02	K02901.1	NT	African swine fever virus, complete genome
10459	23347	36764	0.89	7.0E-02	U27266.1	NT	Rat Ig germline epsilon H-chain gene C-region, 3' end
11811	24732	38223	3.23	7.0E-02	AA724295.1	EST_HUMAN	Human myosin binding protein H (MyBP-H) gene, complete cds
12980	25540	31750	1.88	7.0E-02	11421638	NT	ah9a05.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1327184 3' similar to gb:1.14837
537	13606	26514	9.27	6.9E-02	AL163210.2	NT	TIGHT JUNCTION PROTEIN ZO-1 (HUMAN);
537	13606	26515	9.27	6.9E-02	AL163210.2	NT	Homo sapiens hypothetical protein FLJ20116 (FLJ20116), mRNA
1361	14392		1.08	6.9E-02	4507968	NT	Homo sapiens chromosome 21 segment HS21C010
3857	16886	29770	1.36	6.9E-02	Q06364	SWISSPROT	Homo sapiens chromosome 21 segment HS21C010
3857	16886	29771	1.36	6.9E-02	Q06364	SWISSPROT	Homo sapiens regulator of Gz-selective protein signaling (ZGAP1) mRNA, and translated products
5253	18239	31090	0.93	6.9E-02	AA670299.1	EST_HUMAN	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
6141	19200		0.46	6.9E-02	AF161364.1	NT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
8082	20975		0.56	6.9E-02	AF161997.1	NT	at25608.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032710 3'
8630	21561		0.98	6.9E-02	U12022.1	NT	Homo sapiens HSPC101 mRNA, partial cds
9116	22044	35400	0.96	6.9E-02	BE567435.1	EST_HUMAN	Cahine distemper virus strain A7517, complete genome
9116	22044	35401	0.96	6.9E-02	BE567435.1	EST_HUMAN	Human calmodulin (CALM1) gene, exons 2,3,4,5 and 6, and complete cds
9664	22580	35963	0.7	6.9E-02	U22997.1	NT	601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
12415	25184		5.82	6.9E-02	X74315.1	NT	601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
12571	25276		1.53	6.9E-02	P44621	SWISSPROT	Barbante duck parvovirus REP protein (rep) and three capsid protein VP (vp) genes, complete cds
12780	25409		5.15	6.9E-02	AF159553.1	NT	X laevis XFD2 mRNA for fork head protein
1924	14945	27921	4.83	6.8E-02	AF159673.1	NT	PROTEIN TRANSPORT PROTEIN HOF6 HOMOLOG
1998	15014	28004	0.94	6.8E-02	BE263781.1	EST_HUMAN	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
4247	17263	30129	0.87	6.8E-02	6679250	NT	Homo sapiens putative hepatic transcription factor (WBSOR14) gene, complete cds
							601194141F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537706 5'
							Mus musculus phosphodiesterase 9A (Pde9a), mRNA

Page 138 of 545  
Table 4  
Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4668	17673		0.76	6.8E-02	BE141076.1	EST_HUMAN	MRO-HT0089-071099-001-c05 HT0089 Homo sapiens cDNA
6911	19941		0.66	6.8E-02	P20792	SWISSPROT	CELL SURFACE RECEPTOR DAF-1 PRECURSOR
7228	20137		1.21	6.8E-02	BE061800.1	EST_HUMAN	RC1-B10254-090300-017-409 BT0254 Homo sapiens cDNA
7659	20593	33691	8.39	6.8E-02	AL163269.2	NT	Homo sapiens chromosome 21 segment HS21C068
8137	21049	34376	0.74	6.8E-02	U18859.1	NT	Dicystellum discoidium myosin heavy chain kinase A (MHCK A) mRNA, complete cds
8865	21795	35147	5.72	6.8E-02	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
8865	21795	35148	5.72	6.8E-02	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 6/6
12234	25925		1.63	6.8E-02	T03214.1	EST_HUMAN	FB4A8 Fetal brain, Stralagene Homo sapiens cDNA clone FB4A8 3' end similar to LINE-1
12354	25144		1.7	6.8E-02	AA758014.1	EST_HUMAN	af6705.s1 Soares, testis, NHT Homo sapiens cDNA clone 1320705 3'
12938	25504		2.09	6.8E-02	9910586	NT	Mus musculus latent TGF beta binding protein (Tgfb), mRNA
1551	14582		2.8	6.7E-02	AF115536.1	NT	Oncorhynchus mykiss TAP1 protein (OnmyTAP1) mRNA, OnmyTAP1*01 allele, complete cds
1911	14932	27909	1.47	6.7E-02	AF1220285.1	EST_HUMAN	q97980.x1 Soares, NFL_T_GBC, ST Homo sapiens cDNA clone IMAGE:1841406 3'
3781	16812	29698	5.04	6.7E-02	P17278	SWISSPROT	HOMEBOX PROTEIN HOX-D7 (HOX-A)
4037	17064	29953	0.8	6.7E-02	U53783.1	NT	Cyprinus carpio Rap1b mRNA, complete cds
4037	17064	29954	0.8	6.7E-02	U53783.1	NT	Cyprinus carpio Rap1b mRNA, complete cds
8433	21365	34704	0.82	6.7E-02	X62695.1	NT	H. sapiens DNA for cGMP phosphodiesterase (exons 4-22)
8433	21365	34705	0.82	6.7E-02	X62695.1	NT	H. sapiens DNA for cGMP phosphodiesterase (exons 4-22)
10127	23018	36413	0.64	6.7E-02	AW137359.1	EST_HUMAN	UI-H-B11-acr-g-01-0-UI.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
10127	23018	36414	0.64	6.7E-02	AW137359.1	EST_HUMAN	UI-H-B11-acr-g-01-0-UI.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
1377	14409	27363	0.91	6.9E-02	A1735509.1	EST_HUMAN	at12e09.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2354920 3' similar to SW:LN1_NYCCO P08548 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG. ;
1386	14427	27381	0.96	6.9E-02	AF245116.1	NT	Drosophila melanogaster cactin mRNA, complete cds
2195	15206	28210	2.21	6.9E-02	AJ289241.1	NT	Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcripts
3525	16563	29467	10.68	6.9E-02	R64306.1	EST_HUMAN	yf18b10.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:139579 3'
3537	16575	29479	3.59	6.9E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
3537	16575	29480	3.59	6.9E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
4167	17188	30061	1.93	6.9E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
5100	18097	30943	12.83	6.9E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
5100	18097	30944	12.83	6.9E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
6866	18998	33114	3.37	6.9E-02	X09411.1	NT	P. vulgaris mRNA for chalcone synthase
6901	19931	33148	0.53	6.9E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFEN
6901	19931	33149	0.53	6.9E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFEN
7108	19931	33148	0.65	6.9E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFEN
7108	19931	33149	0.65	6.9E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFEN



Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7437	20134	33374	0.42	6.6E-02	AI243328.1	EST_HUMAN	qh41d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1847233 3'
8390	21294		0.48	6.6E-02	D14567.1	NT	Penicillium urticae mitochondrial rRNA (large rRNA) gene and its flanking region
8526	21467	34800	2.09	6.6E-02	AF052672.1	NT	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds
9043	21972	35331	0.99	6.6E-02	AF006055.1	NT	Dictyostelium discoideum derlin (derA) gene, complete cds
9477	22405	35764	1.14	6.6E-02	9629198	NT	Human respiratory syncytial virus, complete genome
9477	22405	35765	1.14	6.6E-02	9629198	NT	Human respiratory syncytial virus, complete genome
10458	23346	36763	0.54	6.6E-02	AI459752.1	EST_HUMAN	ij97g06.x1 NCJ_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2149498 3'
10589	23475	36902	1.44	6.6E-02	Y07848.1	NT	Homo sapiens EWS, gar22, trp22 and bam22 genes
10622	23508		0.81	6.6E-02	11430559	NT	Homo sapiens vinculin (VCL), mRNA
11400	24316	37763	6.43	6.6E-02	BF374248.1	EST_HUMAN	MR1-SN0064-010600-006-a12 SN0064 Homo sapiens cDNA
12773	25402		2.22	6.6E-02	9937891	NT	Mus musculus DIPB gene (Dipb), mRNA
603	13659	26572	1.49	6.5E-02	BF027639.1	EST_HUMAN	601671045F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954178 5'
1014	14064	27008	1.43	6.5E-02	7706068	NT	Homo sapiens E2F-like protein (LOC51270), mRNA
1418	14449	27403	3.55	6.5E-02	U47824.1	NT	Xenopus laevis alpha(E)-catenin mRNA, complete cds
1764	14790	27780	2.01	6.5E-02	AE000764.1	NT	Aquifex aeolicus section 96 of 109 of the complete genome
5750	18823	31920	1.77	6.5E-02	AA443991.1	EST_HUMAN	zy46h12.61 Soares ovary tumor NIH-HOT Homo sapiens cDNA clone IMAGE:786743 3' similar to gb.M26038
6822	18855	33067	0.89	6.5E-02	BF665340.1	EST_HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-5 BETA CHAIN (HUMAN);
7312	18480	31303	0.9	6.5E-02	U22661.1	NT	602118687F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4276029 5'
10451	23340	36756	0.66	6.5E-02	BE963200.2	EST_HUMAN	Azobacter vinelandii ATCC 9046 negative regulator MucB (mucB) gene, partial cds
10451	23340	36757	0.66	6.5E-02	BE963200.2	EST_HUMAN	601666817R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3865637 3'
10944	23829	37255	0.61	6.5E-02	BF106300.1	EST_HUMAN	601656817R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3865637 3'
11084	24016	37457	6.78	6.5E-02	AA195848.1	EST_HUMAN	601823511F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4043138 5'
12252	25073		4.17	6.5E-02	M21498.1	NT	z32g05.e1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:665144 3'
12578	25280		2.45	6.5E-02	AF102993.1	NT	Rabbit microsomal epoxide hydrolase
597	13664	26566	2.04	6.4E-02	X94549.1	NT	Nectria haematococca kinesis related protein 2 (KRP2) gene, complete cds
3059	16111	29016	0.97	6.4E-02	6965923	NT	A. carterae precursor of peridinin-chlorophyll-a-protein (PCP) gene
5005	16111	29016	1.01	6.4E-02	6965923	NT	Mus musculus histone deacetylase 5 (Hdac5), mRNA
5237	18224	31073	1.56	6.4E-02	AL163247.2	NT	Mus musculus histone deacetylase 5 (Hdac5), mRNA
5635	18711	31611	1.05	6.4E-02	AI191956.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
6097	19158	32291	0.47	6.4E-02	7305186	NT	qe07b01.x1 Soares_testis_NIT Homo sapiens cDNA clone IMAGE:1798249 3' similar to contains LTR8.b3 LTR8 repetitive element
6351	19400	32567	5.29	6.4E-02	AF052733.1	NT	Mus musculus IFN-response element binding factor 1 (IREBF-1), mRNA
6351	19400	32568	5.29	6.4E-02	AF052733.1	NT	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds

Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6687	19705	32800	0.78	6.4E-02	AI672896.1	EST_HUMAN	wer3g12.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2348790 3'
7129	20333	33597	4.59	6.4E-02	BE974448.1	EST_HUMAN	001680425R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950503 3'
7865	20792	34095	0.46	6.4E-02	AL162757.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 6/7
8911	21841		3.15	6.4E-02	6753323	NT	Mus musculus chaperonin subunit 6a (zeta) (Cof6a), mRNA
9223	22151	35503	4.56	6.4E-02	AA093305.1	EST_HUMAN	K1418.seq.F Human fetal heart Lambda ZAP Express Homo sapiens cDNA 5'
9672	22598	35971	0.75	6.4E-02	AF150195.1	EST_HUMAN	AF150195 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone CBDAIA10
10114	23005		0.61	6.4E-02	BE934083.1	EST_HUMAN	RC1-OT0083-150600-014-g08 OT0083 Homo sapiens cDNA
10298	23130	36533	1.86	6.4E-02	AB011128.1	NT	Homo sapiens mRNA for KIAA0354 protein, partial cds
10754	23640	37073	0.68	6.4E-02	AF087150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
10764	23840	37074	0.68	6.4E-02	AF087150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
12131	24972	38475	2.01	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
12131	24972	38476	2.01	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
12483	25844		4.18	6.4E-02	AF107890.1	NT	Homo sapiens mucin 5B (MUC5B) gene, partial cds
12531	25254	31830	2.41	6.4E-02	AJ277174.1	NT	Drosophila melanogaster mRNA for mod(mdg4)51.4 protein
1780	14806	27775	1.92	6.3E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hec701 gene, partial cds; smRNP, G7A, NG23, Muts homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
3666	16700		2.94	6.3E-02	P37092	SWISSPROT	HEAT SHOCK PROTEIN 70 HOMOLOG
5084	18081	30930	1.09	6.3E-02	AI963769.1	EST_HUMAN	wr66g10.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2492706 3'
5365	18347	31190	0.99	6.3E-02	D90912.1	NT	Synechocystis sp. PCC8803 complete genome, 14/27, 1719644-1848241
6376	19425	32591	1.14	6.3E-02	BF210738.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097489 5'
7612	20547		0.71	6.3E-02	X97869.1	NT	H. sapiens gene encoding Le autoantigen
9831	22737	36119	1.1	6.3E-02	AJ243916.1	NT	Drosophila melanogaster Dominica gene, exons 1-3
10517	23404	36816	3.78	6.3E-02	AB010162.1	NT	Hepatitis G virus RNA for polyprotein (NS5A region), partial cds, strain: CMR-152
10764	23650		1.14	6.3E-02	AV698070.1	EST_HUMAN	AV698070 GKO Homo sapiens cDNA clone GKCAHE01 5'
11168	19425	32591	3.33	6.3E-02	BF210736.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097489 5'
4349	17363	30227	2.04	6.2E-02	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
4447	17458		1.05	6.2E-02	AF271235.1	NT	Rattus norvegicus differentiation-associated Na-dependent inorganic phosphate cotransporter (DNPI) mRNA, complete cds
4448	18413		0.83	6.2E-02	U67584.1	NT	Methanococcus jannaschii section 126 of 150 of the complete genome

Page 141 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4696	17701		7.74	6.2E-02	Q82191	SWISSPROT	52 KD RO PROTEIN (SUGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52)
5416	18387		1.07	6.2E-02	AF126399.1	NT	Arabidopsis thaliana weworf (WER) gene, complete cds
7104	20310	33571	0.7	6.2E-02	D49530.1	NT	Spirulina platensis DNA for adenylylase, complete cds
8075	20988	34305	0.86	6.2E-02	U41453.1	NT	Rattus norvegicus PKC binding protein and substrate mRNA, complete cds
8395	21298		0.6	6.2E-02	AL161545.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
8502	25980		0.86	6.2E-02	M61101.1	NT	Porcine group C rotavirus (strain Cowden) outer membrane protein (VP7) mRNA, complete cds
9882	22797	36183	0.84	6.2E-02	AA778450.1	EST_HUMAN	af20a06.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032178 3'
10013	22913	36302	1.31	6.2E-02	6577888	NT	Mus musculus stromal cell derived factor receptor 2 (Sdfr2), mRNA
12342	25959		8.19	6.2E-02	AE000750.1	NT	Aquifex aeolicus section 82 of 109 of the complete genome
12728	25371	31802	3.62	6.2E-02	BF112039.1	EST_HUMAN	7137h08.x1 Soares_NSIF_F8_9w_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523815 3' similar to TR.Q9Y4S6 Q9Y4S6 HYPOTHETICAL 30.3 KD PROTEIN. [1];
276	13370	26285	6	6.1E-02	D16471.1	NT	Human mRNA, Xq terminal portion
2737	15730	28725	1.52	6.1E-02	AA159168.1	EST_HUMAN	z07705.s1 Stralagene pancreas (#637208) Homo sapiens cDNA clone IMAGE:592929 3'
4077	17103		3.55	6.1E-02	U73325.1	NT	Arabidopsis thaliana K+ inward rectifying channel protein (AKC1) gene, complete cds
4765	17770	30635	1.14	6.1E-02	AF119413.1	NT	Lupinus albus 1-aminocyclopropane-1-carboxylate synthase 3 (ACCS3) gene, complete cds
4765	17770	30636	1.14	6.1E-02	AF119413.1	NT	Lupinus albus 1-aminocyclopropane-1-carboxylate synthase 3 (ACCS3) gene, complete cds
6188	19216	32356	0.48	6.1E-02	7662463	NT	Homo sapiens KIAA1052 protein (KIAA1052), mRNA
6158	19216	32357	0.48	6.1E-02	7662463	NT	Homo sapiens KIAA1052 protein (KIAA1052), mRNA
6352	19401		1.67	6.1E-02	4507070	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
7510	20449	33733	0.45	6.1E-02	AJ001497.1	NT	Homo sapiens AFG3L1 gene, exon 2
8839	21769	35115	4.28	6.1E-02	X99268.1	NT	H. sapiens mRNA for B-HLH DNA binding protein
9219	22147	35499	0.78	6.1E-02	BE971853.1	EST_HUMAN	601651086R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934604 3'
9219	22147	35500	0.78	6.1E-02	BE971853.1	EST_HUMAN	601651086R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934604 3'
11171	24099	37545	4.83	6.1E-02	BE179543.1	EST_HUMAN	IL3-HT0618-110500-136-C06 HT0618 Homo sapiens cDNA
12302	25879		34.23	6.1E-02	X70689.1	NT	S. japonicum mRNA for serine-enzyme
12965	25516		6.39	6.1E-02	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
1289	14322	27268	1.14	6.0E-02	AE001777.1	NT	Thermotoga maritima section 89 of 136 of the complete genome
2724	15717	28714	1.5	6.0E-02	AW96848.1	EST_HUMAN	EST380924 MAGE resequences, MAGJ Homo sapiens cDNA
2822	15811		1.63	6.0E-02	AB031289.1	NT	Mesocricetus cori mitochondriai DNA, NADH dehydrogenase subunit 4, tRNA-Gln, tRNA-Phe, tRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2
2979	13213	26125	1.11	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Stralagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
2979	13213	26126	1.11	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Stralagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
3276	16324	29229	1.13	6.0E-02	AA372376.1	EST_HUMAN	EST84268 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein

Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3276	16324	29230	1.13	6.0E-02	AA372376.1	EST_HUMAN	EST184266 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3702	16734		1.22	6.0E-02	BE664443.2	EST_HUMAN	601658150R1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3876060 3'
5089	18086	30637	2.43	6.0E-02	Z67739.2	NT	Streptococcus pneumoniae parC, parE and transposase genes and ORF DNA
5232	18220	31088	0.79	6.0E-02	AF146738.1	NT	Rattus norvegicus testis specific protein mRNA, complete cds
5333	18660		1.93	6.0E-02	AW370211.1	EST_HUMAN	RC3-BT0253-011199-013-504 BT0253 Homo sapiens cDNA
6480	19505	32680	1.03	6.0E-02	AI807537.1	EST_HUMAN	wf48h05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358873 3' similar to contains L1.1 L1 repetitive element;
7328	18498	31271	2.42	6.0E-02	5174698	NT	Homo sapiens stimulated trans-acting factor (60 kDa) (STAF50) mRNA
7328	18498	31272	2.42	6.0E-02	5174698	NT	Homo sapiens stimulated trans-acting factor (60 kDa) (STAF50) mRNA
7652	20489	33778	2.15	6.0E-02	BF382349.1	EST_HUMAN	601815274F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4049228 5'
7670	20604	33902	0.64	6.0E-02	BF210488.1	EST_HUMAN	601874710F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101074 5'
8133	21043	34373	1.78	6.0E-02	AI204275.1	EST_HUMAN	qf59b06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1784189 3'
9812	22718	36100	0.8	6.0E-02	AI623167.1	EST_HUMAN	ts78a06.x1 NCL_CGAP_GCB Homo sapiens cDNA clone IMAGE:2237362 3'
9812	22718	36101	0.8	6.0E-02	AI623167.1	EST_HUMAN	ts78a06.x1 NCL_CGAP_GCB Homo sapiens cDNA clone IMAGE:2237362 3'
9940	22845	36235	1.91	6.0E-02	AJ245365.1	NT	Acipenser baeri partial IGLV gene for immunoglobulin light chain variable region, exons 1-2
9940	22845	36236	1.91	6.0E-02	AJ245365.1	NT	Acipenser baeri partial IGLV gene for immunoglobulin light chain variable region, exons 1-2
10416	23305	36723	0.64	6.0E-02	AA309797.1	EST_HUMAN	EST180664 Jurkat T-cells V Homo sapiens cDNA 5' end similar to heat shock protein 1, 60 kDa-like
10416	23305	36724	0.64	6.0E-02	AA309797.1	EST_HUMAN	EST180664 Jurkat T-cells V Homo sapiens cDNA 5' end similar to heat shock protein 1, 60 kDa-like
11778	24677		1.76	6.0E-02	AA128386.1	EST_HUMAN	zn67c08.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565186 5' similar to gb:X69181.60S RIBOSOMAL PROTEIN L31 (HUMAN);
12893	25483		3.06	6.0E-02	AI809273.1	EST_HUMAN	wf69h03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360885 3' similar to TR:O60298
248	13346	26256	4.63	5.9E-02	AW934719.1	EST_HUMAN	O60298 KIAA0551 PROTEIN;
3025	16077	28980	2.7	5.9E-02	AF190269.1	NT	RC1-DT0001-280100-012-e10 DT0001 Homo sapiens cDNA
7220	25665	33467	0.6	5.9E-02	AF146680.1	NT	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced
9176	22104	35462	2.28	5.9E-02	9055249	NT	Drosophila melanogaster LD23107 sfing (sfing) mRNA, complete cds
9983	21341		0.95	5.9E-02	BF242748.1	EST_HUMAN	Mus musculus Iroquois related homeobox 5 (Drosophila) (Irx5), mRNA
11224	24160		3.86	5.9E-02	6679870	NT	Mus musculus folistatin-like (Fst), mRNA
11459	24374	37622	1.5	5.9E-02	11433356	NT	Homo sapiens ninin (LOC51199), mRNA
11974	24817		1.7	5.9E-02	BF572339.1	EST_HUMAN	602076548F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4243834 5'
11988	24831		1.68	5.9E-02	AJ240733.1	NT	Gallus gallus HKC9 telomere junction
961	14011		4.6	5.8E-02	D90110.1	NT	Thiobacillus ferrooxidans marC, marA genes and URF-1

Page 143 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1687	14717	27678	1.07	5.8E-02	Q61768	SWISSPROT	KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC)
3731	16783	28650	1.44	5.8E-02	AE001775.1	NT	Thermoboga maritima section 87 of 138 of the complete genome
4464	17475	30332	7.89	5.8E-02	AW051927.1	EST_HUMAN	wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4464	17475	30333	7.89	5.8E-02	AW051927.1	EST_HUMAN	wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4863	17693	30537	5.63	5.8E-02	A1247505.1	EST_HUMAN	qh56701.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:U13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4663	17693	30538	5.63	5.8E-02	A1247505.1	EST_HUMAN	qh56701.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:U13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4889	17694	31098	2.93	5.8E-02	AF098264.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
5262	18249	31098	1.1	5.8E-02	Q61768	SWISSPROT	KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC)
5272	18258	31109	0.67	5.8E-02	AF275366.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
5272	18258	31110	0.67	5.8E-02	AF275366.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
8129	19188	32324	0.53	5.8E-02	AA190694.1	EST_HUMAN	zp86at1.s1 Stratigene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627068 3'
8131	21041	34370	2.7	5.8E-02	M99150.1	NT	Human polymorphic microsatellite DNA
8131	21041	34371	2.7	5.8E-02	M99150.1	NT	Human polymorphic microsatellite DNA
9224	22132	35504	0.54	5.8E-02	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
12431	25191		1.5	5.8E-02	AF220177.1	NT	Drosophila melanogaster male fruitless type-A (fru) mRNA, complete cds
12709	25949		4.96	5.8E-02	AA604269.1	EST_HUMAN	no75611.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112684 3'
3105	16156	29051	0.88	5.7E-02	A1081644.1	EST_HUMAN	ou03505.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP-C37A2.2 CE08611;
3119	16170	29085	1.56	5.7E-02	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
3867	16896	29780	3.21	5.7E-02	AW066791.1	EST_HUMAN	EST378865 MAGI resequences, MAGI Homo sapiens cDNA
6094	19155		0.75	5.7E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
7879	20805	34108	0.55	5.7E-02	BE871911.1	EST_HUMAN	601447937F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3851985 5'
7879	20805	34109	0.55	5.7E-02	BE871911.1	EST_HUMAN	601447937F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3851985 5'
7868	20890	34201	0.78	5.7E-02	D78003.1	NT	Xenopus laevis mRNA for fourth component of complement, complete cds
7868	20890	34202	0.78	5.7E-02	D78003.1	NT	Xenopus laevis mRNA for fourth component of complement, complete cds
8733	21693	35008	1.59	5.7E-02	AJ266090.1	NT	Rattus norvegicus mRNA for potassium channel, alpha subunit (Kv9.2 gene)
10364	23253	36673	0.72	5.7E-02	6691260	NT	Mus musculus ec2 oncogene (Ec2), mRNA
11633	24539	38010	3.77	5.7E-02	A1752685.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random

Page 144 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11633	24539	38011	3.77	5.7E-02	AI752685.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random
11787	24709		1.76	6.7E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
12625	25779		8.52	5.7E-02	D50320.1	NT	Pig DNA for SPAL-2, complete cds
12779	25403		1.59	5.7E-02	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
12837	25839		3.1	5.7E-02	AF217490.1	NT	Homo sapiens fragile 16D oxido reductase (FOR) gene, exons 8, 9, and partial cds
12971	25935		5.5	5.7E-02	AF261280.1	NT	Pan troglodytes apolipoprotein-E gene, complete cds
1549	14580	27540	1.35	5.6E-02	AF094455.1	NT	Hydrocotyle rotundifolia ribosomal protein L16 (rp16) gene, intron; chloroplast gene for chloroplast product
4752	17757	30617	1.08	5.6E-02	AB013100.1	NT	Lycopersicon esculentum LE-ACS6 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
4809	17810	30576	1.14	5.6E-02	AA290589.1	EST_HUMAN	Zs45c01.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700416 3'
6954	19993	33207	4.17	6.6E-02	AW172708.1	EST_HUMAN	x02c10.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2656050 3' similar to TR:084979 O94979 KIAA0608 PROTEIN. ;
7218	20218	33495	0.76	5.6E-02	AA866182.1	EST_HUMAN	cd47112.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371119 3' similar to contains Alu repetitive element; contains element L1 repetitive element ;
7512	20451	33736	3.36	5.6E-02	BE080001.1	EST_HUMAN	QVO-BN0147-260400-214-g07 BN0147 Homo sapiens cDNA
7525	20484	33752	0.58	5.6E-02	AI983738.1	EST_HUMAN	wz34f05.x1 NCL_CGAP_Brm53 Homo sapiens cDNA clone IMAGE:2559969 3' similar to gb:X06409 RAF
8364	21268	34602	0.54	5.6E-02	AI183583.1	EST_HUMAN	PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (HUMAN);
9360	22288	35652	2.4	5.6E-02	BE542663.1	EST_HUMAN	q064g11.x1 Sceres testis_NHT Homo sapiens cDNA clone IMAGE:1734308 3'
9360	22288	35653	2.4	5.6E-02	BE542663.1	EST_HUMAN	601067158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'
10328	23217	36631	1.07	5.6E-02	AA482864.1	EST_HUMAN	601067158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'
11897	24838		2.43	5.6E-02	AF260225.1	NT	LAMINA ASSOCIATED POLYPEPTIDE 1C. ;
2703	15697	28591	7.61	5.5E-02	X97869.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
3281	16309	29214	3.96	5.5E-02	6755501	NT	H. sapiens gene encoding Le autoantigen
3882	16911	30192	1.54	5.5E-02	BE968659.1	EST_HUMAN	Mus musculus SH3 domain protein 1B (Sh3d1B), mRNA
4312	17326	30192	1.46	5.5E-02	L41551.1	NT	601650078F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933859 5'
4084	17093	30841	0.72	5.5E-02	AF161266.1	NT	Gallid herpesvirus mRNA fragment
5866	16927	32044	2.87	5.5E-02	Q01174	SWISSPROT	Murray Valley encephalitis virus strain MVE-1-51, complete genome
6258	18927	32044	3.95	5.5E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
7770	20700	34000	1.61	5.5E-02	6755902	NT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
8697	21628	34972	0.74	5.5E-02	AF170911.1	NT	Mus musculus tufelin 1 (Tuf1), mRNA
							Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds

Page 145 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8697	21628	34973	0.74	5.5E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
10180	23071	36470	0.61	5.5E-02	10947034	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
10180	23071	36471	0.61	5.5E-02	10947034	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
10270	23160	36570	1.27	5.5E-02	U69492.1	NT	Mus musculus second IL11 receptor alpha chain (IL11Ra2) gene, exons 1 and 2
11458	24373	37821	7.83	6.5E-02	U09771.1	NT	Citrobacter freundii DSM 30040 cyclopropane fatty acid synthase (cia) gene, partial cds, dihydroxyacetone kinase (dhaK), glycerol dehydrogenase (dhaD), transcriptional activator (dhaR), 1,3-propanediol dehydrogenase (dhaT), glycerol dehydratase (dhaB)>
13089	25901	31362	1.62	5.5E-02	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
3065	16117		0.88	5.4E-02	AJ277468.1	NT	Oryza sativa rbb13-1 gene for putative Bowman Birk trypsin inhibitor
3483	18410		8.2	5.4E-02	BE073468.1	EST_HUMAN	RC5-BT0559-140200-012-C03 BT0559 Homo sapiens cDNA
8702	21633		1.14	5.4E-02	Z99116.1	NT	Bacillus subtilis complete genome (section 13 of 21): from 2395261 to 2613730
11085	24017	37458	1.76	5.4E-02	AU120889.1	EST_HUMAN	AU120889 HEMBB1 Homo sapiens cDNA clone HEMBB1001630 5'
11142	24071	37517	2.53	5.4E-02	U20790.1	NT	Neurospora crassa ubiquinol-cytochrome c oxidoreductase subunit VIII (QCR8) mRNA, complete cds
12515	25770		2.17	5.4E-02	U44894.1	NT	Rana catesbeiana heat shock protein 30 (HSP30) mRNA, complete cds
1080	14124	27061	1.35	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021299-062-a09 ST0213 Homo sapiens cDNA
1080	14124	27062	1.35	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021299-062-a09 ST0213 Homo sapiens cDNA
1526	14556	27517	10.63	5.3E-02	T94759.1	EST_HUMAN	ye37112.1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:119951 5' similar to gb:K01506
2518	15520	28523	3.27	5.3E-02	AJ278408.1	NT	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1), ALPHA CHAIN (HUMAN);
2984	16036	28939	0.88	5.3E-02	M58417.1	NT	Pseudomonas putida tfgS gene
2984	16036	28940	0.88	5.3E-02	M58417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
3195	16243	29138	4.2	5.3E-02	AJ276408.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
4721	17726	30589	1.05	5.3E-02	AJ011048.1	NT	Pseudomonas putida tfgS gene
5223	18212	31058	9.91	5.3E-02	M80463.1	NT	Arabidopsis thaliana eli5 gene, exons 1-11
5502	18581	31429	1.98	5.3E-02	AE000527.1	NT	Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds
5502	18581	31430	1.98	5.3E-02	AE000527.1	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
6340	19390	32559	1.11	5.3E-02	M85289.1	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
7211	20211	33456	4.08	5.3E-02	U32832.1	NT	Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds
7451	20392	33662	1.47	5.3E-02	U32832.1	NT	Lymphocystis disease virus 1, complete genome
7752	20682		2.51	5.3E-02	S78221.1	NT	Haemophilus influenzae Rd section 147 of 163 of the complete genome
8457	21318	34650	0.63	5.3E-02	P38742	SWISSPROT	nuclear protein TIF1 isoform [mca, mRNA, 4053 nt]
8978	21906		0.7	5.3E-02	U10089.1	NT	HYPOTHETICAL 130.0 KD PROTEIN IN SNF6-SPO11 INTERGENIC REGION
9670	22566	35970	1.88	5.3E-02	X03127.1	NT	Mus musculus 129/Sv cystatin C (cst3) gene, complete cds
							Podospora anserina mitochondrial epsilon-sen DNA

Page 146 of 545  
Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10631	23517	36951	0.67	5.3E-02	AB022605.1	NT	Homo sapiens hCMT1b mRNA for mRNA (guanine-7-methyltransferase, complete cds)
10631	23517	36952	0.67	5.3E-02	AB022605.1	NT	Homo sapiens hCMT1b mRNA for mRNA (guanine-7-methyltransferase, complete cds)
10749	23635		0.68	5.3E-02	Y07907.1	NT	D. rerio mRNA for zp-23 POU gene, splice variant (neurula, 9-18 hpf and post-somitogenesis, 20-28 hpf)
10821	23707	37134	1.34	5.3E-02	X68432.1	NT	B. rerio pou1c mRNA for transcription factor
2304	15312		246.31	5.2E-02	5031808	NT	Homo sapiens meprin A, alpha (PABA peptide hydrolase) (MEP1A) mRNA
3160	16210	29100	2.51	5.2E-02	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3160	16210	29101	2.51	5.2E-02	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
4016	17043	29933	0.69	5.2E-02	AF236101.1	NT	Arabidopsis thaliana putative dicarboxylate diiron protein (Crd1) mRNA, complete cds
4376	17390	30253	3.69	5.2E-02	U07132.1	NT	Human steroid hormone receptor Nr-1 mRNA, complete cds
5322	18306	31156	0.72	5.2E-02	AB035201.1	NT	Rattus norvegicus mRNA for thyroglobulin, complete cds
6140	19199	32336	0.46	5.2E-02	U14731.1	NT	Saccharomyces cerevisiae Cdc54p (CDC54) gene, complete cds
6945	19395		1.19	5.2E-02	AI830985.1	EST_HUMAN	wf0e04.x1 NCL CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2409150 3' similar to contains MER15.b1 MER15 repetitive element;
7650	20584	33881	1.12	5.2E-02	P36322	SWISSPROT	DNA POLYMERASE PROCESSIVITY FACTOR (POLYMERASE ACCESSORY PROTEIN) (PAP) (DNA-BINDING GENE 18 PROTEIN)
8773	21703		2.58	5.2E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
10250	23141	36547	2.08	5.2E-02	D10927.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
10250	23141	36548	2.08	5.2E-02	D10927.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
12748	25387		2.04	5.2E-02	Q03030	SWISSPROT	OXAALACETATE DECARBOXYLASE ALPHA CHAIN
2387	15392		0.98	5.1E-02	AL134071.1	EST_HUMAN	DKFZp547D073.1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547D073 5'
4806	17805	30775	0.96	5.1E-02	AF085167.1	NT	Hordeum vulgare receptor-like kinase ARK1AS gene, partial cds
5126	18122		0.99	5.1E-02	AB031740.1	NT	Homo sapiens PBI1 gene for salivary proline-rich protein P.B, complete cds
5181	18173	31018	1.1	5.1E-02	BE957423.2	EST_HUMAN	601653556R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838361 3'
6969	19997	33225	0.74	5.1E-02	AF280369.1	NT	HIV-1 patient 96 from Italy protease (pol) gene, complete cds
7180	18452	31321	1.45	5.1E-02	BF378625.1	EST_HUMAN	QV0-UM0051-250800-350-b08 UM0051 Homo sapiens cDNA
8828	21758	35102	1.08	5.1E-02	M29434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8828	21758	35103	1.08	5.1E-02	M29434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8921	21851	35206	1.65	5.1E-02	AJ131966.1	NT	Spodoptera littoralis mRNA for 3-dehydrocyclohexene 3beta-reductase
9442	22370	35733	0.84	5.1E-02	P02593	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)
9442	22370	35734	0.84	5.1E-02	P02533	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)
10325	23214	36626	8.81	5.1E-02	AF012898.1	NT	Candida albicans protein phosphatase Ssd1 homolog (SSD1) gene, complete cds
10678	23564	36994	2.63	5.1E-02	P40603	SWISSPROT	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN GEX)
11269	24191	37640	2.49	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds



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11209	24191	37641	2.49	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
12756	25390		1.75	5.1E-02	AF062467.1	NT	Cucumis melo polygalacturonase precursor (MPG3) mRNA, complete cds
606	13576	26491	2.29	6.0E-02	AF068004.1	NT	Mus musculus fatty acid amide hydrolase gene, exon 10
1232	14268	27211	7.54	5.0E-02	Z99104.1	NT	Bacillus subtilis complete genome (section 1 of 21): from 1 to 213090
2007	15025	28016	4.26	5.0E-02	P02810	SWISSPROT	SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1/PRP-3) (PRP-2/PRP-4) (PIF-F/PIF-S) (PROTEIN A/PROTEIN C) [CONTAINS: PEPTIDE P-C]
2866	14063	27007	1.71	5.0E-02	U72742.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
3386	16429		1.67	5.0E-02	7305610	NT	Mus musculus Unc-51 like kinase 2 (C. elegans) (Ulk2), mRNA
3656	16692		1.15	5.0E-02	U32782.1	NT	Haemophilus influenzae Rd section 97 of 163 of the complete genome
3750	16782	29671	6.07	5.0E-02	U12769.2	NT	Anihereea parvii period clock protein homolog mRNA, complete cds
4934	17933		1.02	5.0E-02	P40232	SWISSPROT	CASEIN KINASE II BETA CHAIN (CK II)
5087	18084	30835	0.91	5.0E-02	AF188530.1	NT	Homo sapiens ubiquitous tetrahydrocortisol containing protein RoXan mRNA, partial cds
6370	19410	32585	0.73	5.0E-02	AF066264.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
6563	19604		1.09	5.0E-02	AJ242625.1	NT	Mus musculus Dmp-1 gene, exons 1-6
7329	18497	31273	0.52	5.0E-02	P35816	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFL-L)
7967	20889	34200	10.25	5.0E-02	P35816	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFL-L)
8199	21105		0.49	5.0E-02	AW062464.1	EST_HUMAN	MR0-CT0064-100899-002-g10 CT0064 Homo sapiens cDNA
10696	23582	37012	1.55	5.0E-02	AF052338.1	NT	Mus musculus Fas-interacting serine/threonine kinase 3 (Fist3) mRNA, complete cds
11923	24768	38265	2.4	5.0E-02	U67600.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
12312	25607		6.67	5.0E-02	Q04047	SWISSPROT	NO-ON-TRANSIENT A PROTEIN
241	13338		17.96	4.9E-02	M14230.1	NT	Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds
390	13474	26393	2.19	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
390	13474	26394	2.19	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
2917	15970	28967	0.76	4.9E-02	U32636.1	NT	Zea mays phytoene synthase (Y1) gene, complete cds
3332	16378	29278	1.65	4.9E-02	P54258	SWISSPROT	A TROPONIN-1 (DENTATORUBRAL-PALLIDOLYSIAN ATROPHY PROTEIN)
3630	16666		0.72	4.9E-02	AA188940.1	EST_HUMAN	zq48a12.s1 Stralegene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632926 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
3652	16688	29582	0.88	4.9E-02	AA400914.1	EST_HUMAN	z78a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
3652	16688	29583	0.88	4.9E-02	AA400914.1	EST_HUMAN	z78a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
4320	17334	30166	1.06	4.9E-02	AF135438.1	NT	Danio rerio de novo DNA methyltransferase 3 (dnmt3) mRNA, partial cds
4320	17334	30197	1.06	4.9E-02	AF135438.1	NT	Danio rerio de novo DNA methyltransferase 3 (dnmt3) mRNA, partial cds
4391	17405		1	4.9E-02	M23629.1	NT	Drosophila melanogaster developmental protein (rough) gene, complete cds
4954	17952	30810	1.55	4.9E-02	AW167821.1	EST_HUMAN	Xg56g10.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2632386 3'
4954	17952	30811	1.55	4.9E-02	AW167821.1	EST_HUMAN	Xg56g10.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2632386 3'

Page 148 of 545  
Table 4

Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5335	18319	31167	2.64	4.9E-02	7662816	NT	Homo sapiens PRO1848 protein (PRO1848), mRNA
5555	18633	31512	1.76	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
5555	18633	31513	1.76	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
7602	20441	33724	1.16	4.9E-02	AE000980.1	NT	Archaeoglobus fulgidus section 127 of 172 of the complete genome
9175	22103		1.16	4.9E-02	AE002309.1	NT	Chlamydia muridarum, section 40 of 85 of the complete genome
9314	22242	35604	0.86	4.9E-02	AL161559.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
10782	23668	37097	0.68	4.9E-02	P19532	SWISSPROT	TRANSCRIPTION FACTOR E3
11839	24890	38179	3.68	4.9E-02	AF008303.1	NT	Homo sapiens prepro placental TGF-beta gene, complete cds
12681	25941		1.62	4.9E-02	8923880	NT	Homo sapiens CS box-containing WD protein (LOC55884), mRNA
12924	25499		2.96	4.9E-02	M19364.1	NT	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds
350	13438	26352	1.24	4.9E-02	D16471.1	NT	Human mRNA, Xq terminal portion
351	13438	26352	2.14	4.9E-02	D16471.1	NT	Human mRNA, Xq terminal portion
611	13682	26496	6.29	4.9E-02	AF003100.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds
2292	15300	28306	2.06	4.8E-02	W51983.1	EST_HUMAN	gb:M30938 LUPUS KU AUTOANTIGEN PROTEIN P86 (HUMAN);
3254	16302	29208	1.72	4.8E-02	X17144.1	NT	Tetrahymena rostrata histone H3II and histone H4II intergenic DNA
5278	18264	31114	0.86	4.8E-02	U91914.1	NT	Streptococcus constellatus D-alanine:D-alanine ligase gene, partial cds
8716	21647	34993	1.33	4.8E-02	AW388497.1	EST_HUMAN	MR2-ST0129-221099-012-b02 ST0129 Homo sapiens cDNA
9674	22600	35973	0.84	4.8E-02	AJ001398.1	NT	Fugu rubripes rps24 gene
9874	22600	35974	0.84	4.8E-02	AJ001398.1	NT	Fugu rubripes rps24 gene
7143	20251	33503	3.42	4.7E-02	W01153.1	EST_HUMAN	yz9709.r1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:291017 5' similar to contains Alu repetitive element;
7212	20212	33457	0.79	4.7E-02	BF686625.1	EST_HUMAN	602143554F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4304772 5'
7212	20212	33458	0.79	4.7E-02	BF686625.1	EST_HUMAN	602143554F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4304772 5'
7247	20156	33396	1.59	4.7E-02	M62752.1	NT	Rat statin-related protein (s1) gene, complete CDS
8181	21088		0.52	4.7E-02	11431898	NT	Homo sapiens protein x 0001 (LOC51185), mRNA
8826	21756	35100	9.98	4.7E-02	X15543.1	NT	B. taurus mRNA for RF-36-DNA-binding protein
9508	22435	35799	1.23	4.7E-02	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
9527	22454		3.03	4.7E-02	AB026678.1	NT	Gallus gallus Wpksi-B gene, complete cds
9766	22692	36078	8.73	4.7E-02	X16543.1	NT	B. taurus mRNA for RF-36-DNA-binding protein
10173	23064	36461	0.53	4.7E-02	BF503237.1	EST_HUMAN	601892692F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138414 5'
10255	23145		0.57	4.7E-02	AI873042.1	EST_HUMAN	we79c10x1 Soares NFL T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347314 3'
11899	24832	38328	1.5	4.7E-02	U73621.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds

Page 149 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11889	24832	38329	1.5	4.7E-02	U73621.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
12500	26951		1.89	4.7E-02	AV648521.1	EST_HUMAN	AV648521 GLC Homo sapiens cDNA clone GLCBKD02 3'
290	13384	26300	1.01	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
763	13820	26749	2.82	4.6E-02	AE000445.1	NT	Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome
1318	14351		0.83	4.6E-02	AI014255.1	EST_HUMAN	am50d02.s1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1538979 3' similar to TR:P90533
1386	14417	27372	3.79	4.6E-02	AV727059.1	EST_HUMAN	P9C533 LIMA contains element LTR1 repetitive element ;
2511	15512	28515	2.84	4.6E-02	AW236023.1	EST_HUMAN	AV727059 HTC Homo sapiens cDNA clone HTCBW C01 5'
2855	13384	26300	2.24	4.6E-02	BE153583.1	EST_HUMAN	Q12849 G-RICH SEQUENCE FACTOR-1 ;
3378	16104	29008	0.67	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
3555	16104	29008	1.07	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
4219	17235		1.21	4.6E-02	AF220366.1	NT	Mus musculus nucleolar RNA helicase II/Gu (ddk21) gene, complete cds
5936	19003	32122	1.49	4.6E-02	AF076982.1	NT	Heplochromis burtoni gonadotropin-releasing hormone and GnRH-associated peptide precursor (GnRH2) gene, complete cds
6476	19521	32697	3.36	4.6E-02	X61624.1	NT	C.reinhardtii alp2 (alpB) mRNA
6476	19521	32698	3.36	4.6E-02	X61624.1	NT	C.reinhardtii alp2 (alpB) mRNA
7109	20313	33576	1.25	4.6E-02	AI149574.1	EST_HUMAN	qc60b06.x1 Soares_placenta_8to9weeks_2NbHP60gW Homo sapiens cDNA clone IMAGE:1713971 3'
8357	21262	34599	0.52	4.6E-02	6976720	NT	similar to contains L1 t3 L1 repetitive element ;
9214	22142	35497	3.8	4.6E-02	BE154006.1	EST_HUMAN	Rattus norvegicus Calhepsin H (Clsh), mRNA
11840	24691	38180	4.09	4.6E-02	AAG13328.1	EST_HUMAN	PM0-HT0339-060400-009-G12 HT0339 Homo sapiens cDNA
13076	25563		3.4	4.6E-02	X57808.1	NT	gl27h09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524737 3'
469	13540	26463	2.77	4.6E-02	P22448	SWISSPROT	Human germ-line immunoglobulin lambda light chain gene
1246	14282	27224	0.8	4.6E-02	AF005730.1	NT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1246	14282	27225	0.8	4.6E-02	AF005730.1	NT	Marburg virus strain M/S.Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
1826	14849	27826	4.38	4.6E-02	P32182	SWISSPROT	Marburg virus strain M/S.Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
2122	15135	28141	1.85	4.6E-02	AE003964.1	NT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
3787	16818	29706	5.68	4.6E-02	AL163278.2	NT	Xyella fastidiosa, section 110 of 228 of the complete genome
6478	19523	32701	1.5	4.6E-02	AJ400877.1	NT	Homo sapiens chromosome 21 segment HS21C078
6785	19818	33030	0.98	4.6E-02	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
7205	20205	33450	0.64	4.6E-02	L26487.1	NT	Melanostoma aeneum carbon monoxide dehydrogenase large subunit (cdh1A) gene; carbon monoxide dehydrogenase small subunit (cdh1B) gene, complete cds

Page 150 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7205	20205	33451	0.64	4.5E-02	L26487.1	NT	Melanosticta frisia carbon monoxide dehydrogenase large subunit (cdh1A) gene; carbon monoxide dehydrogenase small subunit (cdh1B) gene, complete cds
8994	21894	35251	2.15	4.5E-02	AF036684.1	NT	Arabidopsis thaliana CCAAT-box binding factor HAP3 homolog gene, complete cds
10456	23344	36761	4.29	4.5E-02	AA325218.1	EST_HUMAN	EST28167 Cerebellum II Homo sapiens cDNA 5' end similar to neuro-D4 protein
10712	23598	37025	0.95	4.5E-02	AB000470.1	NT	Gallus gallus mRNA for alpha1 integrin, complete cds
12497	25237	31961	2.73	4.5E-02	11418013	NT	Homo sapiens ret finger protein-like 3 (RFPL3), mRNA
12865	25846	31494	4.18	4.5E-02	AA191097.1	EST_HUMAN	zq43f11.1 Stragene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632493 5'
236	13334		4.12	4.4E-02	BE972733.1	EST_HUMAN	601652154F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935388 5'
2108	15122		5.72	4.4E-02	P31568	SWISSPROT	HYPOTHETICAL PROTEIN (ORF 2280)
2513	15314	28517	1.56	4.4E-02	AW875475.1	EST_HUMAN	QV2-P T0012-010300-070-g02 P T0012 Homo sapiens cDNA
3708	16740	29529	2	4.4E-02	AF159160.1	NT	Myxococcus xanthus serine/threonine kinase Pkn10 (pkn10) gene, complete cds
4740	17745	30005	1.51	4.4E-02	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4740	17745	30606	1.51	4.4E-02	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
5399	18381	31221	1.05	4.4E-02	AF081676.1	NT	Petunia x hybrida flavonoid 3',5'-hydroxylase (Hf1) gene, complete cds
7477	20417	33695	4.16	4.4E-02	AF095824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
7477	20417	33696	4.16	4.4E-02	AF095824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
8273	21178	34514	0.42	4.4E-02	11525868	NT	Homo sapiens hypothetical protein PRO2492 (PRO2492), mRNA
8273	21178	34515	0.42	4.4E-02	11525868	NT	Homo sapiens hypothetical protein PRO2492 (PRO2492), mRNA
9312	22240	35601	2.47	4.4E-02	AA736969.1	EST_HUMAN	rw13h03.s1 NCL_CGAP_S51 Homo sapiens cDNA clone IMAGE:1239221 3'
11510	24420	37875	3.87	4.4E-02	AF060669.1	NT	Hepatitis E virus strain HEV-JUS2 polyprotein (ORF1), (ORF3), and capsid protein (ORF2) genes, complete cds
11646	24552	38023	2.92	4.4E-02	AA496739.1	EST_HUMAN	ae33f04.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897631 5'
12248	25071		2.87	4.4E-02	AB040926.1	NT	Homo sapiens mRNA for KIAA1493 protein, partial cds
12416	25960		1.9	4.4E-02	BF241245.1	EST_HUMAN	601878746F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4107418 5'
807	13663	26798	6.2	4.3E-02	AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
2603	16601	28595	1.87	4.3E-02	AV704878.1	EST_HUMAN	AV704878 ADB Homo sapiens cDNA clone ADBA0H08 5'
3491	16530	29430	10.72	4.3E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3727	16759		1.33	4.3E-02	AF060569.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
5337	18321	31170	1.18	4.3E-02	AI075275.1	EST_HUMAN	oy69g05.x1 NCL_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:1671128 3' similar to contains Alu repetitive element; contains element MER3 repetitive element
6772	19806	33016	4.82	4.3E-02	P30427	SWISSPROT	PLECTIN
6772	19806	33017	4.92	4.3E-02	P30427	SWISSPROT	PLECTIN

Page 151 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7036	20062	33296	0.92	4.3E-02	AA652266.1	EST_HUMAN	ns8c12.s1 NCL CGAP_P12 Homo sapiens cDNA clone IMAGE:118886
8368	21272		0.44	4.3E-02	L15299.1	NT	Yeast para-aminobenzoate synthase gene, complete cds
9079	22008	35364	0.9	4.3E-02	AF293359.1	NT	Homo sapiens desmodulin 3 (DSC3) gene, complete cds, alternatively spliced
9359	22287	35650	1.16	4.3E-02	X55322.1	NT	H. sapiens NCAM mRNA for neural cell adhesion molecule
9359	22287	35651	1.16	4.3E-02	X55322.1	NT	H. sapiens NCAM mRNA for neural cell adhesion molecule
847	13902	26842	2.67	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
891	13944		2.51	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
921	13973	26920	0.87	4.2E-02	AW003645.1	EST_HUMAN	wx34g01.x1 NCL CGAP_P11 Homo sapiens cDNA clone IMAGE:2545584 3' similar to TR:Q63291 Q63291
1749	14776		1.24	4.2E-02	AL445066.1	NT	L1 RETROPOSON, ORF2 MRNA, contains L1.13 L1 L1 repetitive element ;
3732	16764	29651	1.53	4.2E-02	P23091	SWISSPROT	Thermoplasma acidophilum complete genome; segment 4/5
4214	17231	30100	0.79	4.2E-02	BE262605.1	EST_HUMAN	TRANSFORMING PROTEIN MAF
6812	18884	31993	0.73	4.2E-02	AF280107.1	NT	601150933F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503505 5'
5812	18884	31994	0.73	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7323	18491	31294	0.79	4.2E-02	BE268265.1	EST_HUMAN	601124698F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2989319 5'
7950	20872	34183	4.63	4.2E-02	AF270752.1	NT	Legionella pneumophila catalase-peroxidase (katA) gene, complete cds
7976	20897	34210	0.72	4.2E-02	AV730347.1	EST_HUMAN	AV730347 HTF Homo sapiens cDNA clone HTFAVH04 5'
9359	22287	35660	4.41	4.2E-02	P05095	SWISSPROT	ALPHA-ACTININ 3, NON MUSCULAR (F-ACTIN CROSS LINKING PROTEIN)
10660	23546	36980	1.74	4.2E-02	Q16650	SWISSPROT	T-BRAIN-1 PROTEIN (T-BOX BRAIN PROTEIN 1) (TBR-1) (TES-56)
11752	24653	38134	2.3	4.2E-02	BE815822.1	EST_HUMAN	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA
11752	24653	38135	2.3	4.2E-02	BE815822.1	EST_HUMAN	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA
11938	24782	38279	1.69	4.2E-02	AF178458.1	NT	PRRS isolate PRRSV38 envelope glycoprotein gene, complete cds
12761	25889		3.73	4.2E-02	AI983494.1	EST_HUMAN	w49g10.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510350 3'
533	13602	26513	0.67	4.1E-02	AF200629.1	NT	Homo sapiens HPS1 gene, intron 5
2726	15718	28715	1.05	4.1E-02	AE002330.2	NT	Chlamydia muridarum, section 60 of 85 of the complete genome
3969	16997	29882	0.69	4.1E-02	BE297230.1	EST_HUMAN	60117507F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3533353 5'
3969	16997	29883	0.69	4.1E-02	BE297230.1	EST_HUMAN	60117507F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3533353 5'
4585	17593		9.36	4.1E-02	AW693494.1	EST_HUMAN	QV41-NN0012-180400-164-f05 NN0012 Homo sapiens cDNA
5839	18910	32026	0.94	4.1E-02	BE251894.1	EST_HUMAN	601107535F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5'
5839	18910	32026	0.94	4.1E-02	BE251894.1	EST_HUMAN	601107535F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5'

Table 4

## Single Exon Probes Expressed in Adult Liver

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7209	20209		1.02	4.1E-02	X75881.1	NT	A.thaliana mRNA for plasma membrane intrinsic protein 1a
7458	20398	33871	1.51	4.1E-02	AE002132.1	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
7936	20858	34168	1.96	4.1E-02	7562347	NT	Homo sapiens KIAA0867 protein (KIAA0867). mRNA
8045	20958	34273	0.66	4.1E-02	L02110.1	NT	Mus musculus proviral insertion in the cGMP-phosphodiesterase (rd beta PDE) gene, intron 1, with the proviral insert encompassing the env pseudogene (3' end) and 3' LTR
8234	21139	34471	2.95	4.1E-02	AF026198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit>
8785	21715	35062	0.72	4.1E-02	P97857	SWISSPROT	ADAM-TS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 1) (ADAMTS-1) (ADAM-TS1)
9203	22131	36487	0.76	4.1E-02	P34687	SWISSPROT	CUTICLE COLLAGEN 34
9697	22822	36000	0.96	4.1E-02	AA372398.1	EST_HUMAN	EST84297 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
13040	25890	31479	12.28	4.1E-02	AJ271909.1	NT	Brassica napus gln gene for plectid glutamine synthetase, exons 1-12
1669	14699	27659	1.32	4.0E-02	A1675392.1	EST_HUMAN	wp98h01.x1 NCI_CGAP_Pt28 Homo sapiens cDNA clone IMAGE:2313745 3'
3290	16337	29240	4.8	4.0E-02	AB040904.1	NT	Homo sapiens mRNA for KIAA1471 protein, partial cds
3664	16893	29777	1.38	4.0E-02	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
5273	18259	31111	0.7	4.0E-02	AB042297.1	NT	Homo sapiens PTS gene for 6-pyruvoyltetrahydropterin synthase, complete cds
5379	18361	31201	1.06	4.0E-02	BF242746.1	EST_HUMAN	601877607F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106280 5'
5594	18942	31520	5.92	4.0E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
6458	19503	32678	1.61	4.0E-02	BF110434.1	EST_HUMAN	7n52h07.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3593980 3' similar to TR:075296 075296 R29124_1;
8143	21062	34384	6.06	4.0E-02	L23838.1	NT	Strongylocentrotus purpuratus homolog of human bone morphogenetic protein 1 (submp) mRNA, complete cds
8217	21122		0.42	4.0E-02	AL161535.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35
8235	21140	34472	0.88	4.0E-02	AB000391.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
8235	21140	34473	0.88	4.0E-02	AB000391.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
8292	21198	34533	0.48	4.0E-02	AF288153.1	NT	Homo sapiens erythrocyte tropomodulin (E-TMOD) gene, exon 7
9278	22204	35661	2.41	4.0E-02	P08640	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
10170	23061		0.72	4.0E-02	BF676376.1	EST_HUMAN	602153884F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294724 5'
10193	23084	36486	2.36	4.0E-02	AJ000941.1	NT	Methanobacterium thermoautotrophicum strain Marburg. Thiol:fumarate reductase subunit A
10490	23378		0.6	4.0E-02	D43948.1	NT	Human mRNA for KIAA0882 gene, partial cds

Page 153 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12186	25022		1.76	4.0E-02	AJ001018.1	NT	Kluyveromyces fragilis gene for Cat+ ATPase
12403	25730	31668	14.22	4.0E-02	AJ001056.1	NT	Ovis aries mRNA for acetyl-coA carboxylase
1147	14189	27128	2.67	3.9E-02	BF618149.1	EST_HUMAN	UIH-BW1-axh-08-0-JLs1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084134 3'
1373	14405	27958	1.89	3.9E-02	P41047	SWISSPROT	FAS ANTIGEN LIGAND
1973	14993	27976	2.67	3.9E-02	AJ403395.1	NT	Mus musculus DNA for desmin-binding fragment DesD7
2754	15745		1.98	3.9E-02	4506862	NT	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC) mRNA
5884	18757	31680	0.76	3.9E-02	D50608.1	NT	Rat gene for cholecystokinin type-A receptor (CCKAR), complete cds
5894	18757	31681	0.76	3.9E-02	D50608.1	NT	Rat gene for cholecystokinin type-A receptor (CCKAR), complete cds
5893	19000	32120	1.15	3.9E-02	BE66841.1	EST_HUMAN	601849874F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3633642 5'
6071	19132	32266	0.53	3.9E-02	BF675203.1	EST_HUMAN	602138132F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274910 5'
7411	20110	33344	1.21	3.9E-02	BE271437.1	EST_HUMAN	601140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'
8408	21312	34644	0.44	3.9E-02	P48778	SWISSPROT	ANTIGEN GOR
8422	21354	34692	1.67	3.9E-02	BF235613.1	EST_HUMAN	601806848F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134779 5'
8638	21569	34907	0.81	3.9E-02	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
8638	21569	34908	0.81	3.9E-02	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
11844	21312	34644	1.81	3.9E-02	P48778	SWISSPROT	ANTIGEN GOR
12271	25854		13.04	3.9E-02	AB042553.1	NT	Felis catus G-CSF gene for granulocyte colony-stimulating factor, complete cds
12870	25472		2.28	3.9E-02	U66051.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV16S1P, TCRBV15S1, TCRBV14S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2 >
12988	25786		18.85	3.9E-02	AL049886.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mrxq28orf
2133	15146		0.94	3.9E-02	AJ251973.1	NT	Homo sapiens partial steath-1 gene
6040	18037	30893	1.24	3.9E-02	AJ124122.1	EST_HUMAN	AJ124122 NT2RM2 Homo sapiens cDNA clone NT2RM2001698 5'
5628	18702	31601	1.01	3.9E-02	M11228.1	NT	Human protein C gene, complete cds
6324	19374	32542	1.1	3.9E-02	P10284	SWISSPROT	HOMEOBOX PROTEIN HOX-B4 (HOX-2.6)
7702	20634	33931	1.42	3.9E-02	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
8034	20949		0.43	3.9E-02	AA3682700.1	EST_HUMAN	EST06937 Tcslg 1 Homo sapiens cDNA 5' end
9222	22150		1.39	3.9E-02	M60675.1	NT	Human von Willebrand factor gene, exons 23 through 34
11097	24028	37472	2.4	3.9E-02	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
1019	14068	27011	2.9	3.7E-02	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)

Page 154 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1415	1448	27400	1.1	3.7E-02	L14661.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
2252	15262	28271	5.12	3.7E-02	AI084906.1	EST_HUMAN	wf8508.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494502 3'
2615	15613	28508	0.95	3.7E-02	AB018281.1	NT	Homo sapiens mRNA for KIAA0718 protein, partial cds
3097	16148	29045	0.73	3.7E-02	P79844	SWISSPROT	EOMESODERMIN
3099	16150	29046	5.51	3.7E-02	BF312983.1	EST_HUMAN	601898233F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125584 5'
6875	19908	33121	0.47	3.7E-02	A1132405.1	NT	Homo sapiens GDF-9B gene
7434	25980		0.86	3.7E-02	AF000083.1	NT	Aeropyrum pernix genomic DNA, section 817
8146	21055	34387	0.57	3.7E-02	AE003975.1	NT	Xyella fastidiosa, section 121 of 229 of the complete genome
10518	23405		1.05	3.7E-02	AA782516.1	EST_HUMAN	ai65c09.a1 Soares_papillary thyroid tumor_NbHPA Homo sapiens cDNA clone 1360912 3'
12310	25116	38578	9.68	3.7E-02	BF124974.1	EST_HUMAN	601782117F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4024973 5'
12928	25759	31674	2.33	3.7E-02	11418392	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1 (SLC22A1), mRNA
3722	16754	29642	0.88	3.6E-02	X73221.1	NT	H. vulgare Sst1 gene for sucrose synthase
3730	16762	29649	0.88	3.6E-02	AL096806.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens
5812	18688	31568	0.65	3.6E-02	X59403.1	NT	C. glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
5812	18688	31583	0.65	3.6E-02	X59403.1	NT	C. glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
5690	18763	31688	0.54	3.6E-02	AF161722.1	NT	Homo sapiens RUC2AS (RUC2) mRNA, complete cds
7004	20031	33262	5.25	3.6E-02	AW945516.1	EST_HUMAN	CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA
7004	20031	33263	5.25	3.6E-02	AW945516.1	EST_HUMAN	CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA
7294	18463	31333	0.46	3.6E-02	U67575.1	NT	Methanococcus jannaschii section 117 of 150 of the complete genome
7444	20385	33654	1.58	3.6E-02	AF025952.1	NT	Chromatium vibriosulfur globule protein Cyt2 precursor (sgp2) gene, complete cds
7689	20622	33922	2.87	3.6E-02	AA714521.1	EST_HUMAN	hw20e05.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241024 3' similar to gb:J00314_rna2
8081	20993	34311	0.77	3.6E-02	BE143078.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN)
9928	22833	36220	2.52	3.6E-02	U20608.1	NT	MFO-HT0168-030200-003-b08 HT0158 Homo sapiens cDNA
9928	22833	36221	2.52	3.6E-02	U20608.1	NT	Dictyostelium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
10139	23030	36427	0.8	3.6E-02	BF347588.1	EST_HUMAN	Dictyostelium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
11626	24532	38000	1.67	3.6E-02	BF131609.1	EST_HUMAN	602020453F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4156116 5'
11626	24532	38001	1.57	3.6E-02	BF131609.1	EST_HUMAN	601820416F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052570 5'



Page 155 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
920	13972	26919	1.72	3.5E-02	U09506.1	NT	Drosophila melanogaster liggrin mRNA, complete cds
1036	14083	27023	1.29	3.5E-02	AF253417.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
1684	14615	27677	2.74	3.5E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
1584	14615	27578	2.74	3.5E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
4309	17323	30190	2.4	3.5E-02	AE001773.1	NT	Thermotoga maritima section 85 of 136 of the complete genome
4420	17431	30293	1.07	3.5E-02	P53780	SWISSPROT	CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
6466	10511	32886	1.62	3.5E-02	J01238.1	NT	Maize acin 1 gene (Mac1), complete cds
8656	21487		0.8	3.5E-02	H26951.1	EST_HUMAN	yp44a05.r1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:190266 5' similar to contains Alu repetitive element;
9183	22111	35470	3.08	3.5E-02	BE958970.1	EST_HUMAN	60184470 IR2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3929737 3'
10521	23408	36820	1.68	3.5E-02	X76642.1	NT	L. lactis MG1363 grpE and dnaK genes
10567	23453	36874	0.51	3.5E-02	BE861042.1	EST_HUMAN	601344661F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677654 5'
11926	24771	36268	2.03	3.5E-02	AW861641.1	EST_HUMAN	PM1-CT0326-291299-002-h03 CT0326 Homo sapiens cDNA
11926	24771	36269	2.03	3.5E-02	AW861641.1	EST_HUMAN	PM1-CT0326-291299-002-h03 CT0326 Homo sapiens cDNA
12922	25795		6.42	3.5E-02	BE276948.1	EST_HUMAN	601178765F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3543833 5'
600	13667	26569	1.13	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
600	13667	26570	1.13	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
601	13667	26569	2.94	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
601	13667	26570	2.94	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
1077	14121	27058	2.46	3.4E-02	AW274020.1	EST_HUMAN	xv29d07.x1 Soares NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:2814253 3' similar to SW:C211_HUMAN P53801 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR ;
1234	14270		6.05	3.4E-02	11345459	NT	Homo sapiens hypothetical protein FLJ13220 (FLJ13220), mRNA
2415	15419	28420	2.11	3.4E-02	T57160.1	EST_HUMAN	yc20a06.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:81250 5' similar to contains MER29 repetitive element
3492	16531	29431	1.83	3.4E-02	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
3996	17023	29913	4.92	3.4E-02	AW794962.1	EST_HUMAN	RC6-UM0015-210200-021-A10 UM0015 Homo sapiens cDNA
4708	17713	30578	2.88	3.4E-02	X59799.1	NT	M. musculus S-antigen gene promoter region
5195	18187		3	3.4E-02	Q26457	SWISSPROT	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)
6212	18202	31046	1.82	3.4E-02	AJ012469.1	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial
6447	19493		0.62	3.4E-02	BF131628.1	EST_HUMAN	601820446F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052434 5'
7173	18445	31314	5.04	3.4E-02	U24393.1	NT	Human lysyl oxidase-like protein gene, exon 3
8837	21767		3.39	3.4E-02	AI869629.1	EST_HUMAN	w89d04.x1 NCL CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2433031 3'

Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9307	22235	35596	1.05	3.4E-02	AA664886.1	EST_HUMAN	nu70f08.s1 NCL CGAP_AVI Homo sapiens cDNA clone IMAGE:1216071 similar to contains Alu repetitive element; contains element MER25 MER25 repetitive element ;
9474	22402		5.03	3.4E-02	AA194306.1	EST_HUMAN	zq04f11.s1 Stragene muscle 937209 Homo sapiens cDNA clone IMAGE:628749 3' similar to TR:G1017425 G1017425
10297	23187		0.65	3.4E-02	AI092719.1	EST_HUMAN	IPISGKPLPKVTLSDRGVPLKATMRNFTEITAEINLTKESVTADAGRYEITAANSSTGTTKAFINIVLDRPG
393	13477		7.84	3.3E-02	AA388735.1	EST_HUMAN	PPT GPVXVSDITEESVTLKWEPPKYDGGSQVTNLLKRETSIAVW TEVSATYARTMMKVMKL ... ;
1194	14233	27172	10.27	3.3E-02	AB035867.1	NT	0259f08.x1 Soares parathyroid tumor NbfHPA Homo sapiens cDNA clone IMAGE:1683519 3'
1520	14551	27613	0.91	3.3E-02	L16870.1	NT	Cricetulus griseus CYP2A17 mRNA for cytochrome P450 2A17, complete cds
1665	14895	27655	1.13	3.3E-02	AF110763.1	NT	Homo sapiens cytochrome P4502C18 (CYP2C18) gene, exons 2 and 3
1767	14793		0.97	3.3E-02	AE000700.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
2097	15111		2.44	3.3E-02	R09112.1	EST_HUMAN	Aquifex acidicus section 32 of 109 of the complete genome
2476	15478	28479	1.42	3.3E-02	6755862	NT	yf25c09.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:127888 5'
3416	16458	29364	0.89	3.3E-02	H02389.1	EST_HUMAN	Mus musculus tumor rejection antigen gp96 (Tra1), mRNA
4273	14695	27655	3.48	3.3E-02	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
4579	17587	30449	2.71	3.3E-02	6755862	NT	Mus musculus tumor rejection antigen gp96 (Tra1), mRNA
6698	19734	32935	19.31	3.3E-02	BF245995.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
6698	19734	32936	19.31	3.3E-02	BF245995.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
7931	20853	34161	0.53	3.3E-02	AF124162.1	NT	Nicotiana plumbaginifolia molybdopterin synthase sulphurylase (cys5) gene, partial cds
9862	22777	36164	0.84	3.3E-02	BF115921.1	EST_HUMAN	7m92d04.x1 NCL CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3562423 3'
9862	22777	36165	0.84	3.3E-02	BF115921.1	EST_HUMAN	7m92d04.x1 NCL CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3562423 3'
9958	22863	36250	0.63	3.3E-02	AA488202.1	EST_HUMAN	ad08f09.s1 Soares_NHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X709444_cds1 MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN);
9958	22863	36251	0.63	3.3E-02	AA488202.1	EST_HUMAN	ad08f09.s1 Soares_NHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X709444_cds1 MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN);
11087	23951		0.52	3.3E-02	H38109.1	EST_HUMAN	yp5f1f1.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:180989 3'
11581	24470	37936	3.27	3.3E-02	BF691107.1	EST_HUMAN	602247171F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332497 5'
12072	24923	38416	1.4	3.3E-02	AF077337.1	NT	Zea mays heat shock protein 101 (HSP101) gene, complete cds
12404	25227		3.82	3.3E-02	T96545.1	EST_HUMAN	yp40f11.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:121101 5'
12600	25299		1.68	3.3E-02	AF289655.1	NT	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
12628	25311		2.2	3.3E-02	M81890.1	NT	Human Interleukin 11 (IL11) gene, complete mRNA
136	13238	26157	1.46	3.2E-02	AJ002005.1	NT	Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
1163	14184	27132	8.71	3.2E-02	AF096275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds

Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1153	14194	27133	8.71	3.2E-02	AF08275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
2131	15144		1.94	3.2E-02	P28955	SWISSPROT	LARGE TEGUMENT PROTEIN
2885	13238	26157	1.01	3.2E-02	AJ002005.1	NT	Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
3179	16229	29123	17.23	3.2E-02	BE067353.1	EST_HUMAN	601442431F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846727 5'
3777	18808	29696	1.42	3.2E-02	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4315	17329		17.61	3.2E-02	X94788.1	NT	H sapiens RP3 gene (XLRP gene 3)
4880	17879	30744	3.77	3.2E-02	AF114182.1	NT	Saxifraga nidifica maturase (matK) gene, chloroplast gene encoding chloroplast protein, partial cds
4941	17940	30797	0.69	3.2E-02	AF067083.1	NT	Vitreoscilla sp. outer membrane protein homolog gene, complete cds; Ttp repressor binding protein gene, partial cds; and unknown genes
5061	18058		0.92	3.2E-02	AF109906.1	NT	Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSC70L and smRNP genes, complete cds; G7A gene, partial cds; and unknown genes
5725	18798	31890	1.69	3.2E-02	X68709.1	NT	S. griseocarneum whiG-Stv gene
5726	18708	31891	1.69	3.2E-02	X68709.1	NT	S. griseocarneum whiG-Stv gene
6802	19835	33046	2.31	3.2E-02	M32437.1	NT	Rat polyomavirus left junction in cell line W98.14
6805	19838		27.08	3.2E-02	T89387.1	EST_HUMAN	yt33h12.s1 Soares fetal liver spleen TNFLS Homo sapiens cDNA clone IMAGE:110087 3' similar to contains
6895	19925	33140	3.81	3.2E-02	AF173845.1	NT	Alu repetitive element/contains LTR1 repetitive element;
8231	21136	34468	0.9	3.2E-02	11424049	NT	Sagittaria pediculus tissue kallikrein gene, complete cds
8401	21304	34636	0.46	3.2E-02	AA555015.1	EST_HUMAN	Homo sapiens cytochrome P450, subfamily IIB (phenobarbital-inducible) (CYP2B), mRNA
8875	21805	35158	4.16	3.2E-02	6680569	NT	nl07r11.s1 NCI CGAP Pr11 Homo sapiens cDNA clone IMAGE:1029621 similar to gb:X65923 UBIQUITIN-LIKE PROTEIN FUBI (HUMAN);
9496	22424		0.95	3.2E-02	AF109718.1	NT	Mus musculus kinesin family member 3c (Kif3c), mRNA
9766	22690	36075	1.32	3.2E-02	A1278971.1	EST_HUMAN	Homo sapiens chromosome 3 subtelomeric region
9768	22690	36076	1.32	3.2E-02	A1278971.1	EST_HUMAN	qm17b04.x1 NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:1882063 3'
10559	23445		4.52	3.2E-02	AA19795.1	EST_HUMAN	qm17b04.x1 NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:1882063 3'
10844	23730	37153	1.15	3.2E-02	U96762.1	NT	zg5b12.s1 Soares pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:397151 3' similar to
12211	25045		1.43	3.2E-02	AL163302.2	NT	gb:L08441 CYTOCHROME C OXIDASE POLYPEPTIDE III (HUMAN);
1287	14320		2.17	3.1E-02	4603476	NT	Macaca mulatta chemokine receptor COR5 mRNA, complete cds
1331	14365	27314	1.12	3.1E-02	P18845	SWISSPROT	Homo sapiens chromosome 21 segment HS21C102
1970	14931	27908	1.41	3.1E-02	6671564	NT	Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA
1980	15008		1.05	3.1E-02	Z50097.1	NT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)
5445	18528	31252	1.22	3.1E-02	U78104.1	NT	Mus musculus adaptor-related protein complex AP-3, delta subunit (Ap3d), mRNA
						NT	Drosophila melanogaster mRNA for headcase protein
						NT	Human leukemia inhibitory factor receptor (LIFR) gene, promoter and partial exon 1

Page 158 of 545  
Table 4

## Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5545	18623		2.38	3.1E-02	AA278478.1	EST_HUMAN	zs81a06.r1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703868 5'
5844	18915	32031	0.69	3.1E-02	BF687742.1	EST_HUMAN	602068783F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4085789 5'
5916	25836	32104	0.42	3.1E-02	AJ391284.1	NT	Neisseria meningitidis DNA for region 2 (flaB- and flhC-homologs, unknown genes) and flanking genes, strain FAM18
10534	23420	36636	2.6	3.1E-02	AF034779.1	NT	Enterococcus faecalis surface protein precursor, gene, complete cds
1846	14877		1.74	3.0E-02	AF187125.1	NT	Ptyckiaines minutus cytochrome oxidase I gene, partial cds; mitochondrial gene for mitochondrial product
2623	15921	28614	1.41	3.0E-02	AA402242.1	EST_HUMAN	z65h03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727263 5'
3625	16661	29661	1.22	3.0E-02	M94176.1	NT	Saccharomyces cerevisiae stem-loop mutation suppressor SSL2 gene, complete cds
3721	16753	28641	3.17	3.0E-02	AF247644.1	NT	Pseudomonas fluorescens family II aminotransferase gene, complete cds
3808	16838		0.78	3.0E-02	AW820223.1	EST_HUMAN	QV2-S10296-150200-040-e09 ST0286 Homo sapiens cDNA
4027	17054		0.95	3.0E-02	AA364003.1	EST_HUMAN	EST74530 Pineal gland II Homo sapiens cDNA 5' end
5185	18177	31022	8.94	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
6186	18177	31023	8.94	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5576	18654		3.18	3.0E-02	AB046793.1	NT	Homo sapiens mRNA for KIAA1573 protein, partial cds
6503	18547	32724	0.7	3.0E-02	N69615.1	EST_HUMAN	za39a10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294906 5' similar to contains element TAR1 repetitive element:
6503	19547	32725	0.7	3.0E-02	N69615.1	EST_HUMAN	za39a10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294906 5' similar to contains element TAR1 repetitive element:
7098	20304	33563	2.45	3.0E-02	AJ242806.1	NT	Cyprinus carpio mRNA for inducible nitric oxide synthase (NOS gene)
7235	20144	33363	2.96	3.0E-02	BE889948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
7235	20144	33384	2.98	3.0E-02	BE889948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
7426	20125	33363	2.14	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7426	20125	33364	2.14	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7601	20538	33825	1.19	3.0E-02	M86524.1	NT	Human dystrophin gene
8019	20335		0.88	3.0E-02	BF246361.1	EST_HUMAN	601854981F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4074548 5'
9180	22108	35466	0.55	3.0E-02	BE512670.1	EST_HUMAN	601171626F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3845047 5'
9200	22128	35484	0.83	3.0E-02	BF353889.1	EST_HUMAN	IL3-H10704-290600-108-c04 H10704 Homo sapiens cDNA
9351	22279		1.65	3.0E-02	AF276664.1	NT	Ornithorhynchus anatinus coagulation factor X mRNA, complete cds
10939	23824	37251	1.94	3.0E-02	AE001797.1	NT	Thermoboga maritima section 109 of 136 of the complete genome
11025	23909	37350	0.53	3.0E-02	Z21211.1	EST_HUMAN	HSAADTHS TEST1, Human adult Testis tissue Homo sapiens cDNA clone cam test244 (b)
11681	24885	38062	2.47	3.0E-02	M81357.1	NT	Human coagulation factor VII (F7) gene exon 1 and factor X (F10) gene, exon 1

Page 159 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12114	24955	38458	8.71	3.0E-02	AA483216.1	EST_HUMAN	n88704.s1 NCLCGAP_Kid1 Homo sapiens cDNA clone IMAGE:911263
12581	25937	31373	2.56	3.0E-02	R32019.1	EST_HUMAN	Y63304.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:134407 3'
12613	26496		7.82	3.0E-02	AW895665.1	EST_HUMAN	QV4-NN0038-270400-187-h05 NN0038 Homo sapiens cDNA
12952	29931		4.22	3.0E-02	AF048687.1	NT	Rattus norvegicus UDP-Galglucosylceramide beta-1,4-galactosyltransferase mRNA, complete cds
3033	16085	28986	1.12	2.9E-02	BE565644.1	EST_HUMAN	601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680695 5'
3033	16085	28987	1.12	2.9E-02	BE565644.1	EST_HUMAN	601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680695 5'
4004	17031	29921	0.81	2.9E-02	H72805.1	EST_HUMAN	y07e10.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233130 5'
4070	17086	29079	0.66	2.9E-02	O15440	SWISSPROT	MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 5 (ABC TRANSPORTER MOAT-C) (PABC14)
5144	18139	30981	0.91	2.9E-02	X65137.1	NT	S.vulgate pepC gene for PEP carboxylase
5144	18139	30982	0.91	2.9E-02	X65137.1	NT	S.vulgate pepC gene for PEP carboxylase
5260	18474		3.66	2.9E-02	R09112.1	EST_HUMAN	y25609.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127888 5'
6298	16343	32617	1.31	2.9E-02	AF060221.1	NT	Sus scrofa deoxyribonuclease II mRNA, complete cds
6545	19588	32775	6.16	2.9E-02	BF032233.1	EST_HUMAN	601452661F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3656598 5'
7286	20239	33489	0.57	2.9E-02	AJ391284.1	NT	Neisseria meningitidis DNA for region 2 (flaB- and flhC-homologs, unknown genes) and flanking genes, strain FAM18
7619	20554	33847	10.47	2.9E-02	BE271437.1	EST_HUMAN	601140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'
7827	20756	34060	0.54	2.9E-02	D29214.1	EST_HUMAN	HUMNK262 Human epidermal keratinocyte Homo sapiens cDNA clone 262
8577	21508	34853	1.01	2.9E-02	AF129279.1	NT	Buchnera aphidicola natural-host Schlechtendalia chinensis gluconate-6-phosphate dehydrogenase (grd) gene, partial cds
8577	21508	34854	1.01	2.9E-02	AF129279.1	NT	Buchnera aphidicola natural-host Schlechtendalia chinensis gluconate-6-phosphate dehydrogenase (grd) gene, partial cds
10183	23074	36474	2.06	2.9E-02	AW875979.1	EST_HUMAN	CM3-PT0014-071299-051-c04 PT0014 Homo sapiens cDNA
10183	23074	36475	2.06	2.9E-02	AW875979.1	EST_HUMAN	CM3-PT0014-071299-051-c04 PT0014 Homo sapiens cDNA
10386	23275		0.85	2.9E-02	AW976597.1	EST_HUMAN	EST388708 MAGE resequences, MAGN Homo sapiens cDNA
10832	23719	37143	1.17	2.9E-02	AF000064.1	NT	Aeropyrum pernix genomic DNA, section 7/7
11485	18425	31350	2.04	2.9E-02	X55294.1	NT	Sheep gene for ultra high-sulphur keratin protein
12583	25853		1.73	2.9E-02	AI135817.1	EST_HUMAN	AI135817 PLACE1 Homo sapiens cDNA clone PLACE1002962 5'
687	13665		0.78	2.8E-02	AF060663.1	EST_HUMAN	EST382234 MAGE resequences, MAGK Homo sapiens cDNA
3425	16465	29079	1.77	2.8E-02	AF060663.1	NT	Homo sapiens retinal fasciclin (FSCN2) gene, exon 2
3425	16465	29374	1.77	2.8E-02	AF060663.1	NT	Homo sapiens retinal fasciclin (FSCN2) gene, exon 2
5676	18760	31672	10.93	2.8E-02	BE741083.1	EST_HUMAN	601594078F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948067 5'
7120	20324	33598	1.05	2.8E-02	T78960.1	EST_HUMAN	y021508.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108855 5'

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8903	21833	35188	1.61	2.8E-02	AJ005820.1	NT	Cratichneumon plantaginis mRNA for homeodomain leucine zipper protein (hb-1)
9568	22495	35858	0.92	2.8E-02	AA280762.1	EST_HUMAN	z98c05.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:711466 5'
9749	22673	36057	1.23	2.6E-02	AF167872.1	NT	Cavia porcellus inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, complete cds
9853	22768	36193	0.65	2.8E-02	AE001092.1	NT	Archaeoglobus fulgidus section 15 of 172 of the complete genome
12204	25039	38542	1.49	2.8E-02	L33697.1	NT	GMyndomonas reinhardtii kinesin-homologous protein (FLA10) mRNA, complete cds
							Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV6S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV6S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S>
1507	14538	27500	1.38	2.7E-02	U66059.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 9
3493	16532	28432	1.72	2.7E-02	AL161494.2	NT	y86h12.r1 Soares_multiple_sclerosis_2NBMSP Homo sapiens cDNA clone IMAGE:280487 5'
4288	17312	30178	2.1	2.7E-02	N47258.1	EST_HUMAN	y86h12.r1 Soares_multiple_sclerosis_2NBMSP Homo sapiens cDNA clone IMAGE:280487 5'
4298	17312	30178	2.1	2.7E-02	N47258.1	EST_HUMAN	y86h12.r1 Soares_fetal_liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120127 3' similar to contains Alu repetitive element;
5383	18395	31204	1.22	2.7E-02	T95073.1	EST_HUMAN	Alu repetitive element;
5428	18510	31234	0.51	2.7E-02	BF245672.1	EST_HUMAN	60186481F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083075 5'
5627	18703	31602	1.16	2.7E-02	R12245.1	EST_HUMAN	yf33d08.r1 Soares_fetal_liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128657 5' similar to SP:JC2264 JC2264 TISSUE FACTOR PATHWAY INHIBITOR - RHESUS ;
6120	19179	32314	0.88	2.7E-02	X61670.1	NT	T.aestivum pTTH20 mRNA for wheat type V thionin
8204	19280	32407	0.52	2.7E-02	AB004799.1	NT	Oryza sativa mRNA for ascorbate oxidase, partial cds
8886	19919		0.89	2.7E-02	X97580.1	NT	A.blauporus pgkA gene
7421	20120	33357	1.92	2.7E-02	AA933571.1	EST_HUMAN	o86h03.s1 Soares_fetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1824661 3'
8363	21267		0.6	2.7E-02	AK024456.1	NT	Homo sapiens mRNA for FLJ00048 protein, partial cds
8388	21301	34632	0.56	2.7E-02	9256542	NT	Mus musculus G21 protein (G21), mRNA
							contains Alu repetitive element;
8927	21857		1.26	2.7E-02	A377036.1	EST_HUMAN	tc28g08.x1 Soares_fetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2065982 3' similar to
593	13630	26563	1.12	2.6E-02	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
2389	15384	28396	3.01	2.6E-02	AA490021.1	EST_HUMAN	ab02002.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839595 3'
2391	15396	28398	2.97	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2391	15396	28399	2.97	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
							Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70, and smRNP genes, complete cds; G7A gene, partial cds; and unknown genes
2958	16010		1.3	2.6E-02	AF109906.1	NT	zmf3709.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:531305 3'
4019	17046		1.25	2.6E-02	AA071307.1	EST_HUMAN	Homo sapiens EWS, ger22, rrp22 and bam22 genes
4392	17406		1.13	2.6E-02	Y07848.1	NT	Chicken dorsalin-1 mRNA, complete cds
5013	18011	30869	3.87	2.6E-02	L12032.1	NT	

Page 161 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5199	18191	31033	1.29	2.6E-02	AE002014.1	NT	Deinococcus radiodurans R1 section 151 of 229 of the complete chromosome 1 xa52b04.x1 NCI_CGAP_Sar4 Homo sapiens cDNA clone IMAGE:2570383 3' similar to SW.Y069_HUMAN
5227	18216	31062	2.49	2.6E-02	AW241154.1	EST_HUMAN	Q16041 HYPOTHETICAL PROTEIN KIAA0089 ;
6059	19120		0.47	2.6E-02	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
6107	19167		0.51	2.6E-02	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
6464	19509		7.05	2.6E-02	AI206030.1	EST_HUMAN	qg27f11.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1762317 3'
6693	19729	32929	2.29	2.6E-02	BE621748.1	EST_HUMAN	601493473T1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895578 3'
7140	20248	33499	0.78	2.6E-02	Z99064.1	NT	Vaccinia virus ORF1L strain Wyeth
7140	20248	33500	0.78	2.6E-02	Z99064.1	NT	Vaccinia virus ORF1L strain Wyeth
7238	20147	33397	5.57	2.6E-02	6981271	NT	Rattus norvegicus Nerve growth factor receptor, fast (Ngfr), mRNA
7678	20612	33911	0.7	2.6E-02	P21894	SWISSPROT	ALANYL-TRNA SYNTHETASE (ALANINE-TRNA LIGASE) (ALARS)
9072	22001	35355	0.87	2.6E-02	AA86046.1	EST_HUMAN	ak22f04.s1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1406719 3'
9868	22889	36270	1.45	2.6E-02	11432020	NT	Homo sapiens KIAA1070 protein (KIAA1070), mRNA
10236	23127	36529	0.77	2.6E-02	AF114952.1	NT	Saccharomyces cerevisiae NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10236	23127	36530	0.77	2.6E-02	AF114952.1	NT	Saccharomyces cerevisiae NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10888	23773	37199	4.93	2.6E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
11825	24745		2.19	2.6E-02	AA279351.1	EST_HUMAN	zs84c02.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704162 5'
11995	24937	36336	1.87	2.6E-02	AW500547.1	EST_HUMAN	UI-HF-BNO-akj-e-10-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077496 5'
555	13624	26532	1.51	2.5E-02	AI793130.1	EST_HUMAN	on26f09.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
555	13624	26533	1.51	2.5E-02	AI793130.1	EST_HUMAN	on26f09.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
835	13690	26827	13.09	2.5E-02	BE974314.1	EST_HUMAN	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950665 3'
894	13947	26894	4.47	2.5E-02	BE974314.1	EST_HUMAN	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950665 3'
2813	15802		2.54	2.5E-02	U12871.1	NT	Rattus norvegicus rabphilin-3A mRNA, complete cds
2997	16043	28951	1.88	2.5E-02	X99697.1	NT	H. carterae mRNA for fucosanthin chlorophyll a/c binding protein, Fcp1
2997	16049	28952	1.88	2.5E-02	X99697.1	NT	H. carterae mRNA for fucosanthin chlorophyll a/c binding protein, Fcp1
4129	18403	30027	1.28	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
4129	18403	30028	1.28	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
4301	17315	30181	6.15	2.5E-02	AW592114.1	EST_HUMAN	pf66h08.x1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2884015 3'
5381	18363		0.96	2.5E-02	BE271116.1	EST_HUMAN	601176925F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3543822 5'
5912	18981	32099	0.58	2.5E-02	AI732776.1	EST_HUMAN	zx83c10.x5 Soares, ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:810364 3'
6434	19481		4.75	2.5E-02	BE870128.1	EST_HUMAN	7e30a09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284008 3' similar to contains L1.11 L1 repetitive element ;

Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6453	19498		4.42	2.5E-02	BE746888.1	EST_HUMAN	601579393F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928054 5'
6593	19634	32816	0.83	2.5E-02	L29029.1	NT	Chlamydomonas reinhardtii VSP-3 mRNA, complete cds
8110	21027	34953	1.72	2.5E-02	BF528722.1	EST_HUMAN	60207062F1 NCI_OGAP_Brm64 Homo sapiens cDNA clone IMAGE:4213406 5'
8116	21027	34954	1.72	2.5E-02	BF528722.1	EST_HUMAN	602070562F1 NCI_OGAP_Brm64 Homo sapiens cDNA clone IMAGE:4213406 5'
8360	21265	34600	0.46	2.5E-02	AF129458.1	NT	Chlamydomonas reinhardtii class II DNA photolyase (PHR2) gene, complete cds
8558	21489	34828	0.63	2.5E-02	BE252469.1	EST_HUMAN	601108291F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3344278 5'
9384	22312	35674	0.73	2.5E-02	Q91713	SWISSPROT	CHORDIN PRECURSOR (ORGANIZER-SPECIFIC SECRETED DORSALIZING FACTOR)
10588	23454		0.78	2.5E-02	X71303.1	NT	D. radiatum 28S ribosomal RNA, D2 domain
11055	23939	37377	0.66	2.5E-02	A1147615.1	EST_HUMAN	q622a08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1686982 3'
11249	24173	37620	2.37	2.5E-02	Q10335	SWISSPROT	HYPOTHEICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME 1
11249	24173	37621	2.37	2.5E-02	Q10335	SWISSPROT	HYPOTHEICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME 1
11299	24218	37668	4.26	2.5E-02	AJ237936.1	NT	Bos taurus partial stat5B gene, exons 17-19
							Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (IiAlpha) and major histocompatibility protein class II beta chain (IiBeta) genes, complete cds;
11318	24237		3.87	2.5E-02	AF050157.1	NT	butyrophilin-like (NG9), butyrophilin-lp
12181	25017		1.74	2.5E-02	AB007646.1	NT	Homo sapiens gene for LECT2, complete cds
12215	25049		1.43	2.5E-02	X98999.1	NT	Pseudomonas sp. transposon Trn5041 DNA
12477	25865		2.05	2.5E-02	11420078	NT	Homo sapiens similar to ALEX3 protein (H. sapiens) (LOC63634), mRNA
12653	25749		1.7	2.5E-02	11439220	NT	Homo sapiens ribogen-activated protein kinase kinase kinase 13 (MAP3K13), mRNA
12740	25380		2.18	2.5E-02	U60169.1	NT	Dictyostelium discoideum putative protein kinase MicaA (mkaA) gene, complete cds
184	13283	26200	1.01	2.4E-02	A1378582.1	EST_HUMAN	tc72c07.x1 Soares_NbHMPu_S1 Homo sapiens cDNA clone IMAGE:2070156 3'
1621	14651	27614	1.4	2.4E-02	H65984.1	EST_HUMAN	w75f11.r1 Soares_fetal_liver_spleen_1NF1S Homo sapiens cDNA clone IMAGE:211149 5'
2058	15915	28075	1.71	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
2058	15915	28076	1.71	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4475	17486	30345	2.53	2.4E-02	J05110.1	NT	T. thermophila calcium-binding 25 kDa (TCBP 25) protein mRNA, complete cds
4641	17847	30511	1.5	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4641	17847	30512	1.6	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
5294	18279	31129	1.1	2.4E-02	8022702	NT	Homo sapiens hypothetical protein FLJ10844 (FLJ10844), mRNA
6459	19504	32679	1.05	2.4E-02	W86680.1	EST_HUMAN	zhf3h04.st Soares_fetal_liver_spleen_1NF1S_S1 Homo sapiens cDNA clone IMAGE:416791 3'
6620	19860	32844	0.51	2.4E-02	M31050.1	NT	Chicken myristoylated alanine-rich G kinase substrate (MARCKS) mRNA, complete cds
6620	19860	32845	0.51	2.4E-02	M31050.1	NT	Chicken myristoylated alanine-rich G kinase substrate (MARCKS) mRNA, complete cds
7590	20526	33815	0.79	2.4E-02	Z20573.1	EST_HUMAN	H5AAACKVX.T Human adult Rhabdomyosarcoma cell-line Homo sapiens cDNA
7607	20542	33832	0.83	2.4E-02	X12925.1	NT	Rat gene for uncoupling protein (UCP)
7607	20542	33833	0.83	2.4E-02	X12925.1	NT	Rat gene for uncoupling protein (UCP)



Page 163 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8397	21300	34630	0.56	2.4E-02	P98092	SWISSPROT	HEMOCYTIN PRECURSOR (HUMORAL LECTIN)
8397	21300	34631	0.56	2.4E-02	P98092	SWISSPROT	HEMOCYTIN PRECURSOR (HUMORAL LECTIN)
8470	21401		0.74	2.4E-02	AW813007.1	EST_HUMAN	RC3-ST0186-230300-019-h05 ST0186 Homo sapiens cDNA
8522	21453		0.61	2.4E-02	M16760.1	NT	Human retrotansposon 3' long terminal repeat
9009	21938		0.87	2.4E-02	H78376.1	EST_HUMAN	yu12c05.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233576 3' similar to contains Alu repetitive element; contains A39 repetitive element ;
9095	22024	35380	2.18	2.4E-02	N69442.1	EST_HUMAN	za355g11.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294596 3' similar to
9538	22465	35826	0.6	2.4E-02	AE001125.1	NT	gb K02909 JRATSR7K Rat (rRNA); contains A39 repetitive element ;
							Borrelia burgdorferi (section 11 of 70) of the complete genome
9561	22488	35849	0.99	2.4E-02	AA625660.1	EST_HUMAN	zu81c08.s1 Soares testis 1NHT Homo sapiens cDNA clone IMAGE:745354 3' similar to gb:J04422 ISLET
10322	23211	36623	2.67	2.4E-02	AV692954.1	EST_HUMAN	AMYLOID POLYPEPTIDE PRECURSOR (HUMAN); contains Alu repetitive element; contains element XTR
10487	23375	36790	3.35	2.4E-02	AA493894.1	EST_HUMAN	XTR repetitive element ;
							AV692954 GK Homo sapiens cDNA clone GKCDSC03 5'
							nm07b12.e1 NCL CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943583 similar to contains Alu repetitive element; contains element PTR5 repetitive element ;
12005	24847	38344	2.3	2.4E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, Muts homolog, CLCP, NG24, NG25, and NG28 genes, complete cds; and unknown genes
12005	24847	38345	2.3	2.4E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, Muts homolog, CLCP, NG24, NG25, and NG28 genes, complete cds; and unknown genes
12296	25106		4.99	2.4E-02	9627909	NT	Bacteriophage bil07, complete genome
12428	25180	31879	2.48	2.4E-02	6753635	NT	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
12530	25253	31829	1.86	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF) mRNA, complete cds
12530	25253	31807	1.86	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF) mRNA, complete cds
12693	25350		13.1	2.4E-02	AB008599.1	NT	Caenorhabditis elegans mRNA for iron-sulfur subunit of mitochondrial succinate dehydrogenase, complete cds
1895	14916		3.58	2.3E-02	W05340.1	EST_HUMAN	za84q08.r1 Soares fetal lung_NbHL19W Homo sapiens cDNA clone IMAGE:299294 5'
1907	14928		6.73	2.3E-02	U64165.1	NT	4 Homo sapiens mammary tumor-associated protein INT6 (INT6) gene, exon 4
2373	15378	28380	2.77	2.3E-02	Z74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
3749	16781	29670	5.63	2.3E-02	Z20377.1	EST_HUMAN	HSAAACADH P, Human fetal Brain Whole tissue Homo sapiens cDNA
3778	18809		0.69	2.3E-02	L23429.1	NT	Canis beta-galactosides-binding lectin (LGALS3) mRNA, 3' end

Page 164 of 545  
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4248	17264	30130	0.91	2.3E-02	L24799.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4248	17264	30131	0.91	2.3E-02	L24799.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4527	17530	30398	1.12	2.3E-02	AW899107.1	EST_HUMAN	CM4-NN0080-280400-160-b04 NN0080 Homo sapiens cDNA
4559	17568	30427	1.12	2.3E-02	BE935223.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4559	17568	30428	1.12	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4560	18405	30429	1.15	2.3E-02	AW593693.1	EST_HUMAN	xs25d08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2770671 3'
4560	18405	30430	1.15	2.3E-02	AW593693.1	EST_HUMAN	xs25d08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2770671 3'
4705	17710	30573	3.03	2.3E-02	BF026487.1	EST_HUMAN	601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5'
4705	17710	30574	3.03	2.3E-02	BF026487.1	EST_HUMAN	601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5'
5141	18136	30578	0.92	2.3E-02	AI793177.1	EST_HUMAN	q235c03.x5 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2028888 3'
5141	18136	30579	0.92	2.3E-02	AI793177.1	EST_HUMAN	q235c03.x5 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2028888 3'
5164	18156	31003	1.02	2.3E-02	AW844307.1	EST_HUMAN	RC2-CN0051-290100-011-a07 CN0051 Homo sapiens cDNA
5560	18638	31517	3.68	2.3E-02	U86303.1	NT	Caulobacter crescentus topoisomerase IV ParE subunit (parE) gene, complete cds, and propionyl-CoA carboxylase beta chain (pccB) homolog gene, partial cds
6483	19528	32706	0.5	2.3E-02	BF106464.1	EST_HUMAN	601822921R1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4042829 3'
6908	19938	33157	4.37	2.3E-02	AL161505.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17
7320	18488	31260	1.11	2.3E-02	BE141475.1	EST_HUMAN	MRO-HT0060-011099-002-c09 HT0060 Homo sapiens cDNA
7897	20794	34096	0.43	2.3E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
8456	21388	34727	5.56	2.3E-02	U63610.1	NT	Human plectin (PLEC1) gene, exons 3-32, and complete cds
9041	21970	35329	0.97	2.3E-02	AJ298105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
9041	21970	35330	0.97	2.3E-02	AJ298105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
9254	22182	35536	0.8	2.3E-02	AI686380.1	EST_HUMAN	wa78h10.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3'
9254	22182	35537	0.8	2.3E-02	AI686380.1	EST_HUMAN	wa78h10.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3'
9881	22807	35980	0.85	2.3E-02	P41996	SWISSPROT	HYPOTHETICAL 55.6 KD PROTEIN B0280.5 IN CHROMOSOME III PRECURSOR
10373	23262	36684	0.79	2.3E-02	P50532	SWISSPROT	CHROMOSOME ASSEMBLY PROTEIN XCAP-C
10533	23419	36834	1.63	2.3E-02	AE000199.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
10533	23419	36835	1.63	2.3E-02	AE000199.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
11221	24147	37598	2.04	2.3E-02	P08640	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
12214	25048		1.41	2.3E-02	AF159132.1	NT	Metapneus ensis fushi tarazu-factor 1 mRNA, complete cds
12408	25736		5.09	2.3E-02	BE278331.1	EST_HUMAN	601179589F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3540587 5'
12891	25481	31765	3.4	2.3E-02	U39394.1	NT	Streptomyces sp. alpha-1/3/4-fucosidase precursor gene, complete cds
12939	25963		3.37	2.3E-02	U11077.1	NT	Dictyostelium discoideum extracellular signal-regulated protein kinase (ERK1) mRNA, complete cds

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761	13518	26747	2.85	2.2E-02	AF018267.1	NT	Columba livia nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds
1773	14799		1.22	2.2E-02	4557448	NT	Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2) mRNA
2028	15045	28040	1.4	2.2E-02	Z82001.1	NT	S.pneumoniae pcpA gene and open reading frames
2774	15633	28759	1.24	2.2E-02	AF108633.1	NT	Mus musculus ets variant protein ER81 gene, exons 1 through 4
3496	16535		1.99	2.2E-02	AA677785.1	EST_HUMAN	nt24a04.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084782 3'
3715	16747		4.46	2.2E-02	AF083094.1	NT	Infectious bursal disease virus segment B strain IL4 VP1 gene, complete cds
3920	16948	29830	1.15	2.2E-02	AW601317.1	EST_HUMAN	PMO-BT0340-170100-004-b03 BT0340 Homo sapiens cDNA
3995	17022	29912	0.65	2.2E-02	Z74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
4726	17731		0.9	2.2E-02	P16759	SWISSPROT	HYPOTHETICAL PROTEIN UL21
6509	19553	32733	0.51	2.2E-02	BF109222.1	EST_HUMAN	7160b11.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525836 3' similar to TR:Q12899 Q12899 ACID FINGER PROTEIN. ;
7617	20352	33845	3.24	2.2E-02	AV699721.1	EST_HUMAN	AV699721 GKB Homo sapiens cDNA clone GKBAND03 3'
8943	21873	35233	1.89	2.2E-02	AL161515.2	NT	Aradopsis thaliana DNA chromosome 4, contig fragment No. 27
8943	21873	35234	1.89	2.2E-02	AL161515.2	NT	Aradopsis thaliana DNA chromosome 4, contig fragment No. 27
9368	22296	35659	0.8	2.2E-02	X79488.1	NT	P.vulgata alpha tub 2 mRNA
10210	23101	36501	2.26	2.2E-02	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10210	23101	36502	2.26	2.2E-02	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10701	23587		1.17	2.2E-02	6678140	NT	Mus musculus Sjogren syndrome antigen A1 (Ssa1), mRNA
11654	24560	38031	1.69	2.2E-02	BE797601.1	EST_HUMAN	601584309F-1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3638571 5'
12656	25329		2.8	2.2E-02	AA503553.1	EST_HUMAN	ne47h07.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:900541 3' similar to contains Alu repetitive element
442	13513		5.01	2.1E-02	AV761502.1	EST_HUMAN	AV761502 MDS Homo sapiens cDNA clone MDSADG01 5'
471	13542		6.53	2.1E-02	AF029726.1	NT	Dibutyldilium difluoride histidine kinase C (dhkC) mRNA, complete cds
1290	14323	27269	5.86	2.1E-02	U72073.1	NT	Bacillus subtilis cotKLM cluster, CotK (cotK), and spore coat protein CotM (cotM) genes, complete cds
1414	14444	27397	1.05	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1414	14444	27398	1.05	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1806	14832	27800	0.98	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1806	14832	27801	0.98	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1806	14832	27802	0.98	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1977	14995	27979	1.02	2.1E-02	AF160889.1	NT	Tegula aureolincta major acrosomal protein precursor (TMAP) mRNA, complete cds

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2048	15055	28066	0.95	2.1E-02	BE072548.1	EST_HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA
2048	15055	28067	0.95	2.1E-02	BE072548.1	EST_HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA
2624	15622	28615	1.26	2.1E-02	AA225095.1	EST_HUMAN	nc21g03.r1 NCI CGAP_Prl Homo sapiens cDNA clone IMAGE:1008820
2863	13861	26799	3.42	2.1E-02	N29269.1	EST_HUMAN	y43h07.r1 Soares melanocyte 2Nbl-H Homo sapiens cDNA clone IMAGE:264541 5'
3192	15055	28066	0.95	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA
3192	15055	28067	0.95	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA
3645	16681	28578	1.26	2.1E-02	AA461271.1	EST_HUMAN	z63b09.r1 Soares fetal N52HF8 9w Homo sapiens cDNA clone IMAGE:796121 5'
4227	17243	30111	0.72	2.1E-02	Z74293.1	NT	S cerevisiae chromosome IV reading frame ORF YDL245c
4414	17425	30287	0.97	2.1E-02	BF343655.1	EST_HUMAN	602015306F1 NCI CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4151161 5'
4554	17553	30422	2.02	2.1E-02	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2. erpC and erpD genes, complete cds; and unknown genes
4565	17573	30436	1.59	2.1E-02	A1768127.1	EST_HUMAN	wg81d11.x1 Soares NSF FB 9W OT PA P ST Homo sapiens cDNA clone IMAGE:2371509 3'
4823	17824	30693	6.16	2.1E-02	Y08501.1	NT	A.thaliana mitochondrial genome, part A
4933	17932	30791	0.69	2.1E-02	A1623432.1	EST_HUMAN	wh54a05.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384528 3'
5636	18907	32022	0.61	2.1E-02	AW379529.1	EST_HUMAN	GM4-HT0244-111199-040-h05 HT0244 Homo sapiens cDNA
7420	20119	33356	0.78	2.1E-02	BF086199.1	EST_HUMAN	QV3-GN0058-120900-329-a12 GN0058 Homo sapiens cDNA
9084	22013	36370	0.92	2.1E-02	9790238	NT	Mus musculus sorting nexin 1 (Snx1), mRNA
10034	22934	36322	0.61	2.1E-02	AA984288.1	EST_HUMAN	am33e07.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains Alu repetitive element; contains element MER11 repetitive element ;
10157	23048	36447	2.31	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10157	23048	36448	2.31	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10489	23377	36792	1.41	2.1E-02	L29324.1	NT	Streptococcus pneumoniae integrase, excisionase, repressor protein, relaxase, UmuC MucB homolog, and UmuD MucA homolog genes, complete cds; and unknown genes
10563	23449	36871	0.71	2.1E-02	AA984288.1	EST_HUMAN	am33e07.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains Alu repetitive element; contains element MER11 repetitive element ;
12638	19429		13.76	2.1E-02	Y19213.1	NT	Homo sapiens putative psihbA pseudogene for hair keratin, exons 2 to 7
13026	25567	31737	12.1	2.1E-02	AF183913.1	NT	Azospirillum brasilense major outer membrane protein OmsA precursor (omsA) gene, complete cds
18	13134	26020	0.77	2.0E-02	BF002932.1	EST_HUMAN	7g51c08.x1 NCI CGAP_Prl28 Homo sapiens cDNA clone IMAGE:3309998 3' similar to contains MER1.13
19	13135	26021	7.06	2.0E-02	AW805666.1	EST_HUMAN	MER1 repetitive element ;
278	13973	26287	3.1	2.0E-02	6753635	NT	QV4-NN0038-270400-187-h05 NN0038 Homo sapiens cDNA
315	13407	26325	2.79	2.0E-02	AA456536.1	EST_HUMAN	Mus musculus Dinb homolog 1 (E. coli) (Dinb1), mRNA
825	13880	26817	1.99	2.0E-02	6753635	NT	eat15b10.r1 Soares NhmMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
							Mus musculus Dinb homolog 1 (E. coli) (Dinb1), mRNA

Page 167 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1114	14196	27095	135.42	2.0E-02	AL096805.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 1[1p36.33] of Homo sapiens
1227	14264	27207	1.04	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1227	14264	27208	1.04	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1895	14917	27895	1.45	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
1896	14917	27896	1.45	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
2846	15835		2.16	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
3128	13134	26020	1.75	2.0E-02	BF002932.1	EST_HUMAN	7951c08.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:3309998 3' similar to contains MERT1.63
3187	16236		1.42	2.0E-02	7505474	NT	Mus musculus sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B (Sema6b), mRNA
3274	16322		1.54	2.0E-02	AF095588.1	NT	Arabidopsis thaliana C2H2 zinc finger protein FZF mRNA, complete cds
4092	17117	29995	1.44	2.0E-02	M18095.1	NT	P. vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' end
6285	18271	31119	0.65	2.0E-02	AA456538.1	EST_HUMAN	aat15b10.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
5349	18332	31180	0.98	2.0E-02	Z21088.1	EST_HUMAN	HSAAADMIITEST1, Human adult Testis tissue Homo sapiens cDNA clone CA
5370	18352		0.97	2.0E-02	BF085913.1	EST_HUMAN	GM0-GN0038-150900-548-09 GN0038 Homo sapiens cDNA
5831	18902	32017	0.41	2.0E-02	U34778.1	NT	Caenorhabditis elegans sma-2 mRNA, complete cds
6115	19174	32308	0.6	2.0E-02	L35321.2	NT	Dicystostellum discoideum class VII unconventional myosin (myoI) gene, complete cds
7982	20903	34218	0.98	2.0E-02	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (4/7)
7982	20903	34219	0.98	2.0E-02	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (4/7)
10369	23278		2.21	2.0E-02	U70408.1	NT	Japanese encephalitis virus envelope protein mRNA, partial cds
10847	23733	37156	2.12	2.0E-02	AI640342.1	EST_HUMAN	wal7b02.x1 NCI CGAP_KD11 Homo sapiens cDNA clone IMAGE:2298315 3'
11087	24019	37460	5.61	2.0E-02	Z73966.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 93/162
11810	24731	38222	2.1	2.0E-02	D88184.1	NT	Equus caballus DNA for 17alpha-hydroxylase/17,20-lyase, complete cds
12107	24948	38450	1.58	2.0E-02	10947055	NT	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
12107	24948	38451	1.58	2.0E-02	10947055	NT	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
12241	18271	31119	1.98	2.0E-02	AA456538.1	EST_HUMAN	aat15b10.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
12673	15835		1.84	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
13086	26905		6.43	2.0E-02	T80037.1	EST_HUMAN	yd04c09.r1 Soares Infant brain INIB Homo sapiens cDNA clone IMAGE:24675 5'
717	13776	26995	1.72	1.9E-02	AA572764.1	EST_HUMAN	nf16a07.s1 NCI CGAP_P11 Homo sapiens cDNA clone IMAGE:914196 similar to contains L1.11 L1 repetitive element:
1639	14670	27633	1.13	1.9E-02	P18488	SWISSPROT	EMPTY SPIRACLES HOMEOTIC PROTEIN
2053	15070	28070	3.41	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2053	15070	28071	3.41	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103

Table 4  
Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2531	15332	28533	1.27	1.9E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
2949	16001	28902	10.55	1.9E-02	AA713855.1	EST_HUMAN	nv04f05.s1 NCL_CGAP_S51 Homo sapiens cDNA clone IMAGE:1238337 3'
2994	16046	28949	2.01	1.9E-02	AV648669.1	EST_HUMAN	AV648669 GLC Homo sapiens cDNA clone GLOBLH07 3'
3304	16351		0.75	1.9E-02	AB033511.1	NT	Urdichus talpoides mitochondrial gene for cytochrome b, complete cds
3675	16708		1.04	1.9E-02	N52250.1	EST_HUMAN	y223b02.s1 Soares_multiple_sclerosis_2NBHMS Homo sapiens cDNA clone IMAGE:284331 3'
3768	16800		5.45	1.9E-02	BE738088.1	EST_HUMAN	601572682F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839564 5'
4131	17153	30030	1.86	1.9E-02	AF141940.1	NT	Myoplasma imlans Viha1 precursor (Viha1) and Viha2 precursor (Viha2) genes, partial cds
4289	17303	30171	1.76	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4289	17303	30172	1.76	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4637	17662	30530	3.58	1.9E-02	AI452999.1	EST_HUMAN	if6d04.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144551 3' similar to contains Alu repetitive element.
4851	17853		0.9	1.9E-02	AF178754.3	NT	Homo sapiens lithium-sensitive myo-inositol monophosphatase A1 (IMPAT1) gene, promoter region and partial cds
6137	15332	28533	2.44	1.9E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
5499	18578	31426	1.09	1.9E-02	AF037352.1	NT	Mus musculus T cell receptor gamma locus, TOR gamma 1 and gamma 3 gene clusters
5655	18729	31634	1.41	1.9E-02	L47572.1	NT	Meleagris gallopavo paraoxonase-2 (PON2) mRNA, complete cds
5998	19063		0.69	1.9E-02	AB019507.1	NT	Drosophila kanakid gene for glycerol-3-phosphate dehydrogenase, complete cds
7460	20400	33673	1.28	1.9E-02	U19241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
7460	20400	33674	1.28	1.9E-02	U19241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
9134	22062		1.42	1.9E-02	AL162764.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 3/7
9871	22786	36176	1.28	1.9E-02	BF316129.1	EST_HUMAN	601896130F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125482 5'
10235	23128	36528	0.55	1.9E-02	L10114.1	NT	Nicotiana tabacum type II phytochrome (phyb) gene, complete cds
10548	23434	36854	1.2	1.9E-02	BF695832.1	EST_HUMAN	601852385F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076233 5'
10647	23533	36965	0.57	1.9E-02	N39160.1	EST_HUMAN	yy48h08.s1 Soares_multiple_sclerosis_2NBHMS Homo sapiens cDNA clone IMAGE:276639 3'
10746	23632	37065	0.94	1.9E-02	D64001.1	NT	Synechocystis sp. PCC6803 complete genome, 20/27, 2539000-2644794
12438	25741	31671	3.34	1.9E-02	AF101065.1	NT	Hirudo medicinalis intermediate filament gliatin mRNA, complete cds
366	13453	26365	1	1.8E-02	AW771104.1	EST_HUMAN	hr52c06.x1 NCL_CGAP_Cot17 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element
709	13768	26984	1.12	1.8E-02	BF308122.1	EST_HUMAN	MER29 repetitive element;
1187	14226	27165	1.12	1.8E-02	X17684.1	NT	601894329F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139983 5'
2727	15720	28717	1.86	1.8E-02	AE004944.1	NT	H.francisci mRNA for myelin basic protein (MBP)
3257	16305		1.18	1.8E-02	AI805829.1	EST_HUMAN	Pseudomonas aeruginosa PA01, section 105 of 529 of the complete genome
3956	16984	29868	1.13	1.8E-02	AW879122.1	EST_HUMAN	tes2a09.x1 Soares_NFL_T_GRC_ST1 Homo sapiens cDNA clone IMAGE:2090298 3'
3956	16984	29869	1.13	1.8E-02	AW879122.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
							MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA

Page 169 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4174	17195		1.29	1.8E-02	AA861446.1	EST_HUMAN	ak24h04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1408935 3'
4537	17546	30407	1.47	1.8E-02	AW936363.1	EST_HUMAN	QV4-DT0021-301299-071-b11 DT0021 Homo sapiens cDNA
5070	18067	30917	1.71	1.8E-02	O60810	SWISSPROT	HYPOTHETICAL PROTEIN DJ845024.2
6048	19087	32878	0.63	1.8E-02	AE002518.1	NT	Neisseria meningitidis serogroup B strain MC58 section 160 of 208 of the complete genome
6048	19087	32879	0.63	1.8E-02	AE002518.1	NT	Neisseria meningitidis serogroup B strain MC58 section 160 of 208 of the complete genome
7121	20325	33589	0.91	1.8E-02	P14310	SWISSPROT	HYPOTHETICAL 7.9 KD PROTEIN IN FIXW 5'REGION
7873	20800	34103	0.45	1.8E-02	BF125690.1	EST_HUMAN	601763268F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026280 5'
7901	20800	34103	0.54	1.8E-02	BF125690.1	EST_HUMAN	601763268F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026280 5'
8708	21637	34984	0.88	1.8E-02	U37091.1	NT	Mus musculus carbonic anhydrase IV gene, complete cds
9037	21966	35325	0.87	1.8E-02	AW905327.1	EST_HUMAN	QV2-NH1073-220400-169-H09 NN1073 Homo sapiens cDNA
9078	22007	35363	1.33	1.8E-02	6578943	NT	Mus musculus microtubule-associated protein 2 (Mtap2). mRNA
10025	22025	36313	0.57	1.8E-02	BF241924.1	EST_HUMAN	601877026F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
10025	22025	36314	0.57	1.8E-02	BF241924.1	EST_HUMAN	601877026F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
10168	23059		2.33	1.8E-02	AA897543.1	EST_HUMAN	aj8209.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394921 3' similar to gb:U11672 ZINC FINGER PROTEIN 91 (HUMAN);
10565	23451	36872	1.73	1.8E-02	BE778274.1	EST_HUMAN	601463545F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866993 5'
10721	23607	37036	1.4	1.8E-02	X96833.1	NT	L. steinhals mRNA for myomodulin neuropeptide precursor
11037	23921	37363	0.59	1.8E-02	O75330	SWISSPROT	HYALURONAN MEDIATED MOTILITY RECEPTOR (INTRACELLULAR HYALURONIC ACID BINDING PROTEIN) (RECEPTOR FOR HYALURONAN-MEDIATED MOTILITY)
11037	23921	37364	0.59	1.8E-02	O75330	SWISSPROT	HYALURONAN MEDIATED MOTILITY RECEPTOR (INTRACELLULAR HYALURONIC ACID BINDING PROTEIN) (RECEPTOR FOR HYALURONAN-MEDIATED MOTILITY)
11859	23969	37405	1.96	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11859	23969	37406	1.96	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
12040	24882	38368	2.8	1.8E-02	AP000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt, position (8/7)
12052	24893	38396	3.11	1.8E-02	U62749.1	NT	Zea mays acidic ribosomal protein P2a-3 (rpp2a-3) mRNA, partial cds
13030	25720		1.93	1.8E-02	AF202180.1	NT	Plasmodium falciparum erythrocyte membrane-associated giant protein antigen 332 (Ag332) gene, partial cds
931	13983	26928	1.36	1.7E-02	BE394859.1	EST_HUMAN	601310626F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632190 5'
1813	14838	27810	2.31	1.7E-02	AW573183.1	EST_HUMAN	h34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.1 L1 repetitive element;
1813	14838	27811	2.31	1.7E-02	AW573183.1	EST_HUMAN	h34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.1 L1 repetitive element;
1894	14915		2.75	1.7E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2125	15138		10.65	1.7E-02	AB004816.1	NT	Oryctolagus cuniculus mRNA for miteugmin29, complete cds

Page 170 of 545  
Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2312	15320	28321	1.05	1.7E-02	S74186.1	NT	[microsatellite INRA41] [Ovis aries=sheep, Genomic, 361 nt, segment 1 of 2]
2688	15882		44.07	1.7E-02	7657485	NT	Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA
3041	16093	28996	0.74	1.7E-02	AI147615.1	EST_HUMAN	q22a08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1696982 3'
3571	16608		5.93	1.7E-02	AW827388.1	EST_HUMAN	hm46a04.x1 NCI_CGAP_RDF1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains
3691	16724		0.72	1.7E-02	P04929	SWISSPROT	MER19.b1 MER19 repetitive element ; HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
4265	17281		1.14	1.7E-02	AA669618.1	EST_HUMAN	ac1904.s1 Stratagene ovary (#837217) Homo sapiens cDNA clone IMAGE:859927 3' similar to contains Alu
4296	17310		2.21	1.7E-02	R02506.1	EST_HUMAN	repetitive element; contains element MER24 repetitive element ;
4564	17572	30435	1.04	1.7E-02	AI305279.1	EST_HUMAN	ye85f08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124647 5' qm08g07.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881276 3' similar to gb:X52359 ZINC
4645	17651	30516	1.58	1.7E-02	AW573183.1	EST_HUMAN	FINGER PROTEIN 30 (HUMAN);
4827	17828	30696	1.57	1.7E-02	V00641.1	NT	h34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains
4927	17926		8.83	1.7E-02	AI015076.1	EST_HUMAN	L1.1 L1 repetitive element ; Messenger RNA for anglerfish (Lophius americanus) somatostatin II
5200	18192	31034	0.85	1.7E-02	6981289	NT	ov51e02.e1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640858 3' Rattus norvegicus N-arginine dibasic convertase 1 (Nrd1), mRNA
6365	19414	32579	1.74	1.7E-02	AI769247.1	EST_HUMAN	wg35f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367113 3' similar to
6747	19781		0.49	1.7E-02	Z28383.1	NT	contains Alu repetitive element;
6861	19893	33106	1.8	1.7E-02	AI038280.1	EST_HUMAN	T_riveum (ATCC34921) simA gene for cyclosporine synthetase
7403	20102	33337	1.13	1.7E-02	AF190930.1	NT	oy65h03.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1672661 3'
7570	20506	33784	1.89	1.7E-02	8400716	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
7748	20679	33977	0.98	1.7E-02	L07899.1	NT	Homo sapiens nebulin (NEB), mRNA
8207	21113		2.17	1.7E-02	U21854.1	NT	Human apolipoprotein (a) gene, exon 1
9870	21328	34661	1.1	1.7E-02	AI010770.1	NT	Human apolipoprotein (a) gene, exon 1
10221	23112	36514	1.31	1.7E-02	AI040554.1	EST_HUMAN	Homo sapiens hypoxanthine gene, exons 1-50
12199	25034	38534	1.66	1.7E-02	5902007	NT	Caenorhabditis elegans cCAF1 protein gene, complete cds
12953	25891	31480	2.08	1.7E-02	AW903482.1	EST_HUMAN	DKFZp434i0314_r1_434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434i0314 5'
13073	25597	31729	1.63	1.7E-02	AA846926.1	EST_HUMAN	Homo sapiens serum constituent protein (MSE55), mRNA
534	13603		2.07	1.6E-02	AL021929.1	NT	GM4-NN1030-040400-130-f05 NN1030 Homo sapiens cDNA
1683	14713	27675	3.48	1.6E-02	Y18889.1	NT	oe08d04.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1385287 similar to contains element MSR1
							repetitive element ;
							Mycobacterium tuberculosis H37Rv complete genome; segment 13/162
							Treponema maltophilum flaB2, flaB3 and flhD genes for flagellin subunit proteins and CAP protein homologue



Page 171 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2264	16274	28279	1.1	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2284	16274	28280	1.1	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2600	15598	28593	1.31	1.6E-02	AJ006345.1	NT	Homo sapiens KVL071 gene
2691	15585	28694	1.32	1.6E-02	AA484872.1	EST_HUMAN	he81d08.s1 NCL CGAP_Ew1 Homo sapiens cDNA clone IMAGE:910667
2744	15737		1.42	1.6E-02	AB014534.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
3587	16624	29527	5.8	1.6E-02	AW850652.1	EST_HUMAN	IL3-C70219-160200-063-C07 CT0219 Homo sapiens cDNA
							Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
4271	17287		2.09	1.6E-02	AF110520.1	NT	QV2-PT0012-140100-030-107 PT0012 Homo sapiens cDNA
4402	17414	30281	1.14	1.6E-02	AW875407.1	EST_HUMAN	ns71f12.s1 NCL CGAP_P12 Homo sapiens cDNA clone IMAGE:1189103 similar to gb:M24902
5135	18131	30972	0.94	1.6E-02	AA653047.1	EST_HUMAN	PROSTATIC ACID PHOSPHATASE PRECURSOR (HUMAN);
5135	18131	30973	0.94	1.6E-02	AA653047.1	EST_HUMAN	ns71f12.e1 NCL CGAP_P12 Homo sapiens cDNA clone IMAGE:1189103 similar to gb:M24902
5203	18194	31036	1.06	1.6E-02	AI769132.1	EST_HUMAN	PROSTATIC ACID PHOSPHATASE PRECURSOR (HUMAN);
5434	18516	31241	0.52	1.6E-02	AI281386.1	EST_HUMAN	wg34b09.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2366969 3'
5818	18890	32003	1.29	1.6E-02	6671715	NT	qu42b09.x1 NCL CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1967417 3'
6834	19963	33184	2.06	1.6E-02	AB015281.1	NT	Mus musculus CD6 antigen (Cd6), mRNA
7261	20170	33410	0.65	1.6E-02	AB027571.1	NT	Candida albicans CaGGR3 gene, complete cds
7261	20170	33411	0.65	1.6E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
8170	21077	34407	0.86	1.6E-02	AL161508.2	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
8698	21829	34974	0.76	1.6E-02	AJ277662.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
8767	21887		2.09	1.6E-02	X05151.1	NT	Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein
10543	23429		2.79	1.6E-02	AF079794.1	NT	Human apoC-II gene for preproapolipoprotein C-II
10902	23787	37214	1.7	1.6E-02	AA572818.1	EST_HUMAN	Drosophila melanogaster enhancer of polycomb (E(Pc)) mRNA, complete cds
10902	23787	37215	1.7	1.6E-02	AA572818.1	EST_HUMAN	n118g03.s1 NCL CGAP_P11 Homo sapiens cDNA clone IMAGE:914280 similar to SW:TELO_RABIT
11347	25099	37708	2.4	1.6E-02	Z94028.1	NT	P29294 TELOKIN. [1];
11661	24567	38040	2.39	1.6E-02	AL161508.2	NT	P29294 TELOKIN. [1];
11661	24567	38041	2.39	1.6E-02	AL161508.2	NT	G.gallus microsatellite DNA (LEI0260 (=T161111))
11643	24787	38283	2.23	1.6E-02	AI373558.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
12417	16274	28279	2.57	1.6E-02	Q64176	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
							q36e10.x1 Soares_pregnant_uterus_NbhpU Homo sapiens cDNA clone IMAGE:2042442 3'
							LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)

Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12417	15274	28280	2.57	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYL ESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
775	13832		35.52	1.5E-02	8923734	NT	Homo sapiens transcription factor (HSA130894), mRNA
2157	15169	28171	3.69	1.5E-02	N39521.1	EST_HUMAN	yv27607.s1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:243925 3'
2188	15109	28204	1.21	1.5E-02	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
3108	16159	29054	1.11	1.5E-02	AJ006216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3108	16159	29055	1.11	1.5E-02	AJ006216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3788	16819	29707	0.88	1.5E-02	BF092942.1	EST_HUMAN	MR4-TN0116-080900-201-b12 TN0115 Homo sapiens cDNA
4239	17255	30121	0.83	1.5E-02	AA160987.1	EST_HUMAN	z440g10.r1 Stralagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632226 5'
5346	18329	31178	1.06	1.5E-02	4503534	NT	Homo sapiens eukaryotic translation initiation factor 4E (EIF4E) mRNA
6547	19590	32777	1.92	1.5E-02	Q08711	SWISSPROT	HYPOTHETICAL CALCIUM-BINDING PROTEIN C16B11.04 IN CHROMOSOME 1
7703	20635		1.73	1.5E-02	11467282	NT	Cyanophora paradoxa cyanelle, complete genome
7800	20729	34031	1.36	1.5E-02	11418713	NT	Homo sapiens KIAA1009 protein (KIAA1009), mRNA
8315	21220	34556	0.47	1.5E-02	AE004347.1	NT	Vibrio cholerae chromosome II, section 4 of 93 of the complete chromosome
8454	21366	34726	1.7	1.5E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
8481	21392	34734	4.2	1.5E-02	11417739	NT	Homo sapiens valyl-tRNA synthetase 2 (VARS2), mRNA
9359	22317	35679	0.88	1.5E-02	BF345554.1	EST_HUMAN	602019135F1 NC1_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4164504 5'
10001	22818		0.55	1.5E-02	AF095774.1	NT	Homo sapiens kinase-related protein isoform 1 mRNA, complete cds
10099	22948	36337	1.39	1.5E-02	D44606.1	NT	Saccharomyces cerevisiae chromosome VI plasmid GapC
10327	23216	36629	1.48	1.5E-02	R32697.1	EST_HUMAN	yh54b10.r1 Soares placenta Nb2-IP Homo sapiens cDNA clone IMAGE:133531 5'
10327	23216	36630	1.48	1.5E-02	R32697.1	EST_HUMAN	yh54b10.r1 Soares placenta Nb2-IP Homo sapiens cDNA clone IMAGE:133531 5'
11044	23928	37369	0.53	1.5E-02	BE965719.2	EST_HUMAN	601659778R1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3896226 3'
11610	24518	37998	2.52	1.5E-02	L40609.1	NT	Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds's
11650	24556	38025	1.79	1.5E-02	AL111238.1	NT	Boltyls cinerea strain T4 cDNA library under conditions of nitrogen deprivation
12616	25778		2.73	1.5E-02	AW750834.1	EST_HUMAN	RC4-CN0048-140100-011-c11 CN0049 Homo sapiens cDNA
440	13511		1.51	1.4E-02	AE002230.2	NT	Chlamydia pneumoniae AR39, section 59 of 94 of the complete genome
1145	14187	27125	3.19	1.4E-02	7706980	NT	Homo sapiens NESH protein (LOC51225), mRNA
1284	14317		1.27	1.4E-02	U32800.1	NT	Haemophilus influenzae Rd section 115 of 163 of the complete genome
1324	14358		2.43	1.4E-02	U67779.1	NT	Xenopus laevis neurogranin related 1b (X-NGNR-1b) mRNA, complete cds
1638	14568		1.2	1.4E-02	AV723785.1	EST_HUMAN	AV723785 HTB Homo sapiens cDNA clone HTBAH11 5'
3259	16307	29211	2.05	1.4E-02	AF160969.2	NT	Blifidobacterium longum Na+H+ antiporter (nhaB), cytosine deaminase, and alpha-galactosidase (aglL) genes, complete cds; and N-acetylglucosaminylxylase repressor protein (nagC/xylR) gene, partial cds
3458	16499	29402	0.79	1.4E-02	AW074212.1	EST_HUMAN	xb09409.x1 NC1_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575793 3'

Page 173 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3543	16581	29484	6.95	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3543	16581	29485	6.95	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3580	16617	29620	0.95	1.4E-02	4503628	NT	Homo sapiens coagulation factor XII (Hageman factor) (F12), mRNA
3724	16756	29644	6.32	1.4E-02	9999918	NT	Mus musculus histocompatibility 2, complement component factor B (H2-Bf), mRNA
4602	17610	30468	10.81	1.4E-02	AW962688.1	EST_HUMAN	EST1374761 IMAGE: ressequences, MAGG Homo sapiens cDNA
4602	17610	30469	10.81	1.4E-02	AW962688.1	EST_HUMAN	EST1374761 IMAGE: ressequences, MAGG Homo sapiens cDNA
4773	17778	30646	0.97	1.4E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4773	17778	30647	0.97	1.4E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4983	17982	30839	8.31	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
4983	17982	30840	8.31	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
6001	25974		0.53	1.4E-02	X91338.1	NT	H. sapiens LaSS-B pseudogene 3
6682	19718	32918	4.54	1.4E-02	AA669030.1	EST_HUMAN	nl1c04.s1 NCL_CGAP_B2 Homo sapiens cDNA clone IMAGE:1029990 3' similar to contains Alu repetitive element
6682	19718	32919	4.54	1.4E-02	AA669030.1	EST_HUMAN	nl1c04.s1 NCL_CGAP_B2 Homo sapiens cDNA clone IMAGE:1029990 3' similar to contains Alu repetitive element
8717	21648		1.59	1.4E-02	AL022073.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 88/162
9455	22383	35745	1.01	1.4E-02	M81702.1	NT	Candida boidinii methanol oxidase (AOD1) gene, complete cds
9698	22623	36001	1.12	1.4E-02	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
9936	22841	36230	2.26	1.4E-02	BE544551.1	EST_HUMAN	601078239F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464241 5'
11034	23918		0.77	1.4E-02	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
11076	23960	37396	0.54	1.4E-02	XG1308.1	NT	Z.mays Knotted-1 (Krt-1) gene
12337	25132	38166	4.93	1.4E-02	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
12660	25337		2.38	1.4E-02	AF324985.1	NT	Arabidopsis thaliana F21J9.2 mRNA, complete cds
12626	25500		1.89	1.4E-02	11426968	NT	Homo sapiens sperm associated antigen 7 (SPAG7), mRNA
1969	14987	27969	2.17	1.3E-02	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2485	15468	28467	1.07	1.3E-02	AE022445.1	NT	Neisseria meningitidis serogroup B strain MC58 section 87 of 206 of the complete genome
3260	16308	29212	2.24	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
3280	16308	29213	2.24	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
4052	17079		1.23	1.3E-02	AF169288.1	NT	Mus musculus beta-sarcoglycan gene, complete cds
							Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV19S1P, TCRBV16S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ4S1, TCRBJ1S2.>
5039	18036	30892	0.99	1.3E-02	U66061.1	NT	Rice gene for thioredoxin h, complete cds
5314	18298		0.71	1.3E-02	D26547.1	NT	

Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5426	18508	31284	1.31	1.3E-02	AL049866.2	NT	Mus musculus chromosome X contig5; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmxq28orf
5426	18508	31285	1.31	1.3E-02	AL049866.2	NT	Mus musculus chromosome X contig5; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmxq28orf
6405	19453	32625	1.35	1.3E-02	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
6430	19486	32662	0.83	1.3E-02	M62962.1	NT	C. reinhardtii ribulose 1,5-bisphosphate carboxylase/oxygenase activase mRNA, complete cds
7298	18487	31287	1.64	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
7298	18487	31288	1.64	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
8012	20929	34247	4.84	1.3E-02	AI031593.1	EST_HUMAN	ov06g05.x1 Soares, parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1646072 3' similar to contains Alu repetitive element;
8418	21321	34654	0.48	1.3E-02	AF153980.1	NT	Homo sapiens exostosin-like protein 1 (EXTL1) gene, exons 2 through 11, and complete cds
9051	21090	35337	1.97	1.3E-02	AF156981.1	NT	Homo sapiens human endogenous retrovirus W gagC3.37 (3 gag) gene, complete cds
10703	23589	37016	2.22	1.3E-02	M63707.1	NT	Mouse kidney androgen-regulated protein (KAP) gene, complete cds
10771	23657	37086	0.84	1.3E-02	AE001304.1	NT	Chlamydia trachomatis section 31 of 87 of the complete genome
11430	24346	37790	3.79	1.3E-02	AW268593.1	EST_HUMAN	x34e03.x1 Soares_NFL_T_GBC_ST Homo sapiens cDNA clone IMAGE:2815036 3'
11430	24346	37791	3.79	1.3E-02	AW268593.1	EST_HUMAN	x34e03.x1 Soares_NFL_T_GBC_ST Homo sapiens cDNA clone IMAGE:2815036 3'
12318	25914		2.51	1.3E-02	X51780.1	NT	Yeast ABP1 gene for actin binding protein
12788	25397		1.86	1.3E-02	Q633069	NT	Human herpesvirus 6S, complete genome
12831	25712		74.42	1.3E-02	AF152238.1	NT	Homo sapiens V1b vasopressin receptor (VPR3) gene, complete cds
227	13325		16.45	1.2E-02	X87344.1	NT	H. sapiens DMA, DMB, HLA-21, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
375	13461	26376	2.66	1.2E-02	AA059299.1	EST_HUMAN	z165g01.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element L1 repetitive element;
475	13548	26466	1.51	1.2E-02	P38898	SWISSPROT	HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3 REGION
762	13819	26748	10.78	1.2E-02	AI183522.1	EST_HUMAN	qdb8e12.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1734670 3' similar to contains L1.t1 L1 repetitive element;
2190	15201	28206	1.98	1.2E-02	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2467	15470	28470	1.63	1.2E-02	AW172350.1	EST_HUMAN	x37e09.x1 Soares_NFL_T_GBC_ST Homo sapiens cDNA clone IMAGE:2659432 3'
2508	15507	28509	1.5	1.2E-02	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
2520	15521	28524	1.29	1.2E-02	BE538310.1	EST_HUMAN	601088406F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454608 5'
2520	15521	28525	1.29	1.2E-02	BE538310.1	EST_HUMAN	601088406F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454608 5'
2682	15470	28470	1.85	1.2E-02	AW172350.1	EST_HUMAN	x37e09.x1 Soares_NFL_T_GBC_ST Homo sapiens cDNA clone IMAGE:2659432 3'
3148	16198		8.7	1.2E-02	AA075418.1	EST_HUMAN	zm88e03.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:645020 5'

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3331	16377	29277	2.38	1.2E-02	R62805.1	EST_HUMAN	y11b08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138903 3'
4990	17989	30846	1.05	1.2E-02	6754367	NT	Mus musculus interferon regulatory factor 5 (Irif5), mRNA
5025	18022	30860	2.33	1.2E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary hemochromatosis (H1A-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5172	18164		1.62	1.2E-02	AB019786.1	NT	Cynops pyrrhogaster CpUq1T mRNA, partial cds
6219	18209	31065	2.09	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
5883	18952		0.47	1.2E-02	AA759018.1	EST_HUMAN	ai29f10.s1 Soares testis_NHT Homo sapiens cDNA clone 1344235 3'
5959	19026	32146	2.02	1.2E-02	D78589.1	NT	Rana rugosa mRNA for calcitriol, complete cds
6355	19404	32571	0.65	1.2E-02	AF045555.1	NT	Homo sapiens wbscr1 (WBSQR1) and wbscr5 (WBSCR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
7351	20347	33615	5.06	1.2E-02	AF175412.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 2, 3, 4, and 5
7672	20606	33905	1.09	1.2E-02	H02197.1	EST_HUMAN	y34h12.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150695 3'
7696	20628	33927	11.66	1.2E-02	AV732093.1	EST_HUMAN	AV732093 HTF Homo sapiens cDNA clone HTFBJC09 5'
7986	20907	34223	0.57	1.2E-02	BF216650.1	EST_HUMAN	601882949F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095253 5'
8576	21507	34852	2.56	1.2E-02	Q11205	SWISSPROT	CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ALPHA 2,3-ST) (GAL-NAC8S) (GAL-BETA-1,3-GALNAC-ALPHA-2,3-SIALYLTRANSFERASE) (ST3GALA.2) (SIAT4-B)
8705	21636	34982	0.58	1.2E-02	R68831.1	EST_HUMAN	y43f06.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:142019 3'
8770	21700	35045	1.36	1.2E-02	AF193812.1	NT	Homo sapiens fringe protein mRNA, partial cds
8770	21700	35046	1.36	1.2E-02	AF193812.1	NT	Homo sapiens fringe protein mRNA, partial cds
9447	22375		0.9	1.2E-02	I76987.1	EST_HUMAN	y672c08.s1 Soares fetal liver spleen tNfLS Homo sapiens cDNA clone IMAGE:113774 3'
10165	23056	36455	2.49	1.2E-02	AB031013.1	NT	Norwalk-like virus genogroup 2 gene for capsid protein, complete cds
10196	23087	36488	1.4	1.2E-02	AJ246003.1	NT	Homo sapiens Spast gene for spastin protein
12938	23506		5.97	1.2E-02	C18119.1	EST_HUMAN	C18119 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone GEN:557308 5'
1296	14329	27275	1.49	1.1E-02	AA070394.1	EST_HUMAN	zm69e11.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:530924 3'
1735	14762	27733	1.22	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
2052	15069	28069	4.39	1.1E-02	BF345283.1	EST_HUMAN	602018037F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4163808 5'
2920	15973		4.58	1.1E-02	N99523.1	EST_HUMAN	za40e05.r1 Soares fetal liver spleen tNfLS Homo sapiens cDNA clone IMAGE:295040 5'
3584	16621	29625	2.58	1.1E-02	A1653508.1	EST_HUMAN	tq95b10.x1 NCI_CGAP_O123 Homo sapiens cDNA clone IMAGE:2216539 3' similar to SW_XPF_HUMAN
4200	17219		0.71	1.1E-02	AW813796.1	EST_HUMAN	Q92889 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL; RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA

Page 176 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4944	17943	30801	2.43	1.1E-02	AL048383.2	EST_HUMAN	DKFZp586E0924_s1_586 (synonym: hufe1) Homo sapiens cDNA clone DKFZp586E0924
6389	19438	32606	0.84	1.1E-02	U66480.1	NT	Bacillus subtilis SpoVK (spoVK), YnaA (ynaA), YnaB (ynbB), YnaC (ynbC), YnaD (ynbD), YnaE (ynbE), YnaF (ynbF), YnaG (ynbG), YnaH (ynbH), YnaI (ynbI), YnaJ (ynbJ), YnaK (ynbK), YnaL (ynbL), YnaM (ynbM), YnaN (ynbN), YnaO (ynbO), YnaP (ynbP), YnaQ (ynbQ), YnaR (ynbR), YnaS (ynbS), YnaT (ynbT), YnaU (ynbU), YnaV (ynbV), YnaW (ynbW), YnaX (ynbX), YnaY (ynbY), YnaZ (ynbZ)
8040	20954	34269	2.83	1.1E-02	BE149611.1	EST_HUMAN	RC1-HT0256-100300-016-h07 HT0256 Homo sapiens cDNA
8316	21221	34567	0.88	1.1E-02	9631294	NT	Melanoplus sanguinipes entomopoxvirus, complete genome
8832	21762	35108	0.53	1.1E-02	P80394	SWISSPROT	METALLOTHIONEIN (MT-1/MT-2)
8832	21762	35108	0.53	1.1E-02	P80394	SWISSPROT	METALLOTHIONEIN (MT-1/MT-2)
9199	22127	35483	0.7	1.1E-02	AW966160.1	EST_HUMAN	QV3-BN0045-220300-128-h02 BN0045 Homo sapiens cDNA
9381	22309	35670	0.79	1.1E-02	C04803.1	EST_HUMAN	C04803 Human heart cDNA (Ynakamura) Homo sapiens cDNA clone 3NHC4040
9459	22387	35750	7.8	1.1E-02	Q61982	SWISSPROT	NEUROGENIC LOCUS NOTCH 3 PROTEIN
10439	23328	36748	2.31	1.1E-02	AA092578.1	EST_HUMAN	zn24e01.r1 Stratigene neuroepithelium NT2PRAMI 937234 Homo sapiens cDNA clone IMAGE:548328 5'
10596	23492	36911	5.32	1.1E-02	AA314665.1	EST_HUMAN	EST166494 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end
11417	24333	37782	2.52	1.1E-02	11435505	NT	Homo sapiens T-box 5 (TBX5), mRNA
12281	25095		3.66	1.1E-02	AA668239.1	EST_HUMAN	ab77f11.s1 Stratigene fetal retina 837202 Homo sapiens cDNA clone IMAGE:853005 3' similar to contains
7	13122	26010	7.5	1.0E-02	AW846120.1	EST_HUMAN	Alu repetitive element
1545	14576	27536	1.31	1.0E-02	AA366128.1	EST_HUMAN	MR3-CT0176-111099-003-e10 CT0176 Homo sapiens cDNA
2607	15605		1.97	1.0E-02	AA806389.1	EST_HUMAN	CM2-HT0177-041099-017-h12 HT0177 Homo sapiens cDNA
3139	16189	29082	3.21	1.0E-02	BE835556.1	EST_HUMAN	oc22h08.s1 NCJ CGAP GCB1 Homo sapiens cDNA clone IMAGE:1350495 3'
3307	16354	29266	0.99	1.0E-02	BE968699.1	EST_HUMAN	RCO-FN0025-250500-021-c02 FN0025 Homo sapiens cDNA
3567	16504		0.75	1.0E-02	AW845621.1	EST_HUMAN	60184956/RT NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933688 3'
3950	16978	29882	0.66	1.0E-02	AI065086.1	EST_HUMAN	MR0-CT0060-081099-003-h10 CT0060 Homo sapiens cDNA
4807	17615	30476	0.67	1.0E-02	Q61982	SWISSPROT	HA0921 Human fetal liver cDNA library Homo sapiens cDNA
4805	17906	30672	0.91	1.0E-02	AV696614.1	EST_HUMAN	NEUROGENIC LOCUS NOTCH 3 PROTEIN
4889	17888	30763	5.61	1.0E-02	6793521	NT	AV696614 GK Homo sapiens cDNA clone GKCDG05 5'
4957	17955	30813	5.9	1.0E-02	R96567.1	EST_HUMAN	Mus musculus corticotropin releasing hormone receptor 2 (Chr12), mRNA
5142	18137	30980	0.69	1.0E-02	Lo5932.1	NT	yq54h01.r1 Soares fetal liver spleen 'NFLS' Homo sapiens cDNA clone IMAGE:199633 5'
5601	18677	31555	0.84	1.0E-02	H82681.1	EST_HUMAN	Human glycoprotein hormone alpha-subunit (GCA) gene, 5' flank
5953	19020	32140	0.67	1.0E-02	AF309388.1	NT	yq56h11.r1 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:235941 5'
6354	19403	32570	1.17	1.0E-02	AF257303.1	NT	Mus musculus transcription complex subunit NF-ATc4 (Nfatc4) gene, exons 1 and 2
6422	19469	32642	2.64	1.0E-02	AW577113.1	EST_HUMAN	Mus musculus synaptotagmin II (Syn2) gene, complete cds
6422	19469	32643	2.64	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-h01 BT0356 Homo sapiens cDNA
6422	19469	32643	2.64	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-h01 BT0356 Homo sapiens cDNA

Page 177 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7067	20273	33528	1.52	1.0E-02	Z29842.1	NT	Z.mays U3snRNA pseudogene
9929	22834	36222	8.21	1.0E-02	BF036331.1	EST_HUMAN	601459570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5'
9929	22834	36223	8.21	1.0E-02	BF036331.1	EST_HUMAN	601459570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5'
11710	24612		2.1	1.0E-02	AF157559.1	NT	Citridia fasciculata 27 kDa guide RNA-binding protein mRNA, complete cds, mitochondrial product
							ig55h07.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2112733 3' similar to gb:X15183_cde1 HEAT SHOCK PROTEIN HSP 90-ALPHA (HUMAN); contains Alu repetitive element; contains element MERS
11739	24641		1.41	1.0E-02	AI417961.1	EST_HUMAN	repetitive element
11805	24727	38219	1.89	1.0E-02	AV760016.1	EST_HUMAN	AV760016 MDS Homo sapiens cDNA clone MDSBDC10 5'
12355	25971		1.97	1.0E-02	Q62203	SWISSPROT	SPICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
12409	25756	31572	3.12	1.0E-02	AW935521.1	EST_HUMAN	RC2-DT0007-120200-016-h02.DT0007 Homo sapiens cDNA
12422	25805		4.23	1.0E-02	S70330.1	NT	Homo sapiens renal dipeptidase (RDP) gene, complete cds
12917	26855		2.94	1.0E-02	X62654.1	NT	H.sapiens gene for Me491/CD83 antigen
918	13970	26917	1.44	9.0E-03	AI796126.1	EST_HUMAN	wh4209.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2383433 3' similar to contains element
1291	14324		1.51	9.0E-03	BE781889.1	EST_HUMAN	MER22 MER22 repetitive element
2418	15422	28423	2.29	9.0E-03	AL161559.2	NT	601470242F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3873346 5'
2427	15431	28432	1.25	9.0E-03	AF099934.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
2950	16002	28903	1.06	9.0E-03	AI251744.1	EST_HUMAN	Mus musculus MHC class III protein RPI1 (Rp1) mRNA, partial cds
2950	16002	28904	1.08	9.0E-03	AI251744.1	EST_HUMAN	qh90709.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
3693	16002	28903	0.74	9.0E-03	AI251744.1	EST_HUMAN	qh90709.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
3693	16002	28904	0.74	9.0E-03	AI251744.1	EST_HUMAN	qh90709.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
3736	16768	29654	0.83	9.0E-03	J05184.1	NT	S.acidocaldarius thermophilin gene, complete cds
6380	18362	31202	0.91	9.0E-03	AI278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
6021	19083		1.01	9.0E-03	AI809792.1	EST_HUMAN	wf77704.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361631 3'
6920	19950		4.43	9.0E-03	BE745988.1	EST_HUMAN	601573438F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834752 5'
7872	20799	34102	0.59	9.0E-03	AI242219.1	EST_HUMAN	qh87612.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853974 3'
7891	20817	34123	0.9	9.0E-03		NT	Homo sapiens hypothetical protein FLJ10650 (FLJ10650), mRNA
8455	21387		0.64	9.0E-03	AL036991.1	EST_HUMAN	DKFZp434L0412_r1 434 (synonym: hsc3) Homo sapiens cDNA clone DKFZp434L0412 5'
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-40, and partial cdo, alternatively spliced
8924	21754		0.59	9.0E-03	AF223391.1	NT	COLLAGEN ALPHA 1(V) CHAIN PRECURSOR
10376	23265	36687	1.71	9.0E-03	P20908	SWISSPROT	COLLAGEN ALPHA 1(V) CHAIN PRECURSOR
11424	24340		2.36	9.0E-03	Y18000.1	NT	Homo sapiens NF2 gene
11451	24367	37817	1.6	9.0E-03	BE395380.1	EST_HUMAN	601310881F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632181 5'

Page 178 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit --BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12079	24920	38421	1.47	9.0E-03	L11144.1	NT	Homo sapiens preprogalanin (GAL1) gene, exons 1, 2, and 3
12079	24920	38422	1.47	9.0E-03	L11144.1	NT	Homo sapiens preprogalanin (GAL1) gene, exons 1, 2, and 3
12545	25972		1.93	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-291299-001-c09 HT0452 Homo sapiens cDNA
12745	25995		23.57	9.0E-03	BE346385.1	EST_HUMAN	hw17b09.x1 NCL CGAP Lu24 Homo sapiens cDNA clone IMAGE:3183161 3'
13014	25581		33.84	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-291299-001-c09 HT0452 Homo sapiens cDNA
							zh30e03.s1 Scores_pihuel_gland_N3HPG Homo sapiens cDNA clone IMAGE:413596 3' similar to contains
524	13594		2.38	8.0E-03	AA723007.1	EST_HUMAN	Alu repetitive element
1016	14066	27009	23.63	8.0E-03	AF106956.1	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
2172	15184	28189	1.85	8.0E-03	AL163283.2	NT	Homo sapiens chromosome 21 segment HS27C083
							RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
2584	15583	28575	1.03	8.0E-03	P10266	SWISSPROT	ENDONUCLEASE
3412	16454	29360	1.04	8.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
3743	16775	29862	1.75	8.0E-03	P32644	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
3743	16775	29863	1.75	8.0E-03	P32644	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
4355	17369	30233	1.16	8.0E-03	BE840049.1	EST_HUMAN	QV0-FN0181-140700-304-g10 FN0181 Homo sapiens cDNA
4480	17501	30384	5.73	8.0E-03	BF363327.1	EST_HUMAN	GM4-NN0119-300600-223-b05 NN0119 Homo sapiens cDNA
4830	17831	30700	0.71	8.0E-03	P03181	SWISSPROT	HYPOTHETICAL BHLF1 PROTEIN
4830	17831	30701	0.71	8.0E-03	P03181	SWISSPROT	HYPOTHETICAL BHLF1 PROTEIN
5343	18326	31175	1.07	8.0E-03	U02970.1	NT	Prototheca wickerhamii 283-11 complete mitochondrial DNA
							Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, lapasin, RaGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and
5713	18786	31717	4.02	8.0E-03	AF110520.1	NT	RPS18 genes, complete cds; Sacm21 gene, partial>
6440	25648	32663	1.26	8.0E-03	AP000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position (2/7)
7054	20080	33313	4.22	8.0E-03	P55677	SWISSPROT	PROBABILE PEPTIDASE Y4NA
7248	20157		1.2	8.0E-03	V01109.1	NT	Human BK virus (strain MM) genome. (Closely related to SV40.)
7574	20510	33788	1.71	8.0E-03	M17197.1	NT	A.californica (marine gastropod mollusc) neurotrophin gene (bag cell), exon 1, 5' end
7972	20894		1.76	8.0E-03	AB039287.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
							BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
9440	22368	35730	0.76	8.0E-03	P98160	SWISSPROT	PRECURSOR (HSPG) (PERLECAN) (PLC)
9467	22396	35757	3.64	8.0E-03	AW808602.1	EST_HUMAN	MR1-ST0111-111199-011-H08 ST0111 Homo sapiens cDNA
9531	22458	35821	0.94	8.0E-03	9789956	NT	Mus musculus fucosyl 2 (human) (Fuc2), mRNA
10455	23443		6.49	8.0E-03	BE086509.1	EST_HUMAN	QV1-BT0677-040400-131-g03 BT0677 Homo sapiens cDNA
11205	24131	37578	1.76	8.0E-03	BE788441.1	EST_HUMAN	601475519F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3878405 5'
11423	24339		2.75	8.0E-03	Z49632.1	NT	S.cerevisiae chromosome X reading frame ORF YJR152w



Page 179 of 545  
Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Database Source	Top Hit Descriptor
12137	24977	38478	4.04	8.0E-03	AF064589.1	Homo sapiens melanoma-associated antigen (IMAGE-C1) gene, complete cds
12291	25102		2.46	8.0E-03	M69035.1	Oryctolagus cuniculus eIF-2a kinase mRNA, complete cds
12334	25130		5.42	8.0E-03	AB038161.1	Homo sapiens ABCG1 gene for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1), complete cds
718	13776	26696	9.8	7.0E-03	AF097183.1	Cryptosporidium parvum HC-10 gene, complete cds
718	13776	26697	9.8	7.0E-03	AF097183.1	Cryptosporidium parvum HC-10 gene, complete cds
1003	14052	26998	3.55	7.0E-03	AF243376.1	Glycine max glutathione S-transferase GST 21 mRNA, partial cds
1143	14185	27123	2.85	7.0E-03	AV731712.1	AV731712 HTF Homo sapiens cDNA clone HTFAZF10 5'
1391	14422		1.34	7.0E-03	Q61060	FORHEAD BOX PROTEIN D3 (HNF3/TFH TRANSCRIPTION FACTOR GENESIS) (HEPATOCYTE NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2) (HNF-2)
1422	14453	27407	5.81	7.0E-03	AA68298.1	ab79609.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853145 3'
1522	14553	27514	3.36	7.0E-03	AW303599.1	xx21b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813739 3'
2274	16920	28292	1.99	7.0E-03	P04929	HISTIDINE RICH GLYCOPROTEIN PRECURSOR
3631	16861	29744	0.97	7.0E-03	AW444463.1	UI-H-B13-akb-e-10-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733601 3'
3880	16909	29790	0.89	7.0E-03	AF196344.1	Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds
4105	16861	29744	0.7	7.0E-03	AW444463.1	UI-H-B13-akb-e-10-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733601 3'
4709	17714		1.02	7.0E-03	AW630888.1	hh69a05.y1 NCI_CGAP_GL1 Homo sapiens cDNA clone IMAGE:2869936 5'
5110	18107		1.88	7.0E-03	AL183278.2	Homo sapiens chromosome 21 segment HS21C078
5334	18318	31168	0.96	7.0E-03	AI970415.1	wr10b02.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2481099 3' similar to contains Alu repetitive element; contains element LTR5 repetitive element;
6031	19093		0.6	7.0E-03	H71106.1	yr82g01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211824 5' similar to gb:X14723 CLUSTERIN PRECURSOR (HUMAN);
6350	25646		5.23	7.0E-03	AW861059.1	RC1-CT0286-050400-018-c08 CT0286 Homo sapiens cDNA
6569	19810	32795	1.96	7.0E-03	W68251.1	zd33f10.r1 Soares_Fetal_Heart_NBHH19W Homo sapiens cDNA clone IMAGE:342475 5'
6816	19849	33059	2.87	7.0E-03	AA327129.1	EST30874 Colon I Homo sapiens cDNA 5' end
6846	19878	33092	0.93	7.0E-03	BE857385.1	7g34b10.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3308347 3' similar to TR:Q13387
7438	20180	33423	1.98	7.0E-03	BE028133.1	Q13387 HYPOPHYSAL PROTEIN 384D8_2; contains TAR1;2 TAR1 TAR1 repetitive element;
7943	20865	34176	5.7	7.0E-03	Z35838.1	CM2-CT0478-230800-347-b11 CT0478 Homo sapiens cDNA
7943	20865	34177	5.7	7.0E-03	Z35838.1	S.cerevisiae chromosome II reading frame ORF YBL077w
8430	21362	34701	0.57	7.0E-03	AJ229043.1	S.cerevisiae chromosome II reading frame ORF YBL077w
8430	21362	34702	0.57	7.0E-03	AJ229043.1	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
8689	21620	34692	3.04	7.0E-03	BE175687.1	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3

Page 180 of 545  
Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9933	22838		0.76	7.0E-03	AF111169.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes y49c10.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246066 3' similar to contains Alu repetitive element;
10122	23013	36410	0.87	7.0E-03	N52378.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10242	23133	36536	2.8	7.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10242	23133	36537	2.9	7.0E-03	P48982	SWISSPROT	AV687379 GK Homo sapiens cDNA clone GKAP007 5'
10795	23681		1.12	7.0E-03	AV687379.1	EST_HUMAN	wc37609.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2320840 3'
10965	23849		0.97	7.0E-03	AI799734.1	EST_HUMAN	Bos taurus mRNA for NDP52, complete cds
11266	24189	37638	2.46	7.0E-03	AB008852.1	NT	Homo sapiens partial MUC5B gene, exon 1-29
11340	24259	37698	1.65	7.0E-03	AJ004862.1	NT	Homo sapiens partial MUC5B gene, exon 1-29
11340	24259	37699	1.65	7.0E-03	AJ004862.1	NT	Homo sapiens partial MUC5B gene, exon 1-29
12795	25422		1.53	7.0E-03	BE263253.1	EST_HUMAN	601145154F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3180478 5'
12881	25478		1.96	7.0E-03	Y17455.1	NT	Homo sapiens LSPR2 gene, penultimate exon
13003	25955		2.11	7.0E-03	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
1268	14303	27250	8.83	6.0E-03	AW511148.1	EST_HUMAN	hd22805.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2810224 3' similar to SW:FXR_HUMAN 075469 ORPHAN NUCLEAR RECEPTOR FXR ;
1268	14303	27251	8.83	6.0E-03	AW511148.1	EST_HUMAN	hd22805.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2810224 3' similar to SW:FXR_HUMAN 075469 ORPHAN NUCLEAR RECEPTOR FXR ;
2933	15986	28884	4.43	6.0E-03	AA759135.1	EST_HUMAN	ah78e11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3'
2933	15986	28885	4.43	6.0E-03	AA759135.1	EST_HUMAN	ah78e11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3'
3291	16338		2.68	6.0E-03	HT5690.1	EST_HUMAN	y77h04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211351 5'
3350	16396		1.02	6.0E-03	AF190338.1	NT	Nobiscus sp. cytochrome c oxidase subunit II gene, partial cds; mitochondrial gene for mitochondrial product Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, septaplerin reductase and vasotocin genes, complete cds
3440	16481	29388	0.97	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, septaplerin reductase and vasotocin genes, complete cds
3440	16481	29389	0.97	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, septaplerin reductase and vasotocin genes, complete cds
3605	16842		1.36	6.0E-03	W37985.1	EST_HUMAN	zr13a11.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:322172 5'
3728	16760	28647	2.47	6.0E-03	BF510986.1	EST_HUMAN	UJH-B14-aprin-c-06-O-U.s1 NCL CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3087754 3'
3844	16873	29756	1.05	6.0E-03	6764029	NT	Mus musculus glucosamine-6-phosphate deaminase (Gnpl), mRNA
3997	17024	29914	0.65	6.0E-03	AW847284.1	EST_HUMAN	RC0-CT0204-240699-021-b10 CT0204 Homo sapiens cDNA
4040	17067		1.34	6.0E-03	BE250108.1	EST_HUMAN	600942904F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859513 5'
4322	17336	30200	1.36	6.0E-03	AF026272.1	NT	Babesia bigemina RAP-1c (rap-1c) gene, complete cds, and YJRO70c-like protein (YJRO70c-like) gene, partial cds
4433	17444		0.92	6.0E-03	N58946.1	EST_HUMAN	W62h10.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:278179 3'

Page 181 of 545  
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## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4471	17482		2.1	6.0E-03	A016833.1	EST_HUMAN	ov33c11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1639124 3'
4808	17809	30875	8.44	6.0E-03	AA324242.1	EST_HUMAN	EST127116 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
6265	18251		1.08	6.0E-03	L34170.1	NT	Human germline UBETL gene similar to the gene for ubiquitin-activating enzyme, exons 1-22
6274	18280	31112	1.05	6.0E-03	A62527.1	EST_HUMAN	wb61b12.x1 NCJ_CGAP_G06 Homo sapiens cDNA clone IMAGE:2310143 3'
6340	18323	31172	0.86	6.0E-03	AA88972.1	EST_HUMAN	ag95g08.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1404266 3'
6393	25647	32608	0.84	6.0E-03	9627521	NT	Varicella virus, complete genome
7128	20332	33596	0.79	6.0E-03	O14994	SWISSPROT	SYNAPSIN III
7175	18447	31316	0.69	6.0E-03	BE253748.1	EST_HUMAN	801112333F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3353172 5'
7620	20555	33848	0.42	6.0E-03	AA259442.1	EST_HUMAN	EST111949 Uterus tumor I Homo sapiens cDNA 5' end
7620	20555	33849	0.42	6.0E-03	AA259442.1	EST_HUMAN	EST111949 Uterus tumor I Homo sapiens cDNA 5' end
7620	20555	33849	0.42	6.0E-03	AA259442.1	EST_HUMAN	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-10 and complete cds
8095	21007	34332	0.7	6.0E-03	AF128894.1	NT	RAS-RELATED PROTEIN RAP-2B
8308	21212	34549	0.61	6.0E-03	P17964	SWISSPROT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
8359	21264	34599	0.49	6.0E-03	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
8440	21372	34713	14.27	6.0E-03	A033980.1	EST_HUMAN	ov13a04.x1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1646670 3' similar to contains MER10.b1 MER10 repetitive element
8552	21483	34824	2.83	6.0E-03	AW789337.1	EST_HUMAN	RCQ-LM0051-210300-032-g02 UM0051 Homo sapiens cDNA
8624	21555		1.74	6.0E-03	BF038198.1	EST_HUMAN	601454915F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858626 5'
10083	22876	36264	9.14	6.0E-03	D10548.1	NT	Stabacute sclerosing panencephalitis (SSPE) virus mRNA for fusion protein
10546	23432		2.49	6.0E-03	A432961.1	EST_HUMAN	h22c02.x1 NCJ_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131202 3' similar to SW/R13A_HUMAN
10658	23544	36978	1.14	6.0E-03	AJ011849.1	NT	P-40429 60S RIBOSOMAL PROTEIN L13A
10785	23671		0.88	6.0E-03	AF084555.1	NT	Bacillus subtilis fenD gene
10889	23774	37200	0.82	6.0E-03	XG8366.1	NT	Homo sapiens okadaic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds
11185	24111	37559	1.71	6.0E-03	AW982164.1	EST_HUMAN	M.thermophilum complete plasmid pFV1 DNA
11250	24174		2.31	6.0E-03	11545814	NT	EST1974237 MAGE resequences, MAGE Homo sapiens cDNA
11420	24336		5.69	6.0E-03	U14556.1	NT	Homo sapiens hypothetical zinc finger protein FLJ14011 (FLJ14011), mRNA
11421	24337	37785	4.02	6.0E-03	BE737895.1	EST_HUMAN	Homo sapiens hypothetical zinc finger protein mRNA, complete cds
12394	25168		2.77	6.0E-03	AF010496.1	NT	Mus musculus zinc-finger protein mRNA, complete cds
12504	25742		7.19	6.0E-03	AE000833.1	NT	Mus musculus zinc-finger protein mRNA, complete cds
12577	25796		2.38	6.0E-03	U30790.1	NT	Rhodobacter capsulatus strain S81003, partial genome
12627	25310		1.75	6.0E-03	Q82209	SWISSPROT	Methanobacterium thermoautotrophicum from bases 429182 to 450296 (section 30 of 148) of the complete genome
						NT	Pneumocystis carinii f. sp. retii guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
						NT	SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN)

Page 182 of 545  
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12898	25487		2.9	6.0E-03	BE788019.1	EST_HUMAN	601482621F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3885388 5'
12914	25497		1.89	6.0E-03	AJ245480.1	NT	Brassica napus sig gene for S-locus glycoprotein, cultivar T2
228	13326	28243	4.89	5.0E-03	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IIP2, LMP2, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
692	13753	26669	1.93	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
692	13753	26670	1.93	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
693	13753	26669	2.31	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
693	13753	26670	2.31	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
1130	14181	27119	1.03	5.0E-03	AJ010457.1	EST_HUMAN	Arabisopsis thaliana mRNA for DEAD box RNA helicase, RH3
1590	14921		1.11	5.0E-03	AH38977.1	NT	q476005.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1735689 3'
2730	15723	28719	2.35	5.0E-03	AB033006.1	NT	Homo sapiens mRNA for KIAA1180 protein, partial cds
2978	16030	28932	0.79	5.0E-03	BE266057.1	EST_HUMAN	601194796F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538799 5'
3181	16231	29126	5.03	5.0E-03	T87623.1	EST_HUMAN	yc81109.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:22395 3'
3198	16246		2.2	5.0E-03	AL161491.2	NT	Arabisopsis thaliana DNA chromosome 4, contig fragment No. 3
3208	16256	29154	1.43	5.0E-03	R71794.1	EST_HUMAN	Arabisopsis thaliana DNA chromosome 4, contig fragment No. 3
3322	16368		0.97	5.0E-03	AJ297957.1	NT	Arabisopsis thaliana DNA chromosome 4, contig fragment No. 3
3784	16796	29685	6.51	5.0E-03	AF147449.2	NT	Homo sapiens partial LMD1 gene for LIM domains containing protein 1B (ponB) gene, complete cds
3822	16852	29736	0.71	5.0E-03	U38914.1	NT	Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (ponB) gene, complete cds
4026	17053	29943	1.09	5.0E-03	X68366.1	NT	Citrus sinensis seed storage protein cDNA clone IMAGE:155666 3'
4055	17092		1.95	5.0E-03	AA299675.1	EST_HUMAN	M. thermophilum complete plasmid pFV1 DNA
4408	17420	30284	0.84	5.0E-03	H78355.1	EST_HUMAN	EST12218 Uterus tumor 1 Homo sapiens cDNA 5' end
4410	16852	29736	0.99	5.0E-03	U38914.1	NT	EST12218 Uterus tumor 1 Homo sapiens cDNA 5' end
4718	17723	30585	0.92	5.0E-03	AJ131016.1	NT	yc76g10.r1 Soares fetal liver spleen 1N1B Homo sapiens cDNA clone IMAGE:240066 5'
						NT	Citrus sinensis seed storage protein cDNA clone IMAGE:240066 5'
						NT	Homo sapiens SGL gene locus
4832	17833	30703	1.53	5.0E-03	AJ752367.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
5045	16042	30898	1.1	5.0E-03	P16285	SWISSPROT	SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS)
6006	19070	32196	5.58	5.0E-03	P35500	SWISSPROT	SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN)

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6279	19330	32496	2.44	5.0E-03	O00507	SWISSPROT	PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-Y (UBIQUITIN THIOLESTERASE FAF-Y) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF-Y) (DEUBIQUITINATING ENZYME FAF-Y) (FAT FACETS PROTEIN RELATED, Y-LINKED) (UBIQUITIN-SPECIFIC PROTEASE 9, Y CHROMOSOME)
6316	19366		0.99	5.0E-03	AE002234.2	NT	Chlamydomonas reinhardtii AR39, section 82 of 94 of the complete genome
6879	19909		7.95	5.0E-03	BE3000391.1	EST_HUMAN	600944564T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960871 3'
7164	19436	31337	6.52	5.0E-03	AB025024.1	NT	Mus musculus AMD1 gene for S-adenosylmethionine decarboxylase, complete cds
7391	20090		0.97	5.0E-03	AB038287.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
7447	20388	33658	2.03	5.0E-03	6753651	NT	Mus musculus dynein, axon, heavy chain 11 (Dnahtc11), mRNA
7905	20830	34133	0.68	5.0E-03	TO5124.1	EST_HUMAN	EST03012 Fetal brain, Stratagene (cat#606206) Homo sapiens cDNA clone HFB083 similar to EST containing Alu repeat
8041	20855		1.2	5.0E-03	AW854327.1	EST_HUMAN	RC3-CT0255-031099-011-407 CT0255 Homo sapiens cDNA
8236	21141	34474	8.0	5.0E-03	AB016816.1	NT	Homo sapiens MASL1 mRNA, complete cds
8305	21209	34544	0.57	5.0E-03	Q9R001	SWISSPROT	ADAM-15 5 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5) (ADAMTS-5) (ADAM-TS5) (AGGRECANASE-2) (ADMP-2) (IMPLANTIN)
8305	21209	34545	0.57	5.0E-03	Q9R001	SWISSPROT	ADAM-15 5 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5) (ADAMTS-5) (ADAM-TS5) (AGGRECANASE-2) (ADMP-2) (IMPLANTIN)
8815	21745	35093	1.9	5.0E-03	P48982	SWISSPROT	ADAM-15 5 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5) (ADAMTS-5) (ADAM-TS5) (AGGRECANASE-2) (ADMP-2) (IMPLANTIN)
9172	22100		5.91	5.0E-03	M61132.1	NT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9365	22293	36658	1.46	5.0E-03	D90723.1	NT	Mouse complement receptor (CR2) mRNA, 3' end
10354	23243	36663	1.21	5.0E-03	L21710.1	NT	Escherichia coli genomic DNA. (19.1 - 19.4 min)
10477	23365	36778	0.61	5.0E-03	AW821888.1	EST_HUMAN	Plasmodium falciparum 56 kDa phosphoprotein mRNA, partial cds
10822	23708	37135	0.64	5.0E-03		NT	RCO-ST0379-210100-032-c02 ST0379 Homo sapiens cDNA
10957	23841		0.58	5.0E-03	AA653261.1	EST_HUMAN	Homo sapiens PRO0471 protein (PRO0471), mRNA
11163	24091		5.13	5.0E-03	T19566.1	EST_HUMAN	ag49c10.s1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1128290 3'
11378	24294	37739	2.46	5.0E-03	AW170334.1	EST_HUMAN	694F Heart Homo sapiens cDNA clone 684
11378	24294					EST_HUMAN	xr95g05.x1 Soares_NHCCc_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1.12 L1 repetitive element;
11478	24391	37841	2.46	5.0E-03	AW170334.1	EST_HUMAN	xr95g05.x1 Soares_NHCCc_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1.12 L1 repetitive element;
11523	24433	37891	2.08	5.0E-03	T49163.1	EST_HUMAN	y006e04.r1 Stratagene placenta (4637226) Homo sapiens cDNA clone IMAGE:70688 5'
11775	24674		1.76	5.0E-03	10940753	NT	Mus musculus hypochelical protein, MNCb-4760 (LOC58212), mRNA
12519	25917		4.05	5.0E-03	BE048035.1	EST_HUMAN	tz46c04.y1 NCI CGAP_Bn52 Homo sapiens cDNA clone IMAGE:2291622 5'
12649	25324		7.51	5.0E-03	AF047874.1	NT	Gallus gallus glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds
12649	25324		19.86	5.0E-03	AF047253.1	NT	Brugia malayi Y chromosome marker

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12742	25382		2.31	5.0E-03	L10347.1	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
12772	25401		2.16	5.0E-03	AA456597.1	EST_HUMAN	z75a03.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:809548 3' similar to SW:DXA2_MOUSE P14695 PROBABLE DIPHENOL OXIDASE A2 COMPONENT ;
12798	25750		4.71	5.0E-03	BF872332.1	EST_HUMAN	60207774F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4232002 5'
12954	25522	31743	2.44	5.0E-03	AW449109.1	EST_HUMAN	UI-H-B13-akt-f-08-0-UI.s1 NCI CGAP Sub5 Homo sapiens cDNA clone IMAGE:2734216 3'
251	13349	26262	2.07	4.0E-03	AW500196.1	EST_HUMAN	UI-HF-BN0-akc-h-04-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076831 5'
341	13431	26346	1.76	4.0E-03	R46482.1	EST_HUMAN	y65t04.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35988 3'
466	13637	26459	0.89	4.0E-03	P54675	SWISSPROT	PHOSPHATIDYLINOSITOL 3-KINASE 3 (PI3-KINASE) (PI3K)
624	13689	26592	2.29	4.0E-03	AA939339.1	EST_HUMAN	on75g12.s1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:1662566 3'
902	13954	26803	1.77	4.0E-03	R46482.1	EST_HUMAN	y65t04.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35988 3'
936	13988		3.87	4.0E-03	AW749101.1	EST_HUMAN	RC3-BT0333-110100-012-01 BT0333 Homo sapiens cDNA
1178	14218	27167	20.85	4.0E-03	AA099777.1	EST_HUMAN	z181a08.r1 Striatogene colon (#937204) Homo sapiens cDNA
1187	14236	27176	1.87	4.0E-03	AW794740.1	EST_HUMAN	RC8-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
1329	14363	27311	1.09	4.0E-03	AA284374.1	EST_HUMAN	z559a01.r1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701736 5'
1609	14639		1.26	4.0E-03	AV708305.1	EST_HUMAN	AV708305 ADC Homo sapiens cDNA clone ADCAKB06 5'
1771	14797	27767	1.88	4.0E-03	U33472.1	NT	Rattus norvegicus type 1 astrocyte and efferent-imbic associated protein AT1-46 mRNA, complete cds
2031	15048	28045	10.26	4.0E-03	AA099777.1	EST_HUMAN	z181a08.r1 Striatogene colon (#937204) Homo sapiens cDNA clone IMAGE:510998 5'
2262	15272		1.87	4.0E-03	BE410566.1	EST_HUMAN	601304161F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636510 5'
2297	15305	28311	1.46	4.0E-03	AW794740.1	EST_HUMAN	RC8-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
2609	15607	28601	2.01	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2609	15607	28602	2.01	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2741	15734	28728	2.8	4.0E-03	AJ277365.1	NT	CDM protein (CDM), adrenoleukodystrophy protein >
2741	15734	28729	2.8	4.0E-03	AJ277365.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2747	15799	28732	1.28	4.0E-03	AL163284.2	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
3272	16320	29224	1.4	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151299-003-h08 HT0340 Homo sapiens cDNA
3272	16320	29225	1.4	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151299-003-h08 HT0340 Homo sapiens cDNA
3592	16629	29532	0.93	4.0E-03	AW188426.1	EST_HUMAN	x98t04.x1 NCI CGAP_Cot18 Homo sapiens cDNA clone IMAGE:2665279 3'
3592	16629	29533	0.93	4.0E-03	AW188426.1	EST_HUMAN	x98t04.x1 NCI CGAP_Cot18 Homo sapiens cDNA clone IMAGE:2665279 3'
3689	16722	29615	0.68	4.0E-03	Q13606	SWISSPROT	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)

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3701	16733	29624	0.8	4.0E-03	AV646253.1	EST_HUMAN	AV646253 GLC Homo sapiens cDNA clone GLCADO2 3'
3985	16722	29615	0.7	4.0E-03	Q13606	SWISSPROT	OLFATORY RECEPTOR 611 (OLFATORY RECEPTOR-LIKE PROTEIN OLF1)
4005	17032	29922	0.8	4.0E-03	AF060868.1	NT	Mus musculus tumor susceptibility protein 101 (tsg101) gene, complete cds
4081	17106		2.28	4.0E-03	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (end joined CDS)
4723	17728	30592	0.98	4.0E-03	AI732754.1	EST_HUMAN	eb18a08.x5 Stratagene lung (#637210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element
5325	18309	31159	1.59	4.0E-03	AA699995.1	EST_HUMAN	zif6b01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:436009 3'
5386	18368		1.02	4.0E-03	AW816104.1	EST_HUMAN	MR3-ST0220-110100-026-d06 ST0220 Homo sapiens cDNA
5458	18539	31381	1.67	4.0E-03	AF005859.1	NT	Orosophila melanogaster enon207 (enon207) mRNA, complete cds
5584	18661	31536	20.71	4.0E-03	AF169925.1	NT	Rattus norvegicus beta-calactin binding protein mRNA, complete cds
6004	19058	32195	2.46	4.0E-03	P04196	SWISSPROT	(HPRG)
6008	19072	32197	1.6	4.0E-03	P21849	SWISSPROT	MAJOR SURFACE-LABELLED TROPHOZOITE ANTIGEN PRECURSOR
6098	19159	32292	0.85	4.0E-03	AL133871.1	EST_HUMAN	DKFZp7611014_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp7611014 5'
6321	19371		3.62	4.0E-03	U22180.1	NT	Rattus norvegicus opsin gene, complete cds
6481	19528	32704	0.98	4.0E-03	AW590572.1	EST_HUMAN	hg4f6c07.x1 NCL CGAP_GC6 Homo sapiens cDNA clone IMAGE:2948652 3'
6584	19605	32780	1.86	4.0E-03	BE548453.1	EST_HUMAN	601076015F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3461954 5'
6966	19694	33222	1.34	4.0E-03	AA813222.1	EST_HUMAN	aj32f11.61 Soares_testis_NHT Homo sapiens cDNA clone 1392045 3'
7082	20288	33547	1.49	4.0E-03	U76408.1	NT	Lycopodium esculentum knotted 3 protein (TKn3) mRNA, complete cds
7425	20124	33361	1.01	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7425	20124	33362	1.01	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7592	20499	33767	4.55	4.0E-03	Q02817	SWISSPROT	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)
7835	20763	34056	1.04	4.0E-03	AI681483.1	EST_HUMAN	ix37q12.x1 NCL CGAP_L024 Homo sapiens cDNA clone IMAGE:2271814 3'
7837	20765	34068	0.59	4.0E-03	BE670170.1	EST_HUMAN	7831b02.x1 NCL CGAP_L024 Homo sapiens cDNA clone IMAGE:3284043 3'
7948	20870		0.79	4.0E-03	X92109.1	NT	H.sapiens hcgIX gene
8521	21452	34795	0.58	4.0E-03	Q91T92	SWISSPROT	ADAM-TS 5 (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5)
8626	21657	34896	4.61	4.0E-03	AF111944.1	NT	(ADAMTS-5) (ADAM-TS5) (AGGRECANASE-2) (ADMP-2) (ADAM-TS 11)
9273	22201	35558	7.93	4.0E-03	AI555983.1	EST_HUMAN	Dichytellum discoideum AX4 development protein DG1122 (DG1122) gene, partial cds
9446	22374		3.38	4.0E-03	AL163209.2	NT	te49b11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090013 3' similar to contains Alu repetitive element
9456	22384	35746	3.88	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C009
10437	23326	36743	0.52	4.0E-03	H30664.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
10864	23750	37175	0.84	4.0E-03	AL161555.2	NT	yp42g12.r1 Soares retina N259HR Homo sapiens cDNA clone IMAGE:190150 5'
11041	23925		0.58	4.0E-03	AL163281.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 55
						NT	Homo sapiens chromosome 21 segment HS21C081

Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11569	24778	37944	5.77	4.0E-03	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C006
11949	24793	38291	1.57	4.0E-03	AI208703.1	EST_HUMAN	q956c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839176 3'
11949	24793	38292	1.57	4.0E-03	AI208703.1	EST_HUMAN	q956c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839176 3'
12185	25021	38523	1.4	4.0E-03	AE002102.1	NT	Ureaplasma urealyticum cocton 3 of 69 of the complete genome
12490	25933		4.8	4.0E-03	BE815173.1	EST_HUMAN	PM4-BN0138-180600-002-b08 BN0138 Homo sapiens cDNA
12510	25244		1.64	4.0E-03	BE298290.1	EST_HUMAN	601118104F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028095 5'
12585	25264		3.2	4.0E-03	AW504273.1	EST_HUMAN	UI-HF-BN0-alp-g-04-0-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080622 5'
12807	25430		3.15	4.0E-03	BF224125.1	EST_HUMAN	7q74c09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2858932 3' similar to contains Alu repetitive element; contains element MER31 repetitive element ;
12841	25848		2.93	4.0E-03	AW614596.1	EST_HUMAN	h02c07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2858932 3' similar to contains element LTR6 repetitive element ;
12855	25465		1.99	4.0E-03	AW819141.1	EST_HUMAN	RC3-ST0281-240400-015-03 ST0281 Homo sapiens cDNA
392	13476	26396	1.8	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
904	13956	26904	5.12	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
1688	14718	27679	4.85	3.0E-03	AA468110.1	EST_HUMAN	nc73c05.s1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:782984 similar to contains Alu repetitive element;
2275	15284		1.07	3.0E-03	AF055066.1	NT	Homo sapiens MHC class 1 region
2313	15321		5.91	3.0E-03	Z32521.1	NT	S.cereale (cv. Haio) mRNA for triosephosphate isomerase
2314	15322	28322	1.6	3.0E-03	U46858.1	NT	Mus musculus intestinal trefol factor gene, partial cds
2314	15322	28323	1.6	3.0E-03	U46858.1	NT	Mus musculus intestinal trefol factor gene, partial cds
2426	15430	28431	0.99	3.0E-03	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
3034	16086		0.7	3.0E-03	Y06006.1	NT	Arabidopsis thaliana rpm1 gene
3132	16182	29076	2.53	3.0E-03	BE379296.1	EST_HUMAN	601237892F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609933 5'
3194	16242	29137	3.03	3.0E-03	AW802687.1	EST_HUMAN	IL2-JM0076-240300-056-D03 UM0076 Homo sapiens cDNA
3478	16518	29417	2.31	3.0E-03	U34806.1	NT	Mus musculus alpha-1(XVII) collagen (COL18A1) gene, exon 1 and 2
3487	16526		7.8	3.0E-03	Y12500.1	NT	G.elegans samde gene
4062	17088	29973	8.3	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4062	17088	29974	8.3	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4120	17143	30016	2.16	3.0E-03	AI762278.1	EST_HUMAN	402409.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1155689 5'
4502	17512	30378	10.13	3.0E-03	AJ011432.1	NT	Rattus norvegicus gdnf gene
4638	17644	30508	6.24	3.0E-03	AI536141.1	EST_HUMAN	Xu8.P10.H3 contom Homo sapiens cDNA 3'
4948	17947	30805	1.72	3.0E-03	AI732754.1	EST_HUMAN	ab18a08.x5 Stratiagene lung (#937210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element;



Page 187 of 545  
Table 4

Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4963	17961	30819	3.2	3.0E-03	BE787945.1	EST_HUMAN	601482715F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3885483 5'
5291	18276	31124	1.08	3.0E-03	4506414	NT	Homo sapiens RAP1, GTPase activating protein 1 (RAP1GA1) mRNA
5291	18276	31126	1.08	3.0E-03	4506414	NT	Homo sapiens RAP1, GTPase activating protein 1 (RAP1GA1) mRNA
5447	18528	31254	3.58	3.0E-03	8922499	NT	Homo sapiens hypothetical protein FLJ10539, mRNA
5747	18820	31917	1.86	3.0E-03	AJ249981.1	NT	Mus musculus mRNA for hypothetical protein (ORF2 ortholog)
5821	18893	32006	1.02	3.0E-03	U35323.1	NT	Mus musculus H2-M alpha chain (H2-Ma) gene, H2-M beta 2 chain (H2-Mb2) gene, H2-M beta 1 chain (H2-Mb1) gene, low molecular weight protein 2 Lmp2 (Lmp2) gene, complete cds
6834	19866	33060	10.99	3.0E-03	AA456701.1	EST_HUMAN	aa1310.1 Soares_NHIMPu_S1 Homo sapiens cDNA clone IMAGE:813163 5'
7374	20368	33637	0.65	3.0E-03	D37977.1	NT	Fugu rubripes mRNA for sodium channel alpha subunit, partial cds
7571	20507	33795	1.27	3.0E-03	AJ011419.1	NT	Kluyveromyces marxianus popl8 gene for purine-cytosine permease
7948	20868	34180	3.67	3.0E-03	AB021738.1	NT	Oryza sativa gene for bZIP protein, complete cds
8376	21280	34611	0.47	3.0E-03	P26659	SWISSPROT	DNA REPAIR HELICASE RAD15 (RHP3)
8517	21448	34760	0.97	3.0E-03	BF333058.1	EST_HUMAN	RCO-BT0812-250900-032-e07 BT0812 Homo sapiens cDNA
8517	21448	34791	0.97	3.0E-03	BF333058.1	EST_HUMAN	RCO-BT0812-250900-032-e07 BT0812 Homo sapiens cDNA
8734	21664	35009	1.74	3.0E-03	N92580.1	EST_HUMAN	zb27b04.s1 Soares_papillary_tumor_NbHPA Homo sapiens cDNA clone IMAGE:304783 3'
8890	21820		0.65	3.0E-03	M63498.1	NT	S cerevisiae UGA35 gene, complete cds
9029	21958	35318	1.18	3.0E-03	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
9052	21981	35338	1.61	3.0E-03	AL163289.2	NT	Homo sapiens chromosome 21 segment HS21C068
9148	22076		1.4	3.0E-03	Q9QMB1	SWISSPROT	NONSTRUCTURAL PROTEIN V
9543	22470		11.53	3.0E-03	AW613774.1	EST_HUMAN	hh80f10.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969131 3' similar to contains L1.11 L1 repetitive element
9598	22524	35888	4.26	3.0E-03	AL161589.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
9820	22546	35917	7.95	3.0E-03	AJ016731.1	EST_HUMAN	ov03d12.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1636247 3' similar to gb:X67138_rna1
8943	22848		0.85	3.0E-03	D90901.1	NT	Synedocystis sp. PCC6803 complete genome, 3/27, 271600-402289
10162	23053		0.77	3.0E-03	P03355	SWISSPROT	POLYPROTEIN [CONTAINS: PROTEASE, REVERSE TRANSCRIPTASE, RIBONUCLEASE H]
10229	23120		7.22	3.0E-03	P08672	SWISSPROT	CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
							RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
10407	23296	36716	1.65	3.0E-03	P11369	SWISSPROT	ENDONUCLEASE
10501	23369	36800	1.44	3.0E-03	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
10639	23525	36960	4.3	3.0E-03	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
11283	24204		1.87	3.0E-03	5803028	NT	Homo sapiens ATP/GTP-binding protein (HEAB), mRNA
11627	20868	34180	1.63	3.0E-03	AB021736.1	NT	Oryza sativa gene for bZIP protein, complete cds
11819	24740	38231	1.96	3.0E-03	AF009222.1	NT	Pneumocystis carinii kexin-like serine endoprotease mRNA, partial cds

Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11870	23970	37407	1.46	3.0E-03	P22531	SWISSPROT	SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)
11880	23980	37418	2.66	3.0E-03	AF268285.1	NT	Homo sapiens golin-like protein (GLP) gene, complete cds
11912	24750	38256	2.98	3.0E-03	AF094481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11912	24759	38250	2.98	3.0E-03	AF094481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11987	24830	38327	1.76	3.0E-03	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
12285	25762		2.16	3.0E-03	AI525056.1	EST_HUMAN	promrha-5.E07.r bvtumor Homo sapiens cDNA 5'
12370	25877	31831	1.68	3.0E-03	AB006668.1	NT	Homo sapiens gene for CMP-N-acetylneuraminic acid hydroxylase, partial cds
12533	25256	31831	1.61	3.0E-03	AJ296282.1	NT	Rattus norvegicus mRNA for connexin36 (cx36 gene)
538	13607	26516	0.77	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
538	13607	26517	0.77	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
812	15885		11.14	2.0E-03	T70874.1	EST_HUMAN	yt15h03.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:108341 5'
1390	14421	27376	1.75	2.0E-03	M20783.1	NT	Human alpha-2-plasmin inhibitor gene, exon 6 and 7
1393	14424	27378	1.14	2.0E-03	AA661605.1	EST_HUMAN	nu86f01.s1 NCI_CGAP_A1M1 Homo sapiens cDNA clone IMAGE:1217593
1402	14433	27388	13.79	2.0E-03	AF284448.1	NT	Homo sapiens tumor-related protein DRC2 (DRC2) gene, complete cds
1508	14539	27501	1.7	2.0E-03	P48509	SWISSPROT	PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN)
1537	14567	27526	1.8	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1537	14567	27527	1.8	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1614	14644		6.77	2.0E-03	P29400	SWISSPROT	COLLAGEN ALPHA 5(IV) CHAIN PRECURSOR
1796	14822	27760	1.28	2.0E-03	AA450138.1	EST_HUMAN	zx42a10.r1 Soares_fetus NB2HF8 8w Homo sapiens cDNA clone IMAGE:789114 5'
2011	15029	28022	1.35	2.0E-03	AF302691.1	NT	Mus musculus myelin expression factor-3-like protein gene, partial cds
2265	15275	28281	0.92	2.0E-03	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
2617	15815		5.66	2.0E-03	AW137782.1	EST_HUMAN	U1-H-B11-adi-g-10-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717010 3'
3477	16517	29416	4.74	2.0E-03	AA450138.1	EST_HUMAN	zx42a10.r1 Soares_fetus NB2HF8 9w Homo sapiens cDNA clone IMAGE:789114 5'
3484	16523	29422	0.84	2.0E-03	BF568955.1	EST_HUMAN	602183960.T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 3'
3734	16766	29652	7.03	2.0E-03	X87344.1	NT	H sapiens DMA, DMB, HLA-Z1, PP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
4031	17038	29947	0.65	2.0E-03	AB040802.1	NT	Rattus norvegicus mRNA for SREB1, complete cds
4207	17224	30091	3.03	2.0E-03	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]
4270	17266	30154	1.01	2.0E-03	AA176993.1	EST_HUMAN	zp13h01.r1 Strabagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609361 5'
4317	17331		11.71	2.0E-03	U68491.1	NT	Rattus norvegicus 5-hydroxytryptamine7 receptor gene, partial cds

Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4519	17528		1.9	2.0E-03	L35079.1	NT	Porcine rotavirus major outer capsid protein (VP7) mRNA, complete cds
4634	17643		1.19	2.0E-03	AW297380.1	EST_HUMAN	U1-H-BW0-air-g-03-0-UJ.s1 NCI CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2730413 3'
4639	17648	30409	1	2.0E-03	A1064746.1	EST_HUMAN	HA0507 Human fetal liver cDNA library Homo sapiens cDNA
4662	17667	30535	1.95	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds
4662	17667	30536	1.95	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds
4819	17820	30889	1.25	2.0E-03	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4824	17826		1.47	2.0E-03	R87773.1	EST_HUMAN	yo45e02.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:180890 3'
5147	18142	30987	0.93	2.0E-03	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5178	18168	31013	0.71	2.0E-03	P45969	SWISSPROT	HYPOPHYSICAL 37.4 KD PROTEIN T09A5.9 IN CHROMOSOME III
5271	18257	31108	0.94	2.0E-03	AF187974.1	NT	8 Homo sapiens concentrative nucleoside transporter (CNT1) gene, exon 12
5279	18265		0.71	2.0E-03	AJ245167.1	NT	Camelus dromedarius cvhp19 gene for immunoglobulin heavy chain variable region
5383	18345		1.09	2.0E-03	BE019692.1	EST_HUMAN	b22h05.x1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:2964249 3'
5675	18749	31660	1.19	2.0E-03	BF241410.1	EST_HUMAN	601876385F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104692 5'
5822	25533	32007	2.21	2.0E-03	AB014593.1	NT	Homo sapiens mRNA for KIAA0693 protein, partial cds
5909	18978	32095	0.49	2.0E-03	AW796111.1	EST_HUMAN	MR2-UM0025-300300-102-102 UM0025 Homo sapiens cDNA
5910	18979	32097	1.89	2.0E-03	U63711.1	NT	Xenopus laevis xefitin mRNA, complete cds
6348	19398	32564	4.92	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6348	19398	32565	4.92	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6603	19644	32826	2.23	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
6603	19644	32827	2.23	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
6605	19646	32829	7.88	2.0E-03	BF308187.1	EST_HUMAN	601887434F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121408 5'
6645	19684	32875	2.64	2.0E-03	Q8UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
6646	19685	32876	0.85	2.0E-03	AV709075.1	EST_HUMAN	AV709075 ADC Homo sapiens cDNA clone ADCAEF09 5'
6681	19717	32917	1.22	2.0E-03	X94451.1	NT	L. esculentum mRNA for lysyl-tRNA synthetase (LysRS)
6888	19918		1.29	2.0E-03	A1991089.1	EST_HUMAN	wu36h09.x1 Soares Dieckgreffe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522177 3' similar to SW:RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29; contains element MSR1 repetitive element;
6929	19968	33179	0.68	2.0E-03	AA677831.1	EST_HUMAN	z13a11.s1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:430652 3'
7295	18464	31334	1.21	2.0E-03	AB038502.1	NT	Caenorhabditis elegans mRNA for galectin LEC-11, complete cds
7441	20183	33427	3.26	2.0E-03	BE067986.1	EST_HUMAN	CM4-BT0368-061289-054-d01 BT0368 Homo sapiens cDNA

Page 190 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7504	20443	33726	0.7	2.0E-03	A1298883.1	EST_HUMAN	q199d11.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898885 3'
7673	20607	33906	0.74	2.0E-03	T86599.1	EST_HUMAN	y477g10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:114306 5'
8003	20976	34291	1.55	2.0E-03	P07354	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
8629	21560	34898	2.84	2.0E-03	AW592004.1	EST_HUMAN	h37b06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2934035 3' similar to TR:Q60976
8796	21726	35074	6.05	2.0E-03	N20287.1	EST_HUMAN	Q60976 JERKY. ; y42g06.s1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2 L1 repetitive element ;
8798	21726	35075	6.05	2.0E-03	N20287.1	EST_HUMAN	y42g06.s1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2 L1 repetitive element ;
8840	21770	35116	0.54	2.0E-03	Q92350	SWISSPROT	HYPOTHETICAL 32.8 KD PROTEIN C6G9.06 IN CHROMOSOME 1
8863	21793	35145	1.29	2.0E-03	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
8915	21845	35199	0.83	2.0E-03	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8915	21845	35200	0.83	2.0E-03	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8938	21868	35226	1.03	2.0E-03	AU136679.1	EST_HUMAN	AU136679 PLACE1 Homo sapiens cDNA clone PLACE1004839 5'
8980	21919		0.96	2.0E-03	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
9737	18978	32095	0.76	2.0E-03	AW796111.1	EST_HUMAN	MR2-UM0025-300300-102-402 UM0025 Homo sapiens cDNA
9737	18978	32096	0.76	2.0E-03	AW796111.1	EST_HUMAN	MR2-UM0025-300300-102-402 UM0025 Homo sapiens cDNA
9762	22706	36090	0.9	2.0E-03	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
10056	22972	36361	0.98	2.0E-03	H50832.1	EST_HUMAN	y86a09.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194296 3'
10056	22972	36362	0.98	2.0E-03	H50832.1	EST_HUMAN	y86a09.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194296 3'
10087	22880	36266	3.48	2.0E-03	P24821	SWISSPROT	TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEIN) (JII) (MOTENDINUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C) (TN-C)
10192	23083	36484	1.19	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10192	23083	36485	1.19	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10244	23135	36539	0.65	2.0E-03	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
10244	23135	36540	0.65	2.0E-03	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
10426	23315	36732	1.09	2.0E-03	AW894209.1	EST_HUMAN	QV3-OT0064-060400-144-e01 OT0064 Homo sapiens cDNA
10545	23431		6.4	2.0E-03	AA251376.1	EST_HUMAN	zs10a06.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684754 3'
11454	24370		2.49	2.0E-03	M86524.1	NT	Human dystrophin gene
11920	20976	34291	2.33	2.0E-03	P07354	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
11975	24818		2.4	2.0E-03	BF330909.1	EST_HUMAN	RC3-BT0333-310800-115-g04 BT0333 Homo sapiens cDNA

Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11982	24825	38321	11.38	2.0E-03	Z11740.1	NT	H. sapiens variable number tandem repeat (VNTR) locus DNA
12287	26084		3.38	2.0E-03	A1625745.1	EST_HUMAN	Y95H03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2283089 3' similar to SW:VATG_MANSE
12283	25097	38573	4.23	2.0E-03	AF157516.2	NT	Q26532 VACUOLAR ATP SYNTHASE SUBUNIT G ; Homo sapiens SEL1L (SEL1L) gene, partial cds
12306	25113	38577	9.27	2.0E-03	A1084325.1	EST_HUMAN	oy43006.s1 Soares_papillary_tumor_NbhHPA Homo sapiens cDNA clone IMAGE:1658634 3' similar to
12328	18265		8.68	2.0E-03	AJ245167.1	NT	TR:P97535 P97535 PS-PLA1 PRECURSOR ;
12514	25913		2.26	2.0E-03	AV697966.1	EST_HUMAN	Camelus dromedarius cyp19 gene for immunoglobulin heavy chain variable region
							AV697966 GKC Homo sapiens cDNA clone GKCGXD06 5'
12899	25471		1.92	2.0E-03	AF129756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
13025	25743		4.22	2.0E-03	AV697966.1	EST_HUMAN	AV697966 GKC Homo sapiens cDNA clone GKCGXD05 5'
462	13534	26454	1.21	1.0E-03	H06471.1	EST_HUMAN	y98c08.t1 Soares_pinea_gland_N3HPG Homo sapiens cDNA clone IMAGE:232334 5'
854	13908	26852	1.63	1.0E-03	A1720263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
854	13908	26853	1.63	1.0E-03	A1720263.1	EST_HUMAN	Q13825 AU-BINDING PROTEIN/ENOL-COA HYDRATASE ;
1122	14164	27101	1.99	1.0E-03	A1865788.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
1142	14184	27122	1.76	1.0E-03	A1954572.1	EST_HUMAN	Q13826 AU-BINDING PROTEIN/ENOL-COA HYDRATASE ;
							wk8a06.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2422258 3'
							wk8a10.x1 NCI_CGAP_Mel16 Homo sapiens cDNA clone IMAGE:2551242 3'
							wk8a01.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338440 3' similar to contains Alu
1193	14232	27171	1.87	1.0E-03	A1692616.1	EST_HUMAN	repetitive element;
2041	15058	28059	2.6	1.0E-03	P47808	SWISSPROT	HIGH MOLECULAR WEIGHT FORM OF MYOSIN I (HMWMI)
2168	15180	28186	5.51	1.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
3021	16073	28975	1.46	1.0E-03	AB033117.1	NT	Homo sapiens mRNA for KIAA1291 protein, partial cds
3234	16282	29182	1.05	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3234	16282	29183	1.05	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3345	16391	29291	0.88	1.0E-03	P08547	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3733	16765		1.72	1.0E-03	AB044400.1	NT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
4010	17037	29927	0.74	1.0E-03	Z49649.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4541	17550	30410	1.46	1.0E-03	BE939162.1	EST_HUMAN	Homo sapiens SVMT1 gene for synaptic vesicle monoamine transporter, exon 14, 15
							S. cerevisiae chromosome X reading frame ORF YJR149w
							RC1-TN0128-160800-021-g01 TN0128 Homo sapiens cDNA
4589	17597	30455	5.87	1.0E-03	BE246536.1	EST_HUMAN	TCBAP1D4909 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo
							sapiens cDNA clone TCBAP4909

Page 192 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4775	17780	30850	0.73	1.0E-03	U28449.1	NT	Caenorhabditis elegans spliced leader RNA (SL3 alpha), (SL4), and (SL5) genes
4937	17936	30793	2.63	1.0E-03	A1073485.1	EST_HUMAN	ov45c04.x1 Soares testis NIH Homo sapiens cDNA clone IMAGE:1640262 3'
4937	17936	30794	2.53	1.0E-03	A1073485.1	EST_HUMAN	ov45c04.x1 Soares testis NIH Homo sapiens cDNA clone IMAGE:1640262 3'
4938	17937		4.81	1.0E-03	BE154067.1	EST_HUMAN	PV02-HIT0339-200400-010-D02 HT0339 Homo sapiens cDNA
5211	18201	31045	21.62	1.0E-03	O46409	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
5491	18571	31417	1.8	1.0E-03	AA290951.1	EST_HUMAN	Homo sapiens KVLQ1 gene
5587	18664	31540	3.24	1.0E-03	AJ006345.1	NT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5641	18716	31617	2.09	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5641	18716	31618	2.09	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5764	18837	31940	0.9	1.0E-03	BE788491.1	EST_HUMAN	601569841F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3843984 6'
5770	18843	31945	1.63	1.0E-03	Q02388	SWISSPROT	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
5829	18900	32014	0.66	1.0E-03	N41974.1	EST_HUMAN	y07h06.r1 Soares melanocyte 2N6b-IM Homo sapiens cDNA clone IMAGE:270587 5' similar to contains element MER6 repetitive element;
5829	18900	32015	0.66	1.0E-03	N41974.1	EST_HUMAN	y07h06.r1 Soares melanocyte 2N6b-IM Homo sapiens cDNA clone IMAGE:270587 5' similar to contains element MER6 repetitive element;
6110	19170	32302	0.51	1.0E-03	AA773362.1	EST_HUMAN	ab65g12.s1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:845734 3'
6133	19192		0.45	1.0E-03	BF541639.1	EST_HUMAN	602069042F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4066907 5'
6263	19306		3.24	1.0E-03	X07696.1	NT	Mouse nucleolin gene
6294	19345	32513	1.06	1.0E-03	BE963939.2	EST_HUMAN	601657519R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875693 3'
6433	19480		8.63	1.0E-03	T1526170	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
6591	19632	32814	1.11	1.0E-03	T87761.1	EST_HUMAN	y493a11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:115772 5'
6674	19711		1.56	1.0E-03	AW902585.1	EST_HUMAN	QV3-NN1024-260400-171-g05 NN1024 Homo sapiens cDNA
7060	20085	33318	1.5	1.0E-03	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
7513	20452	33737	2.47	1.0E-03	D16826.1	NT	Human gene for fourth somatostatin receptor subtype
7907	20832		2.62	1.0E-03	AJ229042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
8088	21000	34322	1.82	1.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenergic karyostrophy protein >
8167	21074	34404	3.28	1.0E-03	M63376.1	NT	Human TRPM-2 protein gene, exons 1,2 and 3
8224	21129	34460	0.66	1.0E-03	BE980044.1	EST_HUMAN	601491081F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3803276 5'
8469	21400	34740	0.77	1.0E-03	AF274591.1	NT	Homo sapiens proteolisin-releasing peptide receptor gene, 5' flanking region
8528	21459	34802	5.56	1.0E-03	AJ251973.1	NT	Homo sapiens partial steerin-1 gene
8722	21652	34959	0.87	1.0E-03	AA122270.1	EST_HUMAN	z687c09.s1 Soares pregnant uterus, NbHPU Homo sapiens cDNA clone IMAGE:490768 3' similar to contains L1.t1 L1 repetitive element;

Page 183 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8999	21928	35283	0.89	1.0E-03	U29397.1	NT	Rattus norvegicus plasma membrane Ca2+ ATPase isoform 3 (PMCA3) gene, 5' flanking region
9156	22084	35442	0.61	1.0E-03	AA001613.1	EST_HUMAN	zh2e06.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:427810 3'
9156	22084	35443	0.61	1.0E-03	AA001613.1	EST_HUMAN	zh2e06.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:427810 3'
9499	22426		1.62	1.0E-03	Y11204.1	NT	V. carteri gene encoding volvoxapain
9522	22449	35812	0.64	1.0E-03	AW840353.1	EST_HUMAN	QV3-LT0079-170200-092-a07 LT0079 Homo sapiens cDNA
9628	22552						Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (ORTR), CDM protein (CDM), adrenoleukodystrophy protein >
9663	22589	35961	0.88	1.0E-03	U52111.2	NT	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds
9663	22589	35961	3.11	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds
9663	22589	35962	3.11	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds
10134	23025	36420	1.98	1.0E-03	AF011400.1	NT	Thermotoga neapolitana alpha-1,5-galactosidase (aga) gene, complete cds
10134	23025	36421	1.98	1.0E-03	AF011400.1	NT	Thermotoga neapolitana alpha-1,5-galactosidase (aga) gene, complete cds
10336	23224	36639	0.98	1.0E-03	Q01129	SWISSPROT	BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN) (PG40) (DERMATAN SULFATE PROTEOGLYCAN-II) (DSPG)
10659	23545	36979	0.64	1.0E-03	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
10665	23551		0.79	1.0E-03	AF097485.1	NT	Homo sapiens transducin beta-like 2 (TBL2) gene, complete cds
10805	23691	37119	1	1.0E-03	A1024350.1	EST_HUMAN	ov75f08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1643175 3' similar to contains MER39.b1
11109	24040	37484	1.86	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0279-181099-011-a09 CT0279 Homo sapiens cDNA
11109	24040	37485	1.86	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0279-181099-011-a09 CT0279 Homo sapiens cDNA
11191	24117	37664	3.01	1.0E-03	BE170859.1	EST_HUMAN	QV3-HT0543-220300-130-a03 HT0543 Homo sapiens cDNA
11282	24185						tt3e12.x1 NCL CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246446 3' similar to TR:Q26195 Q26195
11330	24249	37687	2.91	1.0E-03	AI583847.1	EST_HUMAN	PVA1 GENE. ;
11597	24508		3.18	1.0E-03	AW759949.1	EST_HUMAN	AV759949 MDS Homo sapiens cDNA clone MDSDDF11 5'
12282	25080	38571	3.88	1.0E-03	BE894488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
12707	25895		5.42	1.0E-03	AI347355.1	EST_HUMAN	tc05h11.x1 NCL CGAP_Co18 Homo sapiens cDNA clone IMAGE:2063013 3' similar to contains Alu repetitive element;
12805	25915	31369	4.03	1.0E-03	BE780572.1	EST_HUMAN	601468376F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872035 5'
6342	18326	31174	2.04	9.0E-04	L11010.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
5369	18371	31210	1.33	9.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5879	18948		1.82	9.0E-04	P08727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
6508	19552		0.7	9.0E-04	AJ006345.1	NT	Homo sapiens KVLQT1 gene
6761	19795	33009	1.11	9.0E-04	P02381	SWISSPROT	MITOCHONDRIAL RIBOSOMAL PROTEIN VAR1

Page 194 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10169	23080		1.57	9.0E-04	AB037203.1	NT	Glycerol dehydrogenase Gbbs1 mRNA for beta-amylin synthase, complete cds
1506	14537		1.07	8.0E-04	X98469.1	NT	Xlaevis mRNA for C4SR protein
3993	17020	29910	0.65	8.0E-04	R07008.1	EST_HUMAN	Y12r10.1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:126691 5'
4276	17260		5.2	8.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4878	17877	30743	3.2	8.0E-04	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
11586	24496		2.53	8.0E-04	AA777084.1	EST_HUMAN	z24c10.s1 Soares fetal heart NbhH19W Homo sapiens cDNA clone IMAGE:377874 3'
11742	24844		2.4	8.0E-04	AA777084.1	EST_HUMAN	ln85a08.x1 NCI CGAP U2 Homo sapiens cDNA clone IMAGE:2176310 3'
1851	14873	27855	1.24	7.0E-04	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
2421	15426	28428	0.93	7.0E-04	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
2783	16785	28760	1.18	7.0E-04	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3324	16370	29271	1.05	7.0E-04	4885170	NT	Homo sapiens chromosome X open reading frame 8 (GXORF8) mRNA
6333	19383	32551	0.79	7.0E-04	AA516212.1	EST_HUMAN	ng65g12.s1 NCI CGAP L1p2 Homo sapiens cDNA clone IMAGE:939718 similar to contains L1.b3 L1 L1 repetitive element;
6549	19591	32778	0.47	7.0E-04	A133675.1	EST_HUMAN	qq08h05.x1 Soares NhrHMPu_S1 Homo sapiens cDNA clone IMAGE:1931981 3' similar to gb:X57025_rna1
6781	19824		2.27	7.0E-04	A1769331.1	EST_HUMAN	INSULIN-LIKE GROWTH FACTOR IA PRECURSOR (HUMAN); contains Alu repetitive element; contains
7597	20533		0.8	7.0E-04	AK024445.1	NT	wg66109.x1 Soares NSF_F9_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367208 3'
10320	23209	36620	0.65	7.0E-04	P13497	SWISSPROT	Homo sapiens mRNA for FLJ00035 protein, partial cds
10320	23209	36621	0.65	7.0E-04	P13497	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
11698	24840		2.33	7.0E-04	U78027.1	NT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
12023	24865	36366	2.84	7.0E-04	Z40561.1	EST_HUMAN	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and F1P3 (F1P3) genes, complete cds
12746	25385		14.51	7.0E-04	BE077841.1	EST_HUMAN	HSC28A072 normalised infant brain cDNA Homo sapiens cDNA clone c-28a07 3'
12963	25521		4.19	7.0E-04	R17336.1	EST_HUMAN	CM1-BT0614-110300-142-b12 BT0614 Homo sapiens cDNA
12960	25549		4.98	7.0E-04	6005855	NT	Yg13c06.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:32298 5'
2746	16736		0.98	6.0E-04	BF341380.1	EST_HUMAN	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
4044	17071	29957	1.77	6.0E-04	A1862525.1	EST_HUMAN	602013395F1 NCI CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4149297 5'
4281	17265	30161	4.06	6.0E-04	U45983.1	EST_HUMAN	wj15a11.x1 NCI CGAP Jld12 Homo sapiens cDNA clone IMAGE:2402876 3'
4552	17561	30420	1.54	6.0E-04	BE173435.1	EST_HUMAN	Homo sapiens COR8 chemokine receptor (CMKBR8) gene, complete cds
4552	17561	30421	1.54	6.0E-04	BE173435.1	EST_HUMAN	RC2-HT0560-190200-011-f09 HT0560 Homo sapiens cDNA
5391	18373	31213	1.08	6.0E-04	P12259	SWISSPROT	RC2-HT0560-190200-011-f09 HT0560 Homo sapiens cDNA
5391	18373	31214	1.08	6.0E-04	P12259	SWISSPROT	COAGULATION FACTOR V PRECURSOR (ACTIVATED PROTEIN C COFACTOR)
8447	21379		3.72	6.0E-04	P46408	SWISSPROT	COAGULATION FACTOR V PRECURSOR (ACTIVATED PROTEIN C COFACTOR)



Page 195 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8584	21525		0.87	6.0E-04	H92947.1	EST_HUMAN	y940t1.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:231966 3' similar to contains LOR1 repetitive element ;
10486	23374		4.07	6.0E-04	AL048507.2	EST_HUMAN	DKFZp586M2024_r1 589 (synonym: huler1) Homo sapiens cDNA clone DKFZp586M2024
10582	23468	36894	2.41	6.0E-04	BE005850.1	EST_HUMAN	RC2-BN0120-250400-012-h11 BN0120 Homo sapiens cDNA
10827	23713		0.65	6.0E-04	AF287478.1	NT	Lytechinus variegatus embryonic blastocoelar extracellular matrix protein precursor (ECM3) mRNA, complete cds
11918	24763	38260	2.88	6.0E-04	AJ228042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
11989	24841	38337	4.92	6.0E-04	AW013847.1	EST_HUMAN	UI-H810-aab-e-09-0-U1.s1 NCI CGAP_Sub01 Homo sapiens cDNA clone IMAGE:2709825 3'
12064	24905		2.18	6.0E-04	Q01768	SWISSPROT	NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B) (NM23-M2) (P18)
12429	25810		3.04	6.0E-04	AW380519.1	EST_HUMAN	RC1-HT0289-261199-012-c08 HT0289 Homo sapiens cDNA
674	13736	26648	5.41	5.0E-04	O10341	SWISSPROT	HYPOTHETICAL 28.3 KD PROTEIN (ORF92)
1521	14552		1.8	5.0E-04	AW651844.1	EST_HUMAN	QV6-CT0225-021099-030-e07 CT0225 Homo sapiens cDNA
3474	16514	29413	1.67	5.0E-04	AA548931.1	EST_HUMAN	nk27e11.s1 NCI CGAP_Cot11 Homo sapiens cDNA clone IMAGE:1014784 3' similar to contains Alu repetitive element;
3778	16810	29697	0.92	5.0E-04	Q9UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
5680	18734	31641	2.82	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6919	19949	33170	5.5	5.0E-04	AA156080.1	EST_HUMAN	z033508.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:568663 5'
7769	20699	33999	13.69	5.0E-04	M23604.1	NT	Gorilla gorilla involucrin gene medium allele, complete cds
8534	21485	34808	5.87	5.0E-04	A1188382.1	EST_HUMAN	qd13f06.x1 Soares_placenta_800weeks_2NBHP809W Homo sapiens cDNA clone IMAGE:1723619 3' similar to gb:X51602_cds1 VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 (HUMAN)/contains Alu repetitive element;
8878	21808	35161	0.83	5.0E-04	AA814519.1	EST_HUMAN	cb96e02.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339226 3' similar to contains element
9817	22723	36108	2.14	5.0E-04	AA846545.1	EST_HUMAN	MER22 repetitive element ;
9910	22888	36285	0.89	5.0E-04	N83765.1	EST_HUMAN	aj58h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394387 3'
10136	23027	36424	4.44	6.0E-04	AW270938.1	EST_HUMAN	KK2745F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK2745 5' similar to REPETITIVE ELEMENT
10770	23646		0.63	5.0E-04	U52871.1	NT	xs06e02.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2788858 3'
11413	24329		2.25	5.0E-04	AL048507.2	EST_HUMAN	[Human familial Alzheimer's disease (STM2) gene, complete cds
12135	18734	31641	14.44	5.0E-04	AF248054.1	NT	DKFZp586M2024_r1 588 (synonym: huler1) Homo sapiens cDNA clone DKFZp586M2024
12375	25751		2.07	5.0E-04	AA568513.1	EST_HUMAN	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds

Page 196 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
413	13486		1.71	4.0E-04	BF241482.1	EST_HUMAN	601876834F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104897 5'
606	13756	26673	1.2	4.0E-04	U32748.1	NT	Haemophilus influenzae Rd section 63 of 163 of the complete genome
072	13925	26872	1.23	4.0E-04	AI720263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEINENOYL-COA HYDRATASE.;
872	13925	26873	1.23	4.0E-04	AI720263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
1484	14515	27476	3.44	4.0E-04	AW753356.1	EST_HUMAN	RC3-CT0254-130700-023-01 CT0254 Homo sapiens cDNA
2088	15110	28114	1.23	4.0E-04	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
2147	15163		1.23	4.0E-04	AL046704.1	EST_HUMAN	DKF2p343d0059_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKF2p343d0059 5'
2673	15663	28668	2.06	4.0E-04	O96615	SWISSPROT	SERPIN-2 (SILK GUM PROTEIN 2)
3414	16493	29362	0.92	4.0E-04	AV696024.1	EST_HUMAN	AV696624 GK6 Homo sapiens cDNA clone GK6FFH07 5'
3936	16664		1.13	4.0E-04	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4428	17440	30288	4.02	4.0E-04	AA576831.1	EST_HUMAN	nh10a10.s1 NCI CGAP_Co1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4429	17440	30300	4.02	4.0E-04	AA576831.1	EST_HUMAN	nh10a10.s1 NCI CGAP_Co1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4683	17659	30526	1.11	4.0E-04	AA086324.1	EST_HUMAN	zn67c08.s1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562670 3'
5222	18211	31057	3.87	4.0E-04	BE560660.1	EST_HUMAN	601345895F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3678910 5'
5309	18293		0.86	4.0E-04	BE178680.1	EST_HUMAN	PM44-H0606-030400-001-h11 HT0606 Homo sapiens cDNA
7644	20579	33674	1.25	4.0E-04	P48442	SWISSPROT	EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL CALCIUM-SENSING RECEPTOR)
7962	20884		4.7	4.0E-04	AL161568.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
8179	21086	34420	0.71	4.0E-04	AU122079.1	EST_HUMAN	AU122079 MAMMA1 Homo sapiens cDNA clone MAMMA1001620 5'
9100	22029	35384	1.02	4.0E-04	BF240712.1	EST_HUMAN	601875985F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:4099700 5'
9108	22036	36390	2.15	4.0E-04	N26507.1	EST_HUMAN	yx39e12.r1 Soares melanocyte 2NHIM Homo sapiens cDNA clone IMAGE:284142 5'
10214	23105	36505	3.89	4.0E-04	A025699.1	EST_HUMAN	ov87h03.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1944341 3'
10366	23244		0.71	4.0E-04	AF022868.1	NT	Mus musculus neuropilin-2(a17) mRNA, alternatively spliced, complete cds
12716	25729		2.21	4.0E-04	AF254822.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
166	13267	26184	3.52	3.0E-04	AL119426.1	EST_HUMAN	DKF2p761J221_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKF2p761J221 5'
208	13307	26224	6.78	3.0E-04	P40269	SWISSPROT	180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2 R)
905	13957	26905	1.67	3.0E-04	U93991.1	NT	Human ahort chain acyl CoA dehydrogenase gene, exons 1 and 2
1863	14855	27665	1.36	3.0E-04	AI262100.1	EST_HUMAN	q228a03.y1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2028197 5'
1878	14899		0.91	3.0E-04	AI398674.1	EST_HUMAN	ht28a02.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:2119082 3'
3354	16399	29296	5.56	3.0E-04	P25147	SWISSPROT	INTERNALIN B PRECURSOR

Page 197 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4047	17074	29960	3.18	3.0E-04	P49448	SWISSPROT	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
4141	17162		1.67	3.0E-04	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
4182	17202		1.41	3.0E-04	BE140609.1	EST_HUMAN	RCO-HT0014-310599-028 HT0014 Homo sapiens cDNA
4930	17929		6.87	3.0E-04	BE153778.1	EST_HUMAN	PVO-HT0339-180200-007-g12 HT0339 Homo sapiens cDNA
4992	17991	30848	0.77	3.0E-04	AW937723.1	EST_HUMAN	QV3-DT0045-221239-046-d09 DT0045 Homo sapiens cDNA
6383	19432		5.49	3.0E-04	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
7132	20240	33490	3.75	3.0E-04	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7331	18489	31275	0.62	3.0E-04	AW893981.1	EST_HUMAN	RC4-NN0027-060400-011-b08 NN0027 Homo sapiens cDNA
8031	20947	34264	0.85	3.0E-04	P23488	SWISSPROT	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)
8836	21765	35112	4.88	3.0E-04	P22607	SWISSPROT	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3)
10431	23320	36737	1.19	3.0E-04	AA454055.1	EST_HUMAN	z48d08.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:795471 5' similar to gb:U62762
10674	23560	36992	0.76	3.0E-04	AI692139.1	EST_HUMAN	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (HUMAN); w75a11.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:2813276 3'
10938	23623	37250	3.8	3.0E-04	AA781201.1	EST_HUMAN	aj24g05.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:2813276 3' RIBOSOMAL PROTEIN L7A (HUMAN); nc38a04.r1 NCJ CGAP_P12 Homo sapiens cDNA clone IMAGE:1010430 similar to contains L1.L2 L1
12332	25934	31372	4.37	3.0E-04	AA228301.1	EST_HUMAN	repetitive element;
12674	25791	31578	2.8	3.0E-04	AB018292.1	NT	Homo sapiens mRNA for KIAA0749 protein, partial cds
13041	25877		2.71	3.0E-04	AL134483.1	EST_HUMAN	DKFZp547L185_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547L185 5'
186	13285	26201	1.65	2.0E-04	AF217788.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M88, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
501	13571	26489	2.23	2.0E-04	AU146707.1	EST_HUMAN	AU146707 HEMBBT Homo sapiens cDNA clone HEMBB1001253 3'
832	13984	26929	8.04	2.0E-04	MB6524.1	NT	Human dystrophin gene
932	13984	26930	8.04	2.0E-04	MB6524.1	NT	Human dystrophin gene
1207	14246		3.43	2.0E-04	AI288021.1	EST_HUMAN	qh98a11.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains
1214	14252		1.51	2.0E-04	AL163203.2	NT	MER3.b2 MER3 repetitive element;
1856	14878		1.22	2.0E-04	AF224268.1	NT	Homo sapiens chromosome 21 segment HS21C003
2109	15210		0.98	2.0E-04	AA478980.1	EST_HUMAN	Mus musculus 5' flanking region of Pib3 gene zu38b05.s1 Soares ovary tumor NHT Homo sapiens cDNA clone IMAGE:740337 3' similar to contains Alu repetitive element;
2611	15609	28804	6.18	2.0E-04	U66061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV18S1P, TCRBV15S1, TCRBV11S1A1T, HYB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRB1S1, TCRB1S2,>

Page 198 of 545  
Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3029	16081	28992	0.98	2.0E-04	AI124529.1	EST_HUMAN	am58c09.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539760 3'
3382	16425	26329	1.02	2.0E-04	5174736	NT	Homo sapiens tubulin, beta, 4 (TUBB4) mRNA
3497	16536	29434	3.47	2.0E-04	BE082317.1	EST_HUMAN	QV2.BT0636-070500-104-b07.BT0636 Homo sapiens cDNA
3524	16592	29496	1.65	2.0E-04	U34374.1	NT	Human tyrosine kinase TXK (btk) gene, exons 9 and 10
3886	17013	29902	0.75	2.0E-04	AW1978441.1	EST_HUMAN	EST390590 MAGE resequences, MAGP Homo sapiens cDNA
4241	17257		7.68	2.0E-04	U01029.1	NT	Phaseolus vulgaris nitrate reductase (PNR2) gene, complete cds
4780	17785	30655	1.65	2.0E-04	H98265.1	EST_HUMAN	yu01e11.1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4780	17785	30656	1.65	2.0E-04	H98265.1	EST_HUMAN	yu01e11.1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4911	17910		1.82	2.0E-04	U09226.1	NT	Gallus gallus proteasome 28 kDa subunit homolog mRNA, complete cds
5194	18186	31028	1.77	2.0E-04	AB037897.1	NT	Danio rerio tagoromo gene, exons 1 to 6, partial cds
5247	18234	31034	1.03	2.0E-04	AF057019.1	NT	Dicystotellum discoideum Interaplin (abpD) gene, complete cds
5302	18288	31138	1	2.0E-04	7262289	NT	Homo sapiens ARP3 (actin-related protein 3, yeast) homolog (ACTR3), mRNA
6302	18288	31139	1	2.0E-04	7262289	NT	Homo sapiens ARP3 (actin-related protein 3, yeast) homolog (ACTR3), mRNA
5735	18808	31902	2.43	2.0E-04	AV654352.1	EST_HUMAN	AV654352 GLC Homo sapiens cDNA clone GLC00H10 3'
5748	18821	31918	1.76	2.0E-04	AI800882.1	EST_HUMAN	It03b11.x1 NCI_QGAP_U13 Homo sapiens cDNA clone IMAGE:2207709 3'
5956	18023	32143	0.96	2.0E-04	AA286652.1	EST_HUMAN	EST11191 Uterus Homo sapiens cDNA 5' end similar to EST containing O family repeat
6172	19228	32375	0.78	2.0E-04	4758179	NT	Homo sapiens cell cycle progression 3 protein (DNJ3) mRNA
6486	19631	32709	1.83	2.0E-04	AF140708.1	NT	Mus musculus G protein coupled receptor gene, complete cds; and unknown gene
7599	20535		2.37	2.0E-04	AU121712.1	EST_HUMAN	AU121712 MAMMA1 Homo sapiens cDNA clone MAMMA1000798 5'
7709	20641		0.74	2.0E-04	AW860963.1	EST_HUMAN	QV0-CT0387-180300-187-e10 CT0387 Homo sapiens cDNA
8068	20931		13.86	2.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
							MYOMESIN 2 (M-PROTEIN) (165 KD TITIN-ASSOCIATED PROTEIN) (165 KD CONNECTIN-ASSOCIATED PROTEIN)
8078	20990	34308	1.11	2.0E-04	P54296	SWISSPROT	ASSOCIATED PROTEIN
8533	21464	34804	0.96	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
8533	21464	34805	0.96	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
8861	21791	35142	1.31	2.0E-04	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8861	21791	35143	1.31	2.0E-04	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
9128	22056	35416	2.28	2.0E-04	AF020503.1	NT	Homo sapiens FRAB8 common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
9302	22230	35590	0.52	2.0E-04	X57331.1	NT	Human immunoglobulin C(mu) and C(delta) heavy chain genes (constant regions)
9953	22858	36246	0.58	2.0E-04	P18715	SWISSPROT	GASTRULA ZINC FINGER PROTEIN XLGF26.1
10181	23368	36781	0.87	2.0E-04	BE148303.1	EST_HUMAN	RC3-HT0254-157099-011-b05 HT0254 Homo sapiens cDNA

Page 199 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10520	23407	36819	2.09	2.0E-04	AA405777.1	EST_HUMAN	z166c11.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:742964 5'
11286	24207	37657	3.82	2.0E-04	AV730373.1	EST_HUMAN	AV730373 HTF Homo sapiens cDNA clone HTFAA01 5'
11618	24526		2.47	2.0E-04	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 6
11760	24651	38132	3.46	2.0E-04	AI440282.1	EST_HUMAN	i01111.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140289 3' similar to contains Alu repetitive element;
11858	24748	38240	2.82	2.0E-04	AW136740.1	EST_HUMAN	UIH-B11-adm-c-04-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717190 3'
13088	25848		130.57	2.0E-04	DB7675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
793	13848	26782	2.47	1.0E-04	H99846.1	EST_HUMAN	y28c09.s1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:262864 3' similar to contains L1.1 L1 repetitive element;
1102	14145	27093	2.17	1.0E-04	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE];
1141	14183	27120	3.59	1.0E-04	AW013847.1	EST_HUMAN	ENDONUCLEASE
1141	14183	27121	3.59	1.0E-04	AW013847.1	EST_HUMAN	UIH-B10-aab-e-09-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1360	14391		2.89	1.0E-04	U62918.1	NT	UIH-B10-aab-e-09-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
						NT	Anguilla anguilla dopamine D1A1 receptor (d1A1) gene, complete cds
						NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1651	14692	27644	2.56	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1651	14692	27645	2.56	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1886	14907	27892	1.23	1.0E-04	AB048342.1	NT	Equus caballus DNA, chromosome 24q14, microsatellite TKY39
2686	15690	28690	1.05	1.0E-04	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
2686	15690	28691	1.05	1.0E-04	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
2736	15731	28726	0.91	1.0E-04	BE218833.1	EST_HUMAN	h45c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176366 3'
2736	15731	28727	0.91	1.0E-04	BE218833.1	EST_HUMAN	h45c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176366 3'
3328	16374	28275	1.42	1.0E-04	Q62203	SWISSPROT	SPLICING FACTOR 3A SUBUNIT 2 (SF3A69)
3798	16829	29716	0.9	1.0E-04	AI440282.1	EST_HUMAN	i01111.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140289 3' similar to contains Alu repetitive element;
4145	17166	30040	1.69	1.0E-04	M14042.1	NT	Mouse alpha 1 type-IV collagen mRNA
4170	17161	30063	1.62	1.0E-04	AV647727.1	EST_HUMAN	AV647727 GLC Homo sapiens cDNA clone GLCBB04 3'
4576	17594	30446	1.03	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5231	18219	31066	1.14	1.0E-04	7662015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5231	18219	31067	1.14	1.0E-04	7662015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
6074	19135	32269	1.74	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG

Page 200 of 545  
Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6148	19207	32345	0.46	1.0E-04	T19615.1	EST_HUMAN	753F Heart Homo sapiens cDNA clone 753
6148	19207	32346	0.46	1.0E-04	T19615.1	EST_HUMAN	753F Heart Homo sapiens cDNA clone 753
6707	19743	32946	0.98	1.0E-04	AA177111.1	EST_HUMAN	nc02a12.s1 NCI_CGAP_P3 Homo sapiens cDNA clone IMAGE:252
7151	20259	33513	0.6	1.0E-04	AA564561.1	EST_HUMAN	n25a04.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:993480 3' similar to gb:M97252
7550	20488	33777	14.75	1.0E-04	A1251980.1	EST_HUMAN	KALLMANN SYNDROME PROTEIN PRECURSOR (HUMAN); contains Alu repetitive element;
8004	20488	33777	15.42	1.0E-04	A1251980.1	EST_HUMAN	q57d10.x1 NCI_CGAP_Ox32 Homo sapiens cDNA clone IMAGE:1885683 3'
8574	21505	34949	1.13	1.0E-04	AA830453.1	EST_HUMAN	ab94g08.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:854654 3'
9876	22791	36181	2.74	1.0E-04	A1806220.1	EST_HUMAN	w26e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2396742 3'
9888	22801	36188	1.38	1.0E-04	O88969	SWISSPROT	CYSTATIN-RELATED EPIDIDYMAL SPERMATOGENIC PROTEIN PRECURSOR (CYSTATIN 8)
9959	22864		0.62	1.0E-04	T77153.1	EST_HUMAN	y472a08.r1 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:113774 5'
10172	23063	36460	1.61	1.0E-04	10863876	NT	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA
10675	23561		5.84	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10711	23597	37024	1.04	1.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11751	24580		2.01	1.0E-04	M28587.1	NT	Mouse alpha leukocyte interferon gene, complete cds
12077	24918	38418	1.85	1.0E-04	AB032688.1	NT	Homo sapiens mRNA for KIAA1142 protein, partial cds
12116	24957	38460	2	1.0E-04	AW269061.1	EST_HUMAN	xv49g12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2816618 3'
12146	24986	38486	1.98	1.0E-04	Q03696	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
12146	24986	38487	1.98	1.0E-04	Q03696	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
12216	25050		1.48	1.0E-04	AJ251893.1	NT	Homo sapiens partial SLG22A2 gene for organic cation transporter (OCT2), exon 1
722	13780	26702	2.01	9.0E-05	AA718933.1	EST_HUMAN	ah45c11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1292468 3'
5382	18364	31203	1.17	9.0E-05	AF156166.1	NT	Homo sapiens putative tumor suppressor mRNA
6190	19247	32393	1.5	9.0E-05	Q60716	SWISSPROT	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
8011	20928	34245	0.79	9.0E-05	AW204958.1	EST_HUMAN	UI-H-B11-aer-4-05-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720289 3'
8011	20928	34246	0.79	9.0E-05	AW204958.1	EST_HUMAN	UI-H-B11-aer-4-05-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720289 3'
10009	22826		2.67	9.0E-05	D85608.1	NT	Homo sapiens gene for cholecystokinin type-A receptor, complete cds
10011	22828	36215	3.12	9.0E-05	AF120982.1	NT	Homo sapiens methyl-CpG binding protein 1 (MBD1) gene, exon 15b
11576	24485	37953	3.04	9.0E-05	AW073078.1	EST_HUMAN	xa34g05.x1 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568728 3' similar to contains L1 t2 L1 repetitive element;
11698	24590	38067	2.15	9.0E-05	AJ287878.1	EST_HUMAN	qv23f06.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1682435 3' similar to contains element MIR repetitive element;
12042	19247	32393	3.66	9.0E-05	Q60716	SWISSPROT	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR

Page 201 of 545  
Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12521	25818		4.85	9.0E-05	AF129756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, IC7, LST-1, LTB, TNF, and LTA genes, complete cds
846	13901	26841	1.38	8.0E-05	AJ251646.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
889	13942		4.34	8.0E-05	AJ251648.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
4595	17603	30459	0.89	8.0E-05	AW044605.1	EST_HUMAN	wy78a04.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2554638 3'
9308	22236	35697	0.53	8.0E-05	Y11686.1	NT	Mus musculus gene for hexokinase II, exon 1 (and joined CDS)
11591	24500	37869	2.95	8.0E-05	M69197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
13070	25904		1.45	8.0E-05	AA278333.1	EST_HUMAN	z88h01.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704893 3' similar to contains Alu repetitive element; contains element MSRT1 repetitive element ;
367	13454	26366	4.31	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220999-011-E04 CT0208 Homo sapiens cDNA
367	13454	26367	4.31	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220999-011-E04 CT0208 Homo sapiens cDNA
589	13657	26560	6.85	7.0E-05	L49075.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
589	13657	26561	6.85	7.0E-05	L49075.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
1082	14128	27084	1.13	7.0E-05	Q22949	SWISSPROT	PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT)
2767	15759	28753	4.27	7.0E-05	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
3201	16249	29145	3.16	7.0E-05	AB009080.1	NT	Dicystidium discoidium gene for TRFA, complete cds
4142	17163		0.81	7.0E-05	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
4479	17490	30350	2.12	7.0E-05	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4536	17565	30423	0.66	7.0E-05	U60980.1	NT	Caenorhabditis elegans Syp1p homolog mRNA, complete cds
5037	18034	30891	0.88	7.0E-05	9845300	NT	Rat cytomegaloovirus Measrich1, complete genome
8803	21793	35082	1.17	7.0E-05	AA505582.1	EST_HUMAN	nh93g01.s1 NCL_CGAP_Br2 Homo sapiens cDNA clone IMAGE:986088 3'
10082	22875	36263	4.71	7.0E-05	T07095.1	EST_HUMAN	EST04984 Fatal brain, Striatum (catf936206) Homo sapiens cDNA clone HFBED60
11600	24509		6.96	7.0E-05	10835049	NT	Homo sapiens sarcoglycan, epsilon (SGCE), mRNA
2040	15057	28057	1.14	6.0E-05	4886170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2040	15057	28058	1.14	6.0E-05	4886170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2628	15626	28620	1.38	6.0E-05	AI656241.1	EST_HUMAN	w54h06.x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:2308631 3' similar to gb.J03250 DNA
2733	15728	28722	1.11	6.0E-05	Z84506.1	NT	TOPOISOMERASE I (HUMAN);
2733	15728	28723	1.11	6.0E-05	Z84506.1	NT	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA28B10
2861	13762	26678	2.66	6.0E-05	AF053630.1	NT	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA28B10
6134	19193	32329	3.87	6.0E-05	Q12860	SWISSPROT	Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)

Page 202 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6134	19193	32330	3.87	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6668	19706	32901	1.46	6.0E-05	N72829.1	EST_HUMAN	y60g11.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246212 5'
7263	20172	33413	0.73	6.0E-05	AA897680.1	EST_HUMAN	y60a03.s1 Soares_NFL_T_CBC_S1 Homo sapiens cDNA clone IMAGE:1604688 3'
8663	21604	34933	1.06	6.0E-05	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-106 BT0311 Homo sapiens cDNA
8803	21694	34934	1.06	6.0E-05	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-106 BT0311 Homo sapiens cDNA
9011	21940	35296	0.56	6.0E-05	AA150482.1	EST_HUMAN	2108c08.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:491726 3' similar to contains element MER28 repetitive element;
9016	21945	35301	3.62	6.0E-05	AW896629.1	EST_HUMAN	P4M-NN0050-310300-001-110 NN0050 Homo sapiens cDNA
9143	22071	35433	0.63	6.0E-05	Q60401	SWISSPROT	COMPLEMENT DECA-ACCELERATING FACTOR PRECURSOR
9794	22758	36143	1.71	6.0E-05	P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
9794	22758	36144	1.71	6.0E-05	P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
10051	22967	36356	0.69	6.0E-05	T94149.1	EST_HUMAN	y628c12.1 Siratagene lung (9337210) Homo sapiens cDNA clone IMAGE:119062 5'
11189	24116	37563	2.41	6.0E-05	R75639.1	EST_HUMAN	y69d08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:143535 3' similar to contains Alu repetitive element; contains LTR7 repetitive element;
11950	24794	38293	3.33	6.0E-05	AA044015.1	EST_HUMAN	zk5902.1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487035 5'
12723	25802	31562	9.53	6.0E-05	AW890110.1	EST_HUMAN	MRO-NT0038-250400-001-109 NT0038 Homo sapiens cDNA
13059	26595	31728	2.44	6.0E-05	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
1429	14460	27412	9.5	6.0E-05	AW362086.1	EST_HUMAN	QV4-ST0234-241199-040-111 ST0234 Homo sapiens cDNA
1888	14909	28573	3.16	6.0E-05	8923891	NT	Homo sapiens 22kDa peroxisomal membrane protein-like (LOC656895), mRNA
2580	15579	28573	1.04	6.0E-05	P23249	SWISSPROT	PROTEIN MOV-10
2903	15957	28575	0.97	6.0E-05	AJ251058.1	NT	Homo sapiens MEPIA gene, promoter region and exon 1
4064	17090	29975	3.75	6.0E-05	AJ251884.1	NT	Homo sapiens partial SLC22A3 gene for extraneuronal monoamine transporter (EMT), exon 1
5301	18285	31136	0.65	6.0E-05	Q26422	SWISSPROT	LIMULUS CLOTTING FACTOR C PRECURSOR (FC)
5301	18285	31137	0.65	6.0E-05	Q26422	SWISSPROT	LIMULUS CLOTTING FACTOR C PRECURSOR (FC)
5716	18788	31719	10.99	6.0E-05	X59855.1	NT	Human MLC1emb gene for embryonic myosin alkaline light chain, 3'UTR
6224	19279	32433	3.28	6.0E-05	AV653544.1	EST_HUMAN	AV653544 GLC Homo sapiens cDNA clone GLCMA06 3'
6409	19457	32631	0.79	6.0E-05	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
7716	20848		1.24	6.0E-05	AB037964.1	NT	Mus musculus gene for calretinin, exon 1
12518	25400		7.16	6.0E-05	P49163	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
12771	25400		5.99	6.0E-05	P49163	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
2854	13343		3.02	6.0E-05	U12821.1	NT	Human retin (REN) gene, 5' flanking region
4596	17604	30460	1.24	6.0E-05	P49163	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4596	17604	30461	1.24	6.0E-05	P49163	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4982	17981		1.2	6.0E-05	AF184488.1	NT	Cryptosporidium parvum isolate Zaire 15 kDa glycoprotein gp15 gene, partial cds



Page 203 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5146	18141	30986	0.74	4.0E-05	AF212313.1	NT	Drosophila melanogaster senseless protein (sens) gene, complete cds
7271	20179	33422	0.69	4.0E-05	U01947.1	NT	Mecaca mulatta haptoglobin (HP) gene, 5' region
10053	22998		7.1	4.0E-05	AF202635.1	NT	Homo sapiens PP1200 mRNA, complete cds
10506	23393	36805	0.61	4.0E-05	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
10891	23778	37202	0.63	4.0E-05	P23780	SWISSPROT	ENDONUCLEASE]
11207	24133	37661	4.6	4.0E-05	AW627946.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE) (ACID BETA-GALACTOSIDASE)
12412	25181	31877	1.69	4.0E-05	AL163252.2	NT	h36c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2974380 3' similar to contains element MIR repetitive element ;
704	13763	26690	0.71	3.0E-05	A1248061.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C052
1086	14130	27068	1.71	3.0E-05	AW273851.1	EST_HUMAN	q164c10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element ;
1158	14199	27135	1.29	3.0E-05	BF037698.1	EST_HUMAN	xx24g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814100 3'
1168	14199	27136	1.29	3.0E-05	BF037698.1	EST_HUMAN	601461463F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3865142 5'
1543	14573	27532	0.99	3.0E-05	BE169211.1	EST_HUMAN	601461463F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3865142 5'
1543	14573	27533	0.99	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
3335	16381		0.71	3.0E-05	A1288919.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4489	17500	30362	0.18	3.0E-05	BE169211.1	EST_HUMAN	q19g11.x1 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:1879748 3' similar to TR:O08632
4489	17500	30363	0.18	3.0E-05	BE169211.1	EST_HUMAN	O08632 GLYCINE TYROSINE-RICH HAIR PROTEIN ;
4578	17586	30447	0.86	3.0E-05	AA368679.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4578	17586	30448	0.86	3.0E-05	AA368679.1	EST_HUMAN	EST79996 Placenta 1 Homo sapiens cDNA similar to similar to p53-associated protein
4732	17737	30599	0.71	3.0E-05	AF149773.1	NT	EST79996 Placenta 1 Homo sapiens cDNA similar to similar to p53-associated protein
4849	17851	30719	0.95	3.0E-05	P97468	SWISSPROT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
4951	13753	26690	0.68	3.0E-05	A1248061.1	EST_HUMAN	CHEMOKINE RECEPTOR-LIKE 1 (G-PROTEIN COUPLED RECEPTOR DEZ)
6749	18822	31919	1.71	3.0E-05	11072102	EST_HUMAN	q164c10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element ;
7062	20086	33319	1.08	3.0E-05	AJ225782.1	NT	Mus musculus myosin light chain 2, precursor lymphocyte-specific (MYL2p1), mRNA
7062	20086	33320	1.08	3.0E-05	AJ225782.1	NT	Homo sapiens SYBL1 gene, exons 6-8
8478	21409	34747	2.38	3.0E-05	BE733167.1	EST_HUMAN	Homo sapiens SYBL1 gene, exons 6-8
9450	22378	35741	1.65	3.0E-05	AW770982.1	EST_HUMAN	601567451F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842202 6'
9454	22382	35744	1.77	3.0E-05	AW770982.1	EST_HUMAN	h94e08.x1 NCJ_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009638 3'
9458	22386	35748	0.73	3.0E-05	P43361	SWISSPROT	Homo sapiens Interleukin-1 receptor antagonist homolog 1 (IL1HY1), mRNA
9675	22801		0.6	3.0E-05	X03273.1	NT	MELANOMA-ASSOCIATED ANTIGEN 8 (MAGE-8 ANTIGEN)
							Human Alu-family cluster 6 of alpha(1)-acid glycoprotein gene

Page 204 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

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9860	22775	36181	1.73	3.0E-05	AA372562.1	EST_HUMAN	EST164475 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
10187	23078		3.49	3.0E-05	A1769331.1	EST_HUMAN	wg36109.x1 Soares_NSF_FB_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
11014	23898	37333	0.9	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NEL-LIKE PROTEIN 2)
11014	23898	37334	0.9	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NEL-LIKE PROTEIN 2)
12420	25186		1.72	3.0E-05	L77570.1	NT	Homo sapiens D1George syndrome critical region, centromeric end
12595	25261		1.5	3.0E-05	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
2346	16354	28357	1.36	2.0E-05	A1286021.1	EST_HUMAN	q198e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3.b2 MER3 repetitive element;
2620	16618	28811	8.89	2.0E-05	M13792.1	NT	Human adenosine deaminase (ADA) gene, complete cds
2762	15764		5.86	2.0E-05	AA160562.1	EST_HUMAN	zq46a12.r1 Stralagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632734 5' similar to contains Alu repetitive element; contains element L1 repetitive element;
3182	16232	29127	1.93	2.0E-05	BE06036.1	EST_HUMAN	RC3-BT0319-120200-014-h08 BT0319 Homo sapiens cDNA
3397	16439	29343	0.92	2.0E-05	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
3427	16498	29377	0.85	2.0E-05	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
3553	16591		0.77	2.0E-05	X95465.1	NT	S. cerevisiae 12.8 Kbp fragment of the left arm of chromosome XV
3875	16904		0.67	2.0E-05	AL039107.1	EST_HUMAN	DKFZp5661064_r1 568 (synonym: htkd2) Homo sapiens cDNA clone DKFZp5661064 5'
4803	17804		1.23	2.0E-05	BE378471.1	EST_HUMAN	601236456F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608663 5'
5866	19033	32154	2.01	2.0E-05	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
6139	19199		0.76	2.0E-05	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
6199	19255	32401	2.23	2.0E-05	Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
6199	19255	32402	2.23	2.0E-05	Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
6398	19446	32617	0.68	2.0E-05	A1149272.1	EST_HUMAN	q672a02.x1 Soares_placenta_8169weeks_2NbHP8tc9W Homo sapiens cDNA clone IMAGE:1715114 3' similar to contains L1.13 L1 repetitive element;
6475	19520	32696	0.52	2.0E-05	P35085	SWISSPROT	CALCIUM-BINDING PROTEIN
6913	19943	33162	2.19	2.0E-05	AA714330.1	EST_HUMAN	rn06d12.s1 NCL_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238519 3'
7230	20139	33378	2	2.0E-05	Y08926.1	NT	P. falciparum mRNA for AARP1 protein, partial
7242	20151	33390	1.15	2.0E-05	A1492960.1	EST_HUMAN	q247b06.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2030003 3' similar to TR:O02711
7252	20161		7.05	2.0E-05	A1891025.1	EST_HUMAN	O02711 PRO-POL-DUTPASE POLYPROTEIN;
							wu35h07.x1 Soares_Diethylgraef_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'

Table 4

## Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7514	20453	33738	2.27	2.0E-05	AF224262.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
7514	20453	33739	2.27	2.0E-05	AF224262.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
7769	20889		0.98	2.0E-05	AF128847.1	NT	Homo sapiens indolethylamine N-methyltransferase (NMT) mRNA, INMT-2 allele, complete cds
8465	21398	34737	2.28	2.0E-05	AI381040.1	EST_HUMAN	ig20105.x1 NCI_CGAP CLL1 Homo sapiens cDNA clone IMAGE:2109369 3'
9666	22592	35965	0.56	2.0E-05	BE244840.1	EST_HUMAN	TCBAP2E1590 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP1590
9666	22592	35966	0.56	2.0E-05	BE244840.1	EST_HUMAN	TCBAP2E1590 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP1590
9807	22713	36095	0.52	2.0E-05	P49457	SWISSPROT	COMPLEMENT DEACY-ACCELERATING FACTOR (CD55)
9807	22713	36096	0.52	2.0E-05	P49457	SWISSPROT	COMPLEMENT DEACY-ACCELERATING FACTOR (CD55)
10434	23323	36741	0.8	2.0E-05	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
10634	23520	36954	0.92	2.0E-05	BF055939.1	EST_HUMAN	775g09.y1 NCI_CGAP_Bm20 Homo sapiens cDNA clone IMAGE:3340576 5'
11062	23946	37383	2.74	2.0E-05	N41751.1	EST_HUMAN	yw91a06.r1 Soares_placenta_8to9weeks_2NHP809W Homo sapiens cDNA clone IMAGE:259570 5'
11062	23946	37384	2.74	2.0E-05	N41751.1	EST_HUMAN	yw91a06.r1 Soares_placenta_8to9weeks_2NHP809W Homo sapiens cDNA clone IMAGE:259570 5'
11089	20161		2.43	2.0E-05	AI991025.1	EST_HUMAN	wu35h07.x1 Soares_Dieckgrafe_cdonr_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'
11883	23968	37424	2.34	2.0E-05	BE175801.1	EST_HUMAN	RC5-HT0562-280300-012-E12 HT0582 Homo sapiens cDNA
12529	25738		5.86	2.0E-05	BE348220.1	EST_HUMAN	hw21a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3183532 3' similar to TR:Q12832
12629	25886		10.39	2.0E-05	AW074604.1	EST_HUMAN	xe89a03.x1 NCI_CGAP_Cot17 Homo sapiens cDNA clone IMAGE:2573832 3' similar to contains L1.b3 L1 repetitive element
12677	25727		2.42	2.0E-05	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
12817	25438	31765	1.45	2.0E-05	AU131513	EST_HUMAN	AU131513 NT2RP3 Homo sapiens cDNA clone NT2RP3002707 5'
13104	25619		2.09	2.0E-05	AI200970.1	EST_HUMAN	q68g11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755236 3'
2286	15294	28302	1.24	1.0E-05	P27448	SWISSPROT	PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78
2745	15932	28731	2.24	1.0E-05	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
3718	16750	29638	2.1	1.0E-05	AF088273.1	NT	Drosophila melanogaster strain Lembo 120 Suppressor of Hairless (Su(H)) gene, partial cds
3881	16910		1.51	1.0E-05	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced

Page 206 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4050	17077	29992	15.85	1.0E-05	P81274	SWISSPROT	MOSAIC PROTEIN LGN
4268	17284	30151	1.2	1.0E-05	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4375	17389	30232	2.22	1.0E-05	AA431119.1	EST_HUMAN	zw69g04.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:781494 5'
4961	17959	30817	2.78	1.0E-05	AW4719134.1	EST_HUMAN	xy49j11x1 NCI CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2859548 3'
5081	18078	30927	0.7	1.0E-05	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
7056	20092	33314	1.68	1.0E-05	AJ246003.1	NT	Homo sapiens Spast gene for spastin protein
7169	18441	31344	0.46	1.0E-05	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7440	20182	33426	3.21	1.0E-05	AA641846.1	EST_HUMAN	ns19g02.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184114 3' similar to contains L1.t1 L1
7442	20383	33552	12.61	1.0E-05	4503844	NT	Homo sapiens phospholipase A2, group X (PLA2G10) mRNA, and translated products
8109	21021	34347	0.63	1.0E-05	BF222646.1	EST_HUMAN	7p57d01.x1 NCI CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3649945 3' similar to contains MER10.b3
8261	21156		2.43	1.0E-05	P19474	SWISSPROT	MER10 repetitive element ;
9472	22400		2.99	1.0E-05	AL163227.2	NT	52 KD RO PROTEIN (SUOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
9612	22538	35908	2.81	1.0E-05	AA452578.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
9827	22733	36115	13.49	1.0E-05	AA236110.1	EST_HUMAN	zx38h12.s1 Soares total_fetus_Nb2HP8_9w Homo sapiens cDNA clone IMAGE:788519 3' similar to gbL02932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
9905	22893	36279	0.77	1.0E-05	AV732190.1	EST_HUMAN	zo05e11.1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:584332 5' similar to contains Alu repetitive element; contains element TAR1 repetitive element ;
10353	23242	36561	0.89	1.0E-05	AW510902.1	EST_HUMAN	AV732190 HTF Homo sapiens cDNA clone HIT FBH01 5'
10353	23242	36562	0.89	1.0E-05	AW510902.1	EST_HUMAN	hd41b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains OFR.11 OFR repetitive element ;
10427	23316	36733	2.56	1.0E-05	AW291521.1	EST_HUMAN	hd41b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains OFR.11 OFR repetitive element ;
10427	23316	36734	2.59	1.0E-05	AW291521.1	EST_HUMAN	UI-H-B12-agk-a-08-0-UI.s1 NCI CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
10681	23567		1.76	1.0E-05	AW469995.1	EST_HUMAN	UI-H-B12-agk-a-08-0-UI.s1 NCI CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
11356	24274	37716	2.1	1.0E-05	U91328.1	NT	ha07c10.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2873010 3' similar to contains L1.12 L1 repetitive element ;
11356	24274	37717	2.1	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
12981	25880	31477	2.31	1.0E-05	AL163303.2	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds

Page 207 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2721	15714	28713	7.88	9.0E-06	AI583811.1	EST_HUMAN	IT73a06.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246386 3'
3143	16193	29086	4.94	9.0E-06	AI218983.1	EST_HUMAN	qg11b08.x1 Soares_placenta_8to6weeks_2NbHP86W Homo sapiens cDNA clone IMAGE:1769191 3'
3874	16707		2.83	9.0E-06	M61755.1	NT	Human alanineglyoxylate aminotransferase (AGXT) gene, exons 1 and 2
6123	19182	32317	2.63	9.0E-06	L23416.1	NT	Homo sapiens differentiation antigen CD20 gene, exons 8, 9
7188	20183	33431	1.03	9.0E-06	BE085042.1	EST_HUMAN	RC1-BT0313-110500-017-a07 BT0313 Homo sapiens cDNA
7844	20771	34074	0.89	9.0E-06	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8246	21151	34486	12.99	9.0E-06	AI034370.1	EST_HUMAN	ox20g01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1656912 3' similar to contains Alu repetitive element;
9033	21892	35322	1.7	9.0E-06	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
9534	22481	35823	3.66	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
9534	22481	35824	3.66	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
9763	22687	36073	3.9	9.0E-06	U35114.1	NT	Human apolipoprotein E (APOE) gene, hepatic control region HCR-2
11377	24293	37738	3.53	9.0E-06	Q10364	SWISSPROT	PUTATIVE SERINE/THREONINE-PROTEIN KINASE C22E12.14C
2557	15926	28556	1.82	8.0E-06	AW362539.1	EST_HUMAN	RC3-CT0283-201189-011-h11 CT0283 Homo sapiens cDNA
11012	23896	37330	0.78	8.0E-06	P34083	SWISSPROT	FASIGLII, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)
11012	23896	37331	0.78	8.0E-06	P34083	SWISSPROT	FASIGLII, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)
1006	14055		1.62	7.0E-06	AA669729.1	EST_HUMAN	ab90f10.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:854251 3' similar to contains
1459	14490	27451	3.05	7.0E-06	7652177	NT	MER20.11 MER20 repetitive element;
2916	15999		15.08	7.0E-06	AI369252.1	EST_HUMAN	Homo sapiens KIAA0553 gene product (KIAA0553), mRNA
3822	16658		0.87	7.0E-06	AA385542.1	EST_HUMAN	qw16g09.x1 NCI_CGAP_U3 Homo sapiens cDNA clone IMAGE:1891298 3' similar to contains Alu repetitive element;
5894	18993		5.3	7.0E-06	AW8693141.1	EST_HUMAN	EST19205 Thyroid Homo sapiens cDNA 5' end similar to EST containing L1 repeat
8015	16078	32203	0.94	7.0E-06	N98845.1	EST_HUMAN	QV2-OT0062-250400-173-R01 OT0062 Homo sapiens cDNA
9347	22275	35637	1.11	7.0E-06	11420709	NT	YJ65C07.r1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:278412 5'
10412	23301		0.56	7.0E-06	Q61147	SWISSPROT	Homo sapiens DNA segment, numerous copies, expressed probes (GS1 gene) (DXF68S1E), mRNA
1288	26806	31366	1.86	7.0E-06	BF216972.1	EST_HUMAN	CERULOPLASMIN PRECURSOR (FERROXIDASE)
2980	16012	28910	1.56	6.0E-06	BE089189.1	EST_HUMAN	601881622F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083972 5'
3758	16790	28880	1.11	6.0E-06	BE089189.1	EST_HUMAN	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA
4866	16036	28938	2.37	6.0E-06	Q01466	SWISSPROT	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA
							OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)

Page 208 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4874	17873	30737	2.75	6.0E-06	AJ040099.1	EST_HUMAN	oxc9e02.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1655738 3' similar to contains MER8.12 MER8 repetitive element
5593	18612	31481	1.37	6.0E-06	AF167441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
5594	18670	31549	1.18	6.0E-06	Q02040	SWISSPROT	PROTEIN XE7
10370	23259		2.19	6.0E-06	AW801912.1	EST_HUMAN	IL5-UM0070-110400-063-g02 UM0070 Homo sapiens cDNA
13061	25587	31740	1.95	6.0E-06	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
6296	19347	32515	4.53	5.0E-06	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
6594	19635	32817	2.11	5.0E-06	U07591.1	NT	Human ABL gene, exon 1b and Intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
7401	20100	33335	0.62	5.0E-06	BE145171.1	EST_HUMAN	CM2-HT0193-191099-022-f06 HT0193 Homo sapiens cDNA
7603	20538	33827	0.97	5.0E-06	AB007546.1	NT	Homo sapiens gene for LECT2, complete cds
9028	21957	35316	0.89	5.0E-06	AW856972.1	EST_HUMAN	RC1-CT0302-120200-013-h02 CT0302 Homo sapiens cDNA
9028	21957	35317	0.89	5.0E-06	AW856972.1	EST_HUMAN	RC1-CT0302-120200-013-h02 CT0302 Homo sapiens cDNA
10603	23499	36918	9.02	5.0E-06	AA313620.1	EST_HUMAN	EST185486 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
10992	23876	37305	0.86	5.0E-06	P06681	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/05 CONVERTASE)
12970	25534	31749	4.21	5.0E-06	A065045.1	EST_HUMAN	HA0877 Human fetal liver cDNA library Homo sapiens cDNA
670	13732	26643	4.55	4.0E-06	R16267.1	EST_HUMAN	y448c03.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:53254 5' similar to contains Alu repetitive element; contains L1 repetitive element
871	13924	26871	9.61	4.0E-06	AW103354.1	EST_HUMAN	xc69g12.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2589574 3' similar to contains Alu repetitive element; contains element MER21 repetitive element
1362	14393	27347	5.1	4.0E-06	A1334928.1	EST_HUMAN	ib33e09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2036168 3'
1362	14393	27348	5.1	4.0E-06	A1334928.1	EST_HUMAN	ib33e09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2036168 3'
1492	14523	27485	3.4	4.0E-06	BF365612.1	EST_HUMAN	GV2-NT0046-200600-250-h07 NT0048 Homo sapiens cDNA
2282	15281	28299	1.85	4.0E-06	AW015401.1	EST_HUMAN	UI-H-BIO-aat-E05-0-U1.a1 NCI_CGAP_Sub1 Homo sapiens cDNA
3111	16192	28058	0.78	4.0E-06	AF198349.1	NT	Galus gallus Dach2 protein (Dach2) mRNA, complete cds
3964	16992	28876	1.26	4.0E-06	AW848295.1	EST_HUMAN	IL3-CT0214-150200-074-B03 CT0214 Homo sapiens cDNA
4922	17921	30784	1.94	4.0E-06	A1889939.1	EST_HUMAN	WER22 repetitive element
9066	21695	35348	0.79	4.0E-06	O15393	SWISSPROT	TRANSMEMBRANE PROTEASE, SERINE 2
9358	22205	35649	4.48	4.0E-06	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TCRBV753A2 to TCRBV12S2 region
10230	23121	36523	1.1	4.0E-06	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
11883	23993	37421	4.56	4.0E-06	AB007955.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0486
2176	15198	28193	1.58	3.0E-06	AA700562.1	EST_HUMAN	z34b08.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1 L1 L1 repetitive element

Page 209 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2176	15198	28194	1.58	3.0E-06	AA700562.1	EST_HUMAN	Z134508.s1 Soares_fetal_liver_spleen_infls_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.11 L1 repetitive element;
2284	15292		1.63	3.0E-06	AF202635.1	NT	Homo sapiens PP1200 mRNA, complete cds
2994	16015	28913	1.26	3.0E-06	AA668218.1	EST_HUMAN	ak48g11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409252 3' similar to contains LTR1.13 LTR1 repetitive element;
3310	16357		2.18	3.0E-06	A1957779.1	EST_HUMAN	w22a05.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2425616 3' similar to TR:O60734 O60734 LINE-1 LIKE PROTEIN; contains L1.12 L1 repetitive element;
3849	16878	29782	1.4	3.0E-06	BE047094.1	EST_HUMAN	h64d12.x1 NCL_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
3849	16878	29783	1.4	3.0E-06	BE047094.1	EST_HUMAN	h64d12.x1 NCL_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
4588	17596	30454	0.71	3.0E-06	T50266.1	EST_HUMAN	y67b10.r1 Stralagene ovary (#937217) Homo sapiens cDNA clone IMAGE:77275 5' similar to contains L1 repetitive element
4677	17682	30550	4.38	3.0E-06	X54816.1	NT	Homo sapiens gene for alpha-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1-microglobulin, N-terminus)
6401	19449	32620	0.79	3.0E-06	AU159412.1	EST_HUMAN	AU59412 THYRO1 Homo sapiens cDNA clone THYRO1001602 3'
7598	20534		2.11	3.0E-06	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8681	21592	34931	0.98	3.0E-06	BE562664.1	EST_HUMAN	601336213F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690314 5'
9242	22170	35522	0.77	3.0E-06	P07743	SWISSPROT	PAROTID SECRETORY PROTEIN PRECURSOR (PSP)
12683	25342		10.28	3.0E-06	AW385282.1	EST_HUMAN	RQO-LT0001-261169-011-A03 LT0001 Homo sapiens cDNA
216	13314		3.41	2.0E-06	P54366	SWISSPROT	HOMEOBOX PROTEIN GOOSECOID
1588	14619		4.75	2.0E-06	P21414	SWISSPROT	POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
2401	15406	28409	1.54	2.0E-06	A1672138.1	EST_HUMAN	w604803.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297088 3' similar to contains MER30.b1 MER30 repetitive element;
2490	15492	28492	2.28	2.0E-06	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2601	15589	28584	2.38	2.0E-06	P08719	SWISSPROT	KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)
3579	16616	29519	1.39	2.0E-06	AV657555.1	EST_HUMAN	AV557555 GLC Homo sapiens cDNA clone GLCFDB05 3'
3823	16856	29739	2.19	2.0E-06	AA173518.1	EST_HUMAN	z02a03.r1 Stralagene ovarian cancer (#937216) Homo sapiens cDNA clone IMAGE:595232 5'
3835	16865	29748	0.88	2.0E-06	AW450215.1	EST_HUMAN	UI-HB18-aky-g-05-UJ.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736176 3'
3843	16872	29755	2.32	2.0E-06	AB030896.1	NT	Mus musculus gene for odorant receptor A16, complete cds
6326	10376		0.79	2.0E-06	AA974832.1	EST_HUMAN	en34h01.s1 NCL_CGAP_Lus Homo sapiens cDNA clone IMAGE:1568609 3' similar to contains Alu repetitive element;
6358	19407	32572	0.77	2.0E-06	A1539448.1	EST_HUMAN	le5105.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090241 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE.;
6709	19745	32948	5.73	2.0E-06	A1819424.1	EST_HUMAN	wj90504.x1 NCL_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410063 3'

Page 210 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7884	20810	34118	0.56	2.0E-06	AA688423.1	EST_HUMAN	nv59c06.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1234090 3' similar to contains L1.13 L1
8496	21427		1.17	2.0E-06	AW869223.1	EST_HUMAN	repetitive element;
8668	21599	34039	0.78	2.0E-06	T12238.1	EST_HUMAN	MR3-SN0067-120400-002-02 SN0067 Homo sapiens cDNA
9394	22322		0.98	2.0E-06	AA772497.1	EST_HUMAN	A447R Heart Homo sapiens cDNA clone A447
9407	22335	35699	1.62	2.0E-06	H62051.1	EST_HUMAN	z17c11.s1 Soares_pituitary_gland_N8HPG Homo sapiens cDNA clone IMAGE:413300 3' similar to
9757	22681	36066	1.09	2.0E-06	AF003529.1	NT	TR:P70467 P70467 REVERSE TRANSCRIPTASE ;
9757	22881	36067	1.09	2.0E-06	AF003529.1	NT	u37c04.f1 Soares_ovaary_tumor_NbHOT Homo sapiens cDNA clone IMAGE:236674 5' similar to gb:X74929
9777	22701		0.6	2.0E-06	AK73450.1	EST_HUMAN	KERATIN, TYPE II CYTOSKELETAL 8 (HUMAN);
10223	23114	36515	0.82	2.0E-06	N30576.1	EST_HUMAN	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
10430	23319		0.66	2.0E-06	AV748969.1	EST_HUMAN	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
12592	25009	31367	1.78	2.0E-06	P23249	SWISSPROT	tf16g10.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141730 3'
12735	25376		3.99	2.0E-06	BE328232.1	EST_HUMAN	yw66e03.s1 Soares_placenta_8to9weeks_2NblHP8c9W Homo sapiens cDNA clone IMAGE:257212 3'
35	13151	26040	1.77	1.0E-06	Q76092	SWISSPROT	AV748969 NPC Homo sapiens cDNA clone NPFCAXD05 5'
680	13742	26657	1.51	1.0E-06	AF084364.1	NT	PROTEIN MOV-10
1470	14501	27462	2	1.0E-06	P27625	SWISSPROT	hs92f02.x1 NCL CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3144699 3' similar to contains L1.12 L1
1546	14577	27537	1.22	1.0E-06	AL163278.2	NT	repetitive element;
1592	14623	27583	1.2	1.0E-06	AA034141.1	EST_HUMAN	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH-AFFINITY SODIUM-DEPENDENT CARNITINE COTRANSPORTER)
1592	14623	27584	1.2	1.0E-06	AA034141.1	EST_HUMAN	Mus musculus D6MME protein (D6MME) mRNA, complete cds
1608	14637		1.18	1.0E-06	P27625	SWISSPROT	MEROZOITE SURFACE PROTEIN CMZ-8
2010	15028	28020	6.69	1.0E-06	AF184614.1	NT	Homo sapiens chromosome 21 segment HS21C078
2010	15028	28021	6.69	1.0E-06	AF184614.1	NT	z106a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428982 3' similar to
4476	17487	30346	15.5	1.0E-06	U07551.1	NT	contains Alu repetitive element;
5246	18233	31082	1.05	1.0E-06	AL163285.2	NT	z106a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428982 3' similar to
5246	18233	31083	1.05	1.0E-06	AL163285.2	NT	contains Alu repetitive element;
5473	18554	31396	4.81	1.0E-06	BF333015.1	EST_HUMAN	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT
							Homo sapiens p47-phox (NCF1) gene, complete cds
							Homo sapiens p47-phox (NCF1) gene, complete cds
							Human ABL gene, exon 1b and intron 1b, and putative M6604 Met protein (M6604 Met) gene, complete cds
							Homo sapiens chromosome 21 segment HS21C085
							Homo sapiens chromosome 21 segment HS21C085
							MR1-BT0800-030700-002-c06 BT0800 Homo sapiens cDNA



Page 211 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5498	18577	31424	1.15	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-090600-001-e04 FN0004 Homo sapiens cDNA
5498	18577	31425	1.15	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-090600-001-e04 FN0004 Homo sapiens cDNA
5663	18737	31645	1.06	1.0E-06	O60613	SWISSPROT	15 KDA SELENOPROTEIN PRECURSOR
6005	19069		0.59	1.0E-06	BE093327.1	EST_HUMAN	GM0-BT0281-031169-087-104 BT0281 Homo sapiens cDNA
7198	20198	33444	5.2	1.0E-06	P02671	SWISSPROT	FIBRINOGEN ALPHA1(A)-E CHAIN PRECURSOR
8209	25987		0.52	1.0E-06	BE185330.1	EST_HUMAN	IL5-HT0730-020500-074-q01 HT0730 Homo sapiens cDNA
8580	21511		0.95	1.0E-06	AA012823.1	EST_HUMAN	cl29c08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524878 3'
8849	21779	35126	1.04	1.0E-06	AI347010.1	EST_HUMAN	q54602.x1 NCL_CGAP_C08 Homo sapiens cDNA clone IMAGE:1928642 3'
							q52309.x1 NCL_CGAP_Lym08 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element
9057	21988	35340	1.5	1.0E-06	AI287878.1	EST_HUMAN	MIR repetitive element ;
9844	22952	36341	1.11	1.0E-06	N74635.1	EST_HUMAN	z55501.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:286472 3'
9918	22903	36295	0.67	1.0E-06	Q39575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
10207	23099	36497	3.3	1.0E-06	U82668.1	NT	Homo sapiens chox gene, alternatively spliced products, complete cds
10207	23099	36498	3.3	1.0E-06	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
10248	23139	36545	5.26	1.0E-06	AA132811.1	EST_HUMAN	z017008.r1 Stragene clone (#937204) Homo sapiens cDNA clone IMAGE:587174 5'
							z040411.e1 Soares_total_fetus_NB2HF8_gw Homo sapiens cDNA clone IMAGE:785493 3' similar to
10307	23197		2.79	1.0E-06	AA449257.1	EST_HUMAN	gb:D26129 RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN);
10966	23850		2.3	1.0E-06	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
12076	24917		3.35	1.0E-06	AW890941.1	EST_HUMAN	RC4-NT0054-120500-012-b03 NT0064 Homo sapiens cDNA
12626	25303	31816	7.93	1.0E-06	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
381	13485	26383	1.26	9.0E-07	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
381	13486	26384	1.26	9.0E-07	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
8978	21908		0.59	9.0E-07	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
11693	24595	38072	3.1	9.0E-07	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
4883	17882	30747	5.27	8.0E-07	AI288596.1	EST_HUMAN	q182g07.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
4883	17882	30748	5.27	8.0E-07	AI288596.1	EST_HUMAN	q182g07.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
5103	19164		7.68	8.0E-07	P21414	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8581	21512		12.29	8.0E-07	AF135416.1	NT	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
12047	24888		7.22	8.0E-07	T07770.1	EST_HUMAN	EST05660 Fetal brain, Stragene (cat#936206) Homo sapiens cDNA clone HFBEN89
12270	25097		5.99	8.0E-07	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5709	18782	31712	0.89	7.0E-07		NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
5709	18782	31713	0.89	7.0E-07		NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
1929	14950	27926	3.2	6.0E-07	AW85558.1	EST_HUMAN	CM3-C10277-221089-024-e11 C10277 Homo sapiens cDNA

Page 212 of 545  
Table 4

## Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2515	15516	28520	2.42	6.0E-07	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (BF), and complement component C2 (C2) genes>
4056	17063		1.98	6.0E-07	P41479	SWISSPROT	HYPOTHETICAL 24.1 KD PROTEIN IN LEE4.P33 INTERGENIC REGION
9684	22610	35984	1.57	6.0E-07	BF001867.1	EST_HUMAN	7g94107.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3314149 3' similar to TR:O75920 O75920 4F5L..
12207	25042	38545	3.58	6.0E-07	A1782950.1	EST_HUMAN	om87105.y6 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1554177 5'
12498	25881		2.14	6.0E-07	AW503222.1	EST_HUMAN	GM4-NN1029-250300-121-112 NN1029 Homo sapiens cDNA
346	13435		1.93	5.0E-07	A1831893.1	EST_HUMAN	wh84f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
1084	14128		2.59	5.0E-07	AA390630.1	EST_HUMAN	EST193615 Supt cells Homo sapiens cDNA 5' end
3078	16129		0.78	5.0E-07	A1831893.1	EST_HUMAN	wh84f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
6359	19408	32573	1.38	5.0E-07	U65067.1	NT	Mus musculus OG-2 homeodomain protein (OG-2) gene, partial cds
6449	19495	32670	0.44	5.0E-07	AA278183.1	EST_HUMAN	Z06e03.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712552 5' similar to gb:X63741_rna1
7418	20117	33353	1.54	5.0E-07	A1393981.1	EST_HUMAN	FIBULIN-1, ISOFORM A PRECURSOR (HUMAN); repetitive element; contains element A3R repetitive element;
7418	20117	33354	1.54	5.0E-07	A1393981.1	EST_HUMAN	tg06b05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element; contains element A3R repetitive element;
7735	20667	33964	15.89	5.0E-07	AW070885.1	EST_HUMAN	xa31a02.x1 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568362 3' similar to gb:X15341 CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER (HUMAN);
8851	21781	35128	1.11	5.0E-07	Q9WUQ1	SWISSPROT	ADAM-TS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 1) (ADAMTS-1) (ADAM-TS1)
9059	21868		1.04	5.0E-07	P09593	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
10854	23740	37163	7.25	5.0E-07	A1908987.1	EST_HUMAN	GM-BT178-220499-014 BT178 Homo sapiens cDNA
11106	24037	37482	1.56	5.0E-07	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11947	24761	38286	3.91	5.0E-07	P11087	SWISSPROT	COLLAGEN ALPHA 1(I) CHAIN PRECURSOR
12012	24854		2.6	5.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
12890	25774		3.27	5.0E-07	AW1662537.1	EST_HUMAN	GV0-CT0383-210400-204-b12 CT0383 Homo sapiens cDNA
4085	17110	29989	1.66	4.0E-07	AW009602.1	EST_HUMAN	ws84h05.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2504897 3'
7542	20481		0.99	4.0E-07	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
7643	20578	33872	0.58	4.0E-07	Q8Z2V6	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)
7643	20578	33873	0.58	4.0E-07	Q8Z2V6	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)
8501	21432	34773	0.85	4.0E-07	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
9604	22530	35897	4.84	4.0E-07	AW116134.1	EST_HUMAN	xy49g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3'

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10814	23700	37128	0.65	4.0E-07	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
11376	24262	37736	3.3	4.0E-07	A1765528.1	EST_HUMAN	w181b08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703 3'
11376	24262	37737	3.3	4.0E-07	A1765528.1	EST_HUMAN	w181b08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703 3'
11670	24574		1.78	4.0E-07	BE001828.1	EST_HUMAN	PM1-BN0083-030300-003-e12 BN0083 Homo sapiens cDNA
464	13536	26456	4.44	3.0E-07	U19719.1	NT	Human microfilament-associated glycoprotein (MFAP2) gene, putative promoter region and alternatively spliced untranslated exons
604	13670	26573	1.46	3.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region, segment 1/2
1401	14432	27387	2.03	3.0E-07	M99149.1	NT	Human polymorphic microsatellite DNA
1649	14680		2.08	3.0E-07	M84857.1	NT	Human IgK subgroup 1 germline gene, exons 1 and 2, V-region 018 allele
2060	15076		1.07	3.0E-07	AA526763.1	EST_HUMAN	nt56509.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:980825 similar to contains Alu repetitive element; contains L1.13 L1 repetitive element
2307	15315	28318	1.77	3.0E-07	M99149.1	NT	Human polymorphic microsatellite DNA
2492	15494	28494	4.09	3.0E-07	BE005077.1	EST_HUMAN	MR0-BN0115-020300-001-F11 BN0115 Homo sapiens cDNA
2492	15494	28495	4.09	3.0E-07	BE005077.1	EST_HUMAN	MR0-BN0115-020300-001-F11 BN0115 Homo sapiens cDNA
3081	16132	29028	0.84	3.0E-07	T84704.1	EST_HUMAN	Yd5071.2.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:111695 5'
3202	16250	29146	2.3	3.0E-07	P38739	SWISSPROT	HYPOPHETICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR
4840	17841	30710	8.54	3.0E-07	AV650201.1	EST_HUMAN	AV650201 GLG Homo sapiens cDNA clone GLGGC001 3'
4876	17876	30740	0.87	3.0E-07	A1767236.1	EST_HUMAN	wed95b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347967 3'
5199	18190	31031	1.7	3.0E-07	T57650.1	EST_HUMAN	yc14h09.s1 Striatogene lung (#937210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to
5198	18190	31032	1.7	3.0E-07	T57650.1	EST_HUMAN	gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
5863	18934	32063	11.51	3.0E-07	O88897	SWISSPROT	db:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
6202	19258	32405	0.81	3.0E-07	O42280	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
7000	20027		4.92	3.0E-07	AA815176.1	EST_HUMAN	(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
7832	20854	34182	4.02	3.0E-07	AW787168.1	EST_HUMAN	WNT-14 PROTEIN PRECURSOR
8114	21026		0.76	3.0E-07	A1691065.1	EST_HUMAN	oc04c10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339890 3'
11931	24776		1.48	3.0E-07	BE439409.1	EST_HUMAN	GV1-JM0036-200300-115-g02 UM0036 Homo sapiens cDNA
12084	24925		2.07	3.0E-07	AF029308.1	NT	tw2811.1.x1 NCI_CGAP_Ov65 Homo sapiens cDNA clone IMAGE:2261037 3' similar to contains Alu repetitive element; contains element MSR1 MSR1 repetitive element ;
13092	25609		6.32	3.0E-07	AJ132352.1	NT	HTM1-025F1 HTM1 Homo sapiens cDNA
30	13146	28034	2.82	2.0E-07	AF262988.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
			6.32	3.0E-07	AJ132352.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
			2.82	2.0E-07	AF262988.1	NT	Homo sapiens TRF2-interacting telomeric RAP1 protein (RAP1) mRNA, complete cds

Page 214 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
164	13265	26182	6.85	2.0E-07	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
164	13265	26183	6.85	2.0E-07	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
183	13291	26206	33.69	2.0E-07	U98949.1	NT	Fugu rubripes beta-cytoplasmic (vascular) actin gene, complete cds
772	13829	26780	3.24	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
772	13829	26781	3.24	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
785	13841		0.88	2.0E-07	P11389	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
971	14022	26966	2.78	2.0E-07	AA223260.1	EST_HUMAN	z08b07.s1 Striatagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650869 3' similar to gb.L31860 GLYCOPHORIN A PRECURSOR (HUMAN); contains Alu repetitive element;
972	14023	26987	7.01	2.0E-07	T63042.1	EST_HUMAN	yc15p04.s1 Striatagene lung (#937210) Homo sapiens cDNA clone IMAGE:30790 3' similar to contains L1 repetitive element ;
1190	14229	27168	0.95	2.0E-07	Q26768	SWISSPROT	I/6 AUTOANTIGEN
1623	14653	27617	2.21	2.0E-07	Q09701	SWISSPROT	HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME 1
3684	16717		0.66	2.0E-07	BF131397.1	EST_HUMAN	601818916F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4044891 5'
3764	16786	28675	26	2.0E-07	AF125348.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
5280	18266		0.78	2.0E-07	AW902219.1	EST_HUMAN	QV3-NN1023-260400-168-h11 NN1023 Homo sapiens cDNA
5528	18607	31455	1.79	2.0E-07	AW898066.1	EST_HUMAN	RC3-NN0088-260400-021-g11 NN0088 Homo sapiens cDNA
6831	26656	33077	0.69	2.0E-07	AW449668.1	EST_HUMAN	UI-H-B13-ake-b-01-0-UI.s1 NOI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734008 3'
6957	19886	33210	1.78	2.0E-07	AI208715.1	EST_HUMAN	qg56d05.x1 Soerres_testis_NHT Homo sapiens cDNA clone IMAGE:1839177 3'
6971	19998	33228	0.57	2.0E-07	AA572953.1	EST_HUMAN	nm33a06.s1 NOI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:1061938 similar to contains Alu repetitive element;
9039	21868		4.65	2.0E-07	AV729390.1	EST_HUMAN	AV729390 HTC Homo sapiens cDNA clone HTCAEG02 5'
9253	22181	35535	1.24	2.0E-07	AA035198.1	EST_HUMAN	zk27g09.s1 Soerres_pregnant_uterus_NBHPU Homo sapiens cDNA clone IMAGE:471808 3'
10281	23171		1.73	2.0E-07	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21G103
10760	23646	37079	7.43	2.0E-07	AW892507.1	EST_HUMAN	CM4-NN0003-280300-124-408 NN0003 Homo sapiens cDNA
10867	23851	37276	1.08	2.0E-07	P00751	SWISSPROT	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B)
10907	23851	37276	1.08	2.0E-07	P00751	SWISSPROT	(GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)
12231	25525		1.88	2.0E-07	BE153717.1	EST_HUMAN	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B)
12309	25776		2.33	2.0E-07	AI732462.1	EST_HUMAN	(GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)
1128	14171		0.97	1.0E-07	AL163282.2	NT	PM0-HT0339-260100-006-H07 HT0339 Homo sapiens cDNA
							z08b11.x5 Striatagene lung carcioma 937218 Homo sapiens cDNA clone IMAGE:565029 3' similar to contains THR.b2 THR repetitive element ;
							Homo sapiens chromosome 21 segment HS21C082

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1986	15004	27991	1.33	1.0E-07	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
1986	15004	27992	1.33	1.0E-07	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2406	15411	28414	0.94	1.0E-07	P10263	SWISSPROT	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
2875	14575	27535	2.43	1.0E-07	P09256	SWISSPROT	GLYCOPROTEIN GPV
3807	14171		1.11	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
4395	17408	30274	3.97	1.0E-07	AV718662.1	EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
4395	17408	30275	3.67	1.0E-07	AV718662.1	EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
							Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>
6780	19813	33025	1.27	1.0E-07	U92671.2	NT	
7192	20192	33435	5.49	1.0E-07	BE047871.1	EST_HUMAN	t243d08.y1 NCL_CGAP_Brm62 Homo sapiens cDNA clone IMAGE:2291339 5'
7192	20192	33436	5.49	1.0E-07	BE047871.1	EST_HUMAN	t243d08.y1 NCL_CGAP_Brm62 Homo sapiens cDNA clone IMAGE:2291339 5'
7914	20858	34141	8.93	1.0E-07	N55081.1	EST_HUMAN	w43c07.s1 Soares fetal liver spleen TNFLS Homo sapiens cDNA clone IMAGE:245484 3'
8097	21009	34334	0.68	1.0E-07	BF375909.1	EST_HUMAN	PM4-TN0024-030800-002-b05 TN0024 Homo sapiens cDNA
8097	21009	34335	0.68	1.0E-07	BF375909.1	EST_HUMAN	PM4-TN0024-030800-002-b05 TN0024 Homo sapiens cDNA
8130	21040	34369	1.32	1.0E-07	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
8354	21259	34593	0.46	1.0E-07	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
8794	21724	35071	2.11	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
8794	21724	35072	2.11	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
9509	22436	35800	3.72	1.0E-07	AA693576.1	EST_HUMAN	ADAM-TS 8 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 8) (ADAMTS-8) (ADAM-TS8) (METH-2)
9810	22716	36098	1.14	1.0E-07	P57110	SWISSPROT	MOTIFS 8) (ADAMTS-8) (ADAM-TS8) (METH-2)
10143	23034	36432	0.58	1.0E-07	BE327843.1	EST_HUMAN	hu28h06.x1 NCL_CGAP_Met15 Homo sapiens cDNA clone IMAGE:3171419 3' similar to contains MER18.13
10445	23334	36752	3.54	1.0E-07	BF674524.1	EST_HUMAN	MER18 repetitive element;
10453	23342	36759	1.25	1.0E-07	AA386311.1	EST_HUMAN	6021371714FT NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274426 5'
10943	23828		1.54	1.0E-07	AL163282.2	NT	EST185054 Brain IV Homo sapiens cDNA
12558	25754	31671	2.88	1.0E-07	BE048770.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
7660	20594	33692	0.75	9.0E-08	AI639362.1	EST_HUMAN	h-53c11.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR:O95722 O95722
10399	23285	36710	2.31	9.0E-08	AV734819.1	EST_HUMAN	DJ1163J1.1;
11626	24533	38002	2.18	9.0E-08	AI891052.1	EST_HUMAN	t551b06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090195 3'
12093	24934	38441	2.86	9.0E-08	AL163301.2	NT	AV734819 cda Homo sapiens cDNA clone cdaBF806 5'
							w30a07.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2446932 3' similar to contains OFR.12
							OFR repetitive element;
							Homo sapiens chromosome 21 segment HS21C101

Page 216 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12509	25243		2.37	9.0E-08	AJ251973.1	NT	Homo sapiens partial steirin-1 gene
630	16879		3.17	8.0E-08	AB111352.1	EST_HUMAN	wd16505.x1 Scars_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2328273 3'
1076	14120		0.81	8.0E-08	BE795469.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
3603	16840		1.22	8.0E-08	BE795469.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
9298	22226	35586	3.14	8.0E-08	AJ752387.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
9298	22226	35587	3.14	8.0E-08	AJ752387.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
10153	23044	36443	3.47	8.0E-08	AW1970693.1	EST_HUMAN	EST382776 MAGE resequences, MAGK Homo sapiens cDNA
11692	24594		2.08	8.0E-08	AF253417.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
63	13193	26109	2.1	7.0E-08	Q02357	SWISSPROT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
1368	14419	27374	6.53	7.0E-08	X04809.1	NT	Rat mRNA for ribosomal protein L31
3637	16673	29571	1.33	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
11253	24177		2.02	7.0E-08	A1535743.1	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
12098	24933	38443	5.9	7.0E-08	U24070.1	NT	cong3.P11.A5 conom Homo sapiens cDNA 3'
12942	16673	29570	3.2	7.0E-08	P15305	SWISSPROT	Rattus norvegicus Munc13-1 mRNA, complete cds
12942	16673	29571	3.2	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
842	13897	26834	3.05	6.0E-08	AL163248.2	NT	DYNEIN HEAVY CHAIN (DYHC)
842	13897	26835	3.05	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2386	15391	28395	1.7	6.0E-08	BE144398.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
3109	16160	29056	0.99	6.0E-08	7662473	NT	Homo sapiens KIAA1074 protein (KIAA1074), mRNA
4346	17369	30225	1.12	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
8529	21460		0.7	6.0E-08	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
9868	22783		0.66	6.0E-08	AA827075.1	EST_HUMAN	ob56c05.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1335368 3' similar to contains
11848	24698	38189	2.34	6.0E-08	P11369	SWISSPROT	MER12.b3 MER12 repetitive element ;
11964	24807		1.64	6.0E-08	AL163209.2	NT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
87	13200	26113	2.33	5.0E-08	AL163303.2	NT	ENDONUCLEASE
2251	15251	28270	2.16	5.0E-08	AA493851.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C009
12272	25088		6.77	5.0E-08	P06881	SWISSPROT	Homo sapiens chromosome 21 segment HS21C103
12448	25201	31849	1.58	5.0E-08	AW851878.1	EST_HUMAN	h03b08.s1 NCL_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943193 similar to contains Alu repetitive element;
							COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
							QV0-CT0225-131099-034-a12 CT0225 Homo sapiens cDNA

Page 217 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1785	14811	27779	1.19	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
1785	14811	27780	1.19	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
2027	15080		0.06	4.0E-08	AL079581.1	EST_HUMAN	DKFZp434J0426_r1_434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434J0426 5'
3112	16163		1.35	4.0E-08	AI078417.1	EST_HUMAN	cd05e02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1674458 3' similar to contains Alu repetitive element
3987	17014	29903	0.72	4.0E-08	U82658.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
6670	19707	32902	1.08	4.0E-08	P52624	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
9356	22284	35646	0.79	4.0E-08	O15393	SWISSPROT	TRANSMEMBRANE PROTEIN, SERINE 2
9682	22608	35981	0.84	4.0E-08	L42571.1	NT	Cricetulus griseus ribosomal transcription factor (UBF2) mRNA, complete cds
10171	23062		0.95	4.0E-08	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10819	23705		1.48	4.0E-08	AI016342.1	EST_HUMAN	cd78d12.s1 Soares_fetal_liver_9w Homo sapiens cDNA clone IMAGE:1622803 3'
10874	23760	37187	4.41	4.0E-08	AI060027.1	EST_HUMAN	an22d10.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1699411 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
11512	24422	37878	1.69	4.0E-08	AA393627.1	EST_HUMAN	z76b08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728247 5' similar to TR:G505579
11512	24422	37879	1.69	4.0E-08	AA393627.1	EST_HUMAN	z76b08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728247 5' similar to TR:G505579
11533	24443	37903	3.91	4.0E-08	BF682493.1	EST_HUMAN	G505579 NA/CA, K-EXCHANGER ;
11533	24443	37904	3.91	4.0E-08	BF682493.1	EST_HUMAN	602248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5'
12277	25888		1.86	4.0E-08	W76159.1	EST_HUMAN	602248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5'
12878	25476		2.28	4.0E-08	AI343353.1	EST_HUMAN	z465g03.r1 Soares_fetal_heart_NBT-H19W Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L1.t1 L1 repetitive element;
5805	18877	31984	2.76	3.0E-08	BE018348.1	EST_HUMAN	tb95a11.x1 NCL_CGAP_C016 Homo sapiens cDNA clone IMAGE:2062076 3' similar to contains MER18.b3
7316	18484	31308	4.02	3.0E-08	AI762737.1	EST_HUMAN	MER18 MER18 repetitive element;
7969	20891	34203	1.5	3.0E-08	AL163246.2	NT	b679a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z158 Q9Z158
8216	21121		3.33	3.0E-08	AI436352.1	EST_HUMAN	SYNTAXIN 17. ;
10410	23293		0.67	3.0E-08	AF055066.1	NT	qs7611.y5 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:1944045 5'
12006	24849	38346	1.53	3.0E-08	R86279.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
							th63h09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126273 3' similar to
							TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE ;
							Homo sapiens MHC class 1 region
							yp12h10.s1 Soares_breast_3NBHst Homo sapiens cDNA clone IMAGE:187195 3' similar to gb:M34079 TAT
							BINDING PROTEIN-1 (HUMAN);

Page 218 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12006	24848	38347	1.53	3.0E-08	R88279.1	EST_HUMAN	yp12b10.s1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:187195 3' similar to gb:M34079 TAT BINDING PROTEIN-1 (HUMAN);
12247	25070		28.09	3.0E-08	R18420.1	EST_HUMAN	yg0204.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30948 5' similar to contains Alu repetitive element
219	13318		6.29	2.0E-08	AW30296.1	EST_HUMAN	x87f06.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2767139 3' zw48107.r1 Soares total fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773317 5' similar to contains Alu repetitive element; contains element MER15 repetitive element ;
246	13344		5.67	2.0E-08	AA425598.1	EST_HUMAN	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
519	13589	28502	2.35	2.0E-08	AF189349.1	NT	MR0-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
663	13745	26659	8.21	2.0E-08	AW886438.1	EST_HUMAN	MR0-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
663	13745	26660	8.21	2.0E-08	AW886438.1	EST_HUMAN	MR0-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
1017	14097		19.93	2.0E-08	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5' Homo sapiens chromosome 21 segment HS21C047
1371	14403	27357	1.66	2.0E-08	AL163247.2	NT	601570463F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845199 5' xp4311.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743149 3'
1769	14795		2.44	2.0E-08	BE734871.1	EST_HUMAN	Sheep Hls-RNA-GUG
1879	14900		3.29	2.0E-08	AW270271.1	EST_HUMAN	WNT-14 PROTEIN PRECURSOR
2574	15573		1.96	2.0E-08	K00216.1	NT	WNT-14 PROTEIN PRECURSOR
3263	16301	26206	6.87	2.0E-08	O42280	SWISSPROT	RC3-ST0197-181099-Q12-B03 ST0197 Homo sapiens cDNA
3926	16954	29207	2.68	2.0E-08	AW813820.1	EST_HUMAN	Homo sapiens shox gene, alternatively spliced products, complete cds
4164	17185	30058	0.73	2.0E-08	U82668.1	NT	aa28c07.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814380 5' similar to contains L1.L2 L1 repetitive element ;
4511	17521		2.15	2.0E-08	AA459040.1	EST_HUMAN	he17h08.x2 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2918327 3' similar to contains Alu repetitive element;
5072	18069		4.82	2.0E-08	AW572881.1	EST_HUMAN	al80h11.s1 Soares testis_NHT Homo sapiens cDNA clone 1377189 3'
5832	18903	32018	0.9	2.0E-08	AA813204.1	EST_HUMAN	xd32c04.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2595462 3' similar to contains MER18.b3 MER18 MER18 repetitive element ;
6046	19108	32238	0.87	2.0E-08	AW088924.1	EST_HUMAN	POL POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8583	21514	34858	0.95	2.0E-08	P10272	SWISSPROT	ab02g06.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839674 3'
8688	21619	34961	1.57	2.0E-08	AA490121.1	EST_HUMAN	AUT39978 PLACE1 Homo sapiens cDNA clone PLACE1011719 5'
9631	22657		1.1	2.0E-08	AU139978.1	EST_HUMAN	W72f02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.b3 LTR1 repetitive element ;
10999	23883	37314	0.91	2.0E-08	N78097.1	EST_HUMAN	W72f02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.b3 LTR1 repetitive element ;
10999	23883	37315	0.91	2.0E-08	N78097.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ11342 (FLJ11342), mRNA
13008	25929		1.77	2.0E-08	11431678	NT	



Page 219 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1529	15903	27519	1.33	1.0E-08	P31792	SWISSPROT	POL POLYPROTEIN (CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE)
1800	14826	27794	1.79	1.0E-08	AF125348.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
2065	15080		2.52	1.0E-08	BE141859.1	EST_HUMAN	PM2-HT0130-150900-001-f12 HT0130 Homo sapiens cDNA
3235	16283	29184	1.16	1.0E-08	BE246844.1	EST_HUMAN	TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HQSC project=TCBA Homo sapiens cDNA clone TCBAP5232
3235	16283	29185	1.16	1.0E-08	BE246844.1	EST_HUMAN	TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HQSC project=TCBA Homo sapiens cDNA clone TCBAP5232
6793	18665	31973	3.89	1.0E-08	AJ010770.1	NT	Homo sapiens hyperin gene, exons 1-50
8238	21143	34476	1.14	1.0E-08	P18474	SWISSPROT	52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
9111	22039	35395	2.15	1.0E-08	AJ015304.1	EST_HUMAN	cd35a05.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1618736 3'
9746	22670	36053	0.75	1.0E-08	BE072572.1	EST_HUMAN	PM2-BT0546-210100-004-d02 BT0546 Homo sapiens cDNA
10472	23360	36774	0.95	1.0E-08	P70110	SWISSPROT	TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (CTP)
11032	23916	37359	0.65	1.0E-08	P98063	SWISSPROT	(TRICARBOXYLATE CARRIER PROTEIN)
11760	24661	38148	4.28	1.0E-08	AF044083.1	NT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
12622	25307	38219	1.89	1.0E-08	X51755.1	NT	Homo sapiens major histocompatibility locus class III region
4341	17355	30219	5.3	9.0E-09	AL163279.2	NT	Human lambda-immunoglobulin constant region complex (germline)
4341	17355	30220	5.3	9.0E-09	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
10584	23450		0.59	9.0E-09	T97950.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C079
6756	19790		0.57	8.0E-09	AI270615.1	EST_HUMAN	ys58a12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121818 3'
7639	20574	33868	7.89	8.0E-09	AI183500.1	EST_HUMAN	q386c11.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:1978984 3' similar to contains L1.13 L1 repetitive element
8679	21510	34856	2.58	8.0E-09	AW900159.1	EST_HUMAN	q42807.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1732164 3' similar to contains MSR1.t1 MSR1 repetitive element
9540	22467		3.07	8.0E-09	AA938892.1	EST_HUMAN	GM0-NN1004-100300-273-e06 NN1004 Homo sapiens cDNA
3670	16703		2.5	7.0E-09	D86842.1	NT	op74408.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1682575 3'
4093	17118		2.83	7.0E-09	U50871.1	NT	Homo sapiens DNA for 3-ketoacyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3
8625	21556		0.94	7.0E-09	AA256200.1	EST_HUMAN	Human familial Alzheimer's disease (STM2) gene, complete cds
9802	22708	36091	2.99	7.0E-09	L09709.1	NT	zr80c05.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:681892 5' similar to contains L1.12 L1 repetitive element
10680	23566	36996	1.66	7.0E-09	BE254850.1	EST_HUMAN	Human lysosomal membrane glycoprotein-2 (LAMP2) gene, 5' end and flanking region
10833	23719		1.72	7.0E-09	AA058626.1	EST_HUMAN	60111173F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3361834 5'
							z558e07.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381156 3' similar to contains L1.12 L1 repetitive element

Page 220 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11117	24047		3.29	7.0E-09	T97960.1	EST_HUMAN	ye58a12.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:121918 3'
5102	18059	30947	9.39	6.0E-09	BE169421.1	EST_HUMAN	PM1-J-H70527-180200-001-h05 HT0527 Homo sapiens cDNA
5392	18374	31215	1.19	6.0E-09	AA557940.1	EST_HUMAN	nl7a11.s1 NCL_CGAP_HSC1 Homo sapiens cDNA clone IMAGE:1040924 similar to contains L1.12 L1
5585	18643	31521	8.92	6.0E-09	AW195784.1	EST_HUMAN	repetitive element ;
9139	22067	35428	1.4	6.0E-09	BE161653.1	EST_HUMAN	xt85h108.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:27013111 3'
9718	22843	36024	2.66	6.0E-09		NT	MR3-HT0446-280300-201-h12 HT0446 Homo sapiens cDNA
10769	23655		4.23	6.0E-09	AF200923.2	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
11173	24100	37546	1.41	6.0E-09	BF108755.1	EST_HUMAN	Homo sapiens testis-specific kinase substrate (TSKS) gene, complete cds
12122	24963	38466	1.8	6.0E-09	P08547	SWISSPROT	7145e10.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29 b2 MER29 repetitive element ;
12122	24963	38467	1.8	6.0E-09	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12187	25032	38633	1.49	6.0E-09	C01803.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
1438	14469	27425	4.58	5.0E-09	BE149264.1	EST_HUMAN	HUMGS0003762 Human adult (K. Okubo) Homo sapiens cDNA
1877	14898	27882	1.16	5.0E-09	AL163284.2	NT	RC2-HT0252-120200-014-h10 HT0252 Homo sapiens cDNA
6875	19712	32806	3.42	5.0E-09	AA359454.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
							EST168746 Fetal lung II Homo sapiens cDNA 5' end
							Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3
7166	18438	31340	0.63	5.0E-09	U66059.1	NT	TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3,
10597	23483	36912	3.23	5.0E-09	AW769887.1	EST_HUMAN	TCRBV637P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV5S2A2P, TCRBV7S2A1N4T,
544	13613		1.75	4.0E-09	AL163282.2	NT	TCRBV13S9/13S>
981	14041		1.82	4.0E-09	AL163285.2	NT	PM2-UM0053-240300-005-c09 UM0053 Homo sapiens cDNA
1488	14519	27480	1.57	4.0E-09	9558718	NT	Homo sapiens chromosome 21 segment HS21C082
2036	15053	28051	1.23	4.0E-09	AF176325.1	NT	Homo sapiens chromosome 21 segment HS21C085
2036	15053	28052	1.23	4.0E-09	AF175925.1	NT	Homo sapiens hypothetical protein (AF038169), mRNA
2454	15458	28435	4.22	4.0E-09	AA350878.1	EST_HUMAN	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
8429	21361	34700	0.74	4.0E-09	AA495747.1	EST_HUMAN	EST58385 Infant brain Homo sapiens cDNA 5' end similar to similar to heat shock protein, 90 kDa
11514	24424	37882	1.58	4.0E-09	AB88401.1	EST_HUMAN	zw04c08.r1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:768298 5'
							wm04f10.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2443627 3'
11587	24465		1.62	4.0E-09	AA195142.1	EST_HUMAN	z34a12.r1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:865278 5' similar to gbL07807
2374	15379	28381	4.49	3.0E-09	BE222239.1	EST_HUMAN	DYNAMIN-1 (HUMAN);
							hu09e09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
							MER18 repetitive element ;

Page 221 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2587	15585	28579	1.65	3.0E-09	BE222239.1	EST_HUMAN	hu09e09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
2699	15693	28687	1.11	3.0E-09	P23249	SWISSPROT	MER18 repetitive element ; PROTEIN MOV-10
3376	16420	29322	1.03	3.0E-09	BE222239.1	EST_HUMAN	hu09e09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
3434	16475		0.75	3.0E-09	AA442272.1	EST_HUMAN	MER18 repetitive element ; z564804.t1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757422 5'
4187	17207		0.64	3.0E-09	X16674.1	NT	H.sapiens PADPRP-I gene for NAD(+) ADP-ribosyltransferase
4533	17542	30404	4	3.0E-09	AF15325.1	NT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
4633	17639	30502	2.44	3.0E-09	Q9Y3R5	SWISSPROT	258.1 KDA PROTEIN C2TORF5 (KIAA0933)
5327	18311		0.9	3.0E-09	D86842.1	NT	Homo sapiens DNA for 3-ketoadacyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3
8480	21411	34748	1.19	3.0E-09	BE465780.1	EST_HUMAN	hx80e02.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3194090 3' similar to TR:O56091
10741	23627	37057	2.07	3.0E-09	AL163247.2	NT	O56091 IMPACT PROTEIN ; Homo sapiens chromosome 21 segment HS21C047
11460	24375	37823	4.02	3.0E-09	BF109943.1	EST_HUMAN	7172c08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
11460	24375	37824	4.02	3.0E-09	BF109943.1	EST_HUMAN	7172c08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
1265	14318	27266	5.55	2.0E-09	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1685	14715		6.07	2.0E-09	AL118573.1	EST_HUMAN	DKFZp761B1710.J1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761B1710 5'
2348	15356	28358	1.41	2.0E-09	Q9Y3R5	SWISSPROT	258.1 KDA PROTEIN C2TORF5 (KIAA0933)
4013	17040	29929	4.32	2.0E-09	O60241	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
5368	18350	31192	0.99	2.0E-09	P25823	SWISSPROT	MATERNAL TUDOR PROTEIN
5921	18988	32107	0.61	2.0E-09	AI004062.1	EST_HUMAN	047508.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1618897 3'
6390	19439		0.62	2.0E-09	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
7087	20293		0.68	2.0E-09	AA357407.1	EST_HUMAN	EST66142 Kidney IX Homo sapiens cDNA 5' end similar to EST containing L1 repeat
7855	20782	34085	8.73	2.0E-09	AA461430.1	EST_HUMAN	zx63h06.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:766187 5' similar to contains Alu repetitive element ;
7947	20859	34181	0.64	2.0E-09	W28634.1	EST_HUMAN	52d11 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
8269	21174	34509	0.46	2.0E-09	AI243732.1	EST_HUMAN	qh88g10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854114 3'
8347	21262	34586	0.63	2.0E-09	AW862126.1	EST_HUMAN	MR1-C10352-240200-105-b06 CT0352 Homo sapiens cDNA
9271	22199	35557	1.27	2.0E-09	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
11712	24614	36090	1.87	2.0E-09	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
12761	18422		15.23	2.0E-09	X16674.1	NT	H.sapiens PADPRP-I gene for NAD(+) ADP-ribosyltransferase
12820	25957		1.74	2.0E-09	AA226070.1	EST_HUMAN	nc11c02.r1 NCL_CGAP_P-r1 Homo sapiens cDNA clone IMAGE:1007810 similar to contains Alu repetitive element ;

Page 222 of 545  
Table 4

## Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1022	14071		1.98	1.0E-09	W78152.1	EST_HUMAN	z479d03.s1 Soares_fetal_heart_Nb-H10W Homo sapiens cDNA clone IMAGE:346863 3' similar to gb:U02932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
1136	14178	27115	1.51	1.0E-09	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
1136	14178	27116	1.51	1.0E-09	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
1659	14888		0.91	1.0E-09	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
2625	15526		1.28	1.0E-09	AJ356086.1	EST_HUMAN	qy64e11.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2016812 3' similar to contains MER12.12
2931	15984	28883	1.74	1.0E-09	U80017.1	NT	MER12 repetitive element;
2968	16020	28917	2.04	1.0E-09	M28698.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (napi) and survival motor neuron protein (smn) genes, complete cds
2968	16020	28918	2.04	1.0E-09	M28698.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
3085	16136	29032	0.86	1.0E-09	BE535440.1	EST_HUMAN	Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
4914	17013		6.56	1.0E-09	AA710297.1	EST_HUMAN	601058802F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445177 5'
5693	18766	31690	1.1	1.0E-09	AL163283.2	NT	zh35c03.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:2330481 3' similar to contains
6043	19105	32235	1.39	1.0E-09	U07000.1	NT	Alu repetitive element; contains element MER22 repetitive element;
6384	19433	32600	3.04	1.0E-09	P26604	SWISSPROT	Homo sapiens chromosome 21 segment HS21C083
8329	21234	34668	0.69	1.0E-09	AV728645.1	EST_HUMAN	Human breakpoint cluster region (BCR) gene, complete cds
8961	21891	35250	0.68	1.0E-09	AI688474.1	EST_HUMAN	CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
10803	23689		2.91	1.0E-09	AL163283.2	NT	wd39b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330481 3' similar to contains
12198	25033		1.88	1.0E-09	AL163283.2	NT	MER25 t1 MER25 repetitive element;
12670	25897	31481	1.52	1.0E-09	T1418127	NT	Homo sapiens chromosome 21 segment HS21C083
12778	25407		1.52	1.0E-09	T57366.1	EST_HUMAN	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
13084	25821		2.18	1.0E-09	AF260225.1	NT	y657g12.s1 Stralagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:74758 3'
1335	14369	27319	1.6	9.0E-10	AW867740.1	EST_HUMAN	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
2881	15936	28841	5.32	9.0E-10	AI870071.1	EST_HUMAN	MRO-SN0040-050500-002-c07 SN0040 Homo sapiens cDNA
7147	20256	33607	4.61	9.0E-10	AI452882.1	EST_HUMAN	we78h03.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2347253 3' similar to
157	13257	26175	8.63	8.0E-10	U63630.2	NT	SW:RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29; contains element PTR0 repetitive element;
3391	16434	29337	0.93	8.0E-10	BE080748.1	EST_HUMAN	TR:Q00372 O00372 PUTATIVE P150.;
4297	17311	30177	4.63	8.0E-10	AA376832.1	EST_HUMAN	Homo sapiens MCM4 (MCM4) and DNA-PKcs (PRKDC) genes, partial cds

Page 223 of 545  
Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10471	23359		3.22	8.0E-10	U36308.2	NT	Homo sapiens lens major intrinsic protein (MIP) gene, complete cds
725	13763	26707	17.53	7.0E-10	7706225	NT	Homo sapiens TPA inducible protein (LOC51586), mRNA
725	13763	26708	17.58	7.0E-10	7706225	NT	Homo sapiens TPA inducible protein (LOC51586), mRNA
1645	14676	27640	2.31	7.0E-10	Q13342	SWISSPROT	LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100)
2594	15592		20.7	7.0E-10	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3137	16187	29079	2.65	7.0E-10	X00856.1	NT	H. sapiens DHFR gene, exon 3
6426	19473	32647	4.28	7.0E-10	AA345220.1	EST_HUMAN	EST151247 Gall bladder II Homo sapiens cDNA 5' end
7817	20746	34051	1.38	7.0E-10	BF352883.1	EST_HUMAN	IL3-H10819-110700-209-D12 H10819 Homo sapiens cDNA
8105	21017		1.81	7.0E-10	P36084	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
8554	21485	34825	1.44	7.0E-10	AF029701.2	NT	Homo sapiens presenilin-1 gene, exons 1 and 2
8554	21485	34826	1.44	7.0E-10	AF029701.2	NT	Homo sapiens presenilin-1 gene, exons 1 and 2
12085	24926	38430	1.82	7.0E-10	AW778769.1	EST_HUMAN	hot2402.x1 NCL CGAP_Co14 Homo sapiens cDNA clone IMAGE:3037202 3' similar to contains Alu repetitive element; contains MERY.b1 MER7 repetitive element;
938	13990	26932	2.8	6.0E-10	AJ400877.1	NT	Homo sapiens ASOL3 gene, CEGP1 gene, C11orf14 gene, C11orf16 gene and C11orf17 gene
2726	15719	28716	1.66	6.0E-10	AK24405.1	EST_HUMAN	h02d07.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:2095021 3'
4606	17614	30475	0.66	6.0E-10	Q02817	SWISSPROT	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)
4852	17854		3.3	6.0E-10	AW853719.1	EST_HUMAN	RC3-CT0254-031089-012-g12 CT0254 Homo sapiens cDNA
9342	22270	35632	1.03	6.0E-10	P33730	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E)
9342	22270	35633	1.03	6.0E-10	P33730	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E)
10160	23051	36452	0.7	6.0E-10	P98073	SWISSPROT	ENTEROPEPTIDASE PRECURSOR (ENTEROKINASE)
786	13842		5.7	5.0E-10	AL046804.1	EST_HUMAN	DKF2p434N219.1 434 (synonym: htes3) Homo sapiens cDNA clone DKF2p434N219 5'
7706	20638		1.88	5.0E-10	BF105159.1	EST_HUMAN	G0182184F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4042413 5'
10065	22981	36371	2.15	5.0E-10	P34678	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
10065	22981	36372	2.15	5.0E-10	P34678	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
115	13223		1.09	4.0E-10	A1221083.1	EST_HUMAN	qg08709.x1 Soares, placenta, 8to9weeks, 2NbhP8to9w Homo sapiens cDNA clone IMAGE:1759049 3' similar to contains LTR8.b2 LTR8 repetitive element;
2012	15030	28023	1.34	4.0E-10	AW594709.1	EST_HUMAN	hg58g03.x1 NCL CGAP_C06 Homo sapiens cDNA clone IMAGE:2949844 3' similar to contains Alu repetitive element;
2810	15603	28603	7.51	4.0E-10	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7540	20479	33787	18.76	4.0E-10	AF224659.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds

Page 224 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10926	23811	37239	0.95	4.0E-10	AI267342.1	EST_HUMAN	eq53h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653
940	13661	26934	1.42	3.0E-10	N36113.1	EST_HUMAN	Y32106.s1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:272863 3' similar to contains L1.t1 L1 repetitive element
1380	14412		5.11	3.0E-10	AY005150.1	NT	Homo sapiens extracellular glycoprotein lectin precursor, gene, complete cds
4652	17656	30524	1.06	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4652	17658	30525	1.06	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
5640	18715	31616	0.82	3.0E-10	N50109.1	EST_HUMAN	Y21p08.s1 Soares multiple_sclerosis_2NBHMSP Homo sapiens cDNA clone IMAGE:282782 3'
6444	19490	32667	1.99	3.0E-10	P220350	SWISSPROT	RHOMBOLD PROTEIN (VEINLET PROTEIN)
6609	19650	32834	2.88	3.0E-10	BE302970.1	EST_HUMAN	ba76408.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2906319 5'
8228	21133	34463	1.77	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'
8228	21133	34494	1.77	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'
9289	22217	35575	1.21	3.0E-10	H87208.1	EST_HUMAN	Y574b12.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:220511 3' similar to contains MER29 repetitive element
9602	22528	35894	1.72	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA
9602	22528	35895	1.72	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B08 CT0219 Homo sapiens cDNA
9879	22794		0.66	3.0E-10	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
10941	23826		1.4	3.0E-10	T85691.1	EST_HUMAN	Yc11e12.r1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:80398 5'
11065	23949		1.37	3.0E-10	AA769294.1	EST_HUMAN	nc236g03.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1286808 3'
12911	25494	31768	2.23	3.0E-10	BE179517.1	EST_HUMAN	IL3-HT0618-110500-138-E07 HT0618 Homo sapiens cDNA
37	13153	26042	1.43	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
37	13153	26043	1.43	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
1915	14936		2.21	2.0E-10	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds
3028	16080		0.65	2.0E-10	BF075047.1	EST_HUMAN	602138640F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273377 5'
5362	18344	31188	1.52	2.0E-10	P11227	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; RIBONUCLEASE H ] (HPRG)
6014	19077		2.91	2.0E-10	Q28640	SWISSPROT	
6499	19543	32719	1.52	2.0E-10	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7772	20702	34001	8.3	2.0E-10	BE791082.1	EST_HUMAN	601586208F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3940824 5'
8592	21523	34867	0.7	2.0E-10	P26809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; RIBONUCLEASE H ]
8592	21523	34868	0.7	2.0E-10	P26809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; RIBONUCLEASE H ]

Page 225 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9842	22747		1.18	2.0E-10	BF434565.1	EST_HUMAN	7078d08.x1 NCL_CGAP_Kid111 Homo sapiens cDNA clone IMAGE:3642303 3' similar to contains L1.13 L1 repetitive element:
1528	14559		1.5	1.0E-10	AW867767.1	EST_HUMAN	MRO-SN0038-290300-001-01 SN0038 Homo sapiens cDNA
1620	14659	27622	3.22	1.0E-10	AV652123.1	EST_HUMAN	AV652123 GLC Homo sapiens cDNA clone GLCXA11 3'
2619	15617		1.64	1.0E-10	AW852001.1	EST_HUMAN	QV6-C10225-191199-058-c08 C10225 Homo sapiens cDNA
3558	16595	29489	0.95	1.0E-10	AW832912.1	EST_HUMAN	QV2-T10003-161169-013-g10 T10003 Homo sapiens cDNA
3600	16637		0.74	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N1317 5'
3913	16637		0.99	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N1317 5'
4101	17126		8.43	1.0E-10	AF213684.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
4225	17241	30108	7.39	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4225	17241	30109	7.39	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4233	17249	30118	2.13	1.0E-10	AB031059.1	NT	CDM protein (CDM), adrenoleukodystrophy protein >
4266	17282		2.53	1.0E-10	M30629.1	NT	Homo sapiens PCCX1 mRNA for protein containing CXXC domain 1, complete cds
5316	18300		1.02	1.0E-10	AI797745.1	EST_HUMAN	we8204.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347615 3' similar to contains MER31.11 MER31 repetitive element:
7014	20041	33275	0.43	1.0E-10	AA631233.1	EST_HUMAN	nc81a05.s1 NCL_CGAP_Cx8 Homo sapiens cDNA clone IMAGE:1153704 3'
7130	20334	33598	0.45	1.0E-10	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
7895	20821		0.73	1.0E-10	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8136	21045	34375	0.55	1.0E-10	AU128584.1	EST_HUMAN	AUT28584 NT2RP2 Homo sapiens cDNA clone NT2RP2003751 5'
8816	21746	35094	1.46	1.0E-10	AW408990.1	EST_HUMAN	IB_6A4 Fetal brain library Homo sapiens cDNA
9213	22141		1.27	1.0E-10	AI268340.1	EST_HUMAN	qmo04e10.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1880874 3' similar to contains L1.11 L1 repetitive element:
10698	23564		8.22	1.0E-10	AA081888.1	EST_HUMAN	zn29g08.r1 Strategene neurospineHum NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:548314 5'
11352	24270	37712	2.96	1.0E-10	AI038280.1	EST_HUMAN	ov65103.x1 Soares_fetal_liver_spleen_TNFL3_S1 Homo sapiens cDNA clone IMAGE:1672691 3'
281	13375	26200	0.82	9.0E-11	BE145600.1	EST_HUMAN	IL2-HT0203-291039-016-c08 HT0203 Homo sapiens cDNA
2116	15129	28134	6.04	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225.1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'
2116	15129	28135	6.04	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225.1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'

Page 226 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3442	16483	29391	3.25	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'
3442	16483	29392	3.25	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'
4621	17628	30492	0.99	9.0E-11	AA775985.1	EST_HUMAN	aa78f0.1e1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:970297 3'
5769	18839		4.2	9.0E-11	BE079760.1	EST_HUMAN	RC6-BT0827-140200-011-E06 BT0827 Homo sapiens cDNA
10851	23537	36970	1.49	9.0E-11	AA324960.1	EST_HUMAN	EST27872 Cerebellum II Homo sapiens cDNA 5' end
10851	23537	36971	1.49	9.0E-11	AA324960.1	EST_HUMAN	EST27872 Cerebellum II Homo sapiens cDNA 5' end
12599	25295	31844	3.3	9.0E-11	C16635.1	EST_HUMAN	C16635 Clontech human aorta polyA+ mRNA (H6572) Homo sapiens cDNA clone GEN:506808 5'
3181	16211		15.85	8.0E-11	H19971.1	EST_HUMAN	Yn63f11.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:172173 3' similar to contains L1 repetitive element;
4046	17073	28959	0.69	8.0E-11	AL478817.1	EST_HUMAN	Im64c09.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161936 3'
4127	17150	30025	7.52	8.0E-11	N23712.1	EST_HUMAN	yw46e06.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:255298 3'
5311	18295	31148	6.12	8.0E-11	AI056038.1	EST_HUMAN	oa46b04.s1 Soares fetal_Nb2HF8_0w Homo sapiens cDNA clone IMAGE:1659343 3' similar to gb.L02832 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
6003	19097	32194	0.72	8.0E-11	AW674316.1	EST_HUMAN	ba60g04.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900982 3'
6968	19996		0.56	8.0E-11	AW166158.1	EST_HUMAN	x145h11.x1 NCL CGAP_Brt50 Homo sapiens cDNA clone IMAGE:2621061 3' similar to contains MER10.11 MER10 repetitive element;
1467	14498	27459	1.62	7.0E-11	AA330642.1	EST_HUMAN	EST34392 Embryo_6 week1 Homo sapiens cDNA 5' end
9065	21994	35347	2.34	7.0E-11	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
10724	23610		1.45	7.0E-11	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
12733	25374		1.71	7.0E-11	AV701656.1	EST_HUMAN	AV701650 ADB Homo sapiens cDNA clone ADBABC08 5'
435	13506	26431	4.25	6.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
435	13506	26432	4.25	6.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
7023	20049	33262	1.04	6.0E-11	L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's
8147	21056	34388	3.32	6.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8936	21866	35224	11.62	6.0E-11	AV727859.1	EST_HUMAN	AV727859 HTC Homo sapiens cDNA clone HTCCSC06 5'
9854	22769	36154	0.81	6.0E-11	BE063509.1	EST_HUMAN	GMC-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
12	13127	26073	0.84	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3421	13127	26073	1.23	6.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
4328	17342	30208	2	5.0E-11	P46034	SWISSPROT	ALDEHYDE OXIDASE
6794	19927	33037	1.56	5.0E-11	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
7955	20877	34188	11.23	5.0E-11	11416709	NT	Homo sapiens protocadherin beta 3 (PCDH3), mRNA
1426	14457		1.32	4.0E-11	AA436042.1	EST_HUMAN	zu01b12.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:730559 5'



Page 227 of 545  
Table 4

## Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2838	15827	28823	11.8	4.0E-11	BE885900.1	EST_HUMAN	G01607531F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3809296 5'
3010	16062	28966	1.57	4.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4731	17736	30598	0.89	4.0E-11	D44866.1	EST_HUMAN	HUMSUPY089 Human brain cDNA Homo sapiens cDNA clone 089
6750	18784	32897	2.67	4.0E-11	P20096	SWISSPROT	PRE-MRNA SPLICING FACTOR RNA HELICASE PRP2
7345	20341	33607	1.19	4.0E-11	AA442630.1	EST_HUMAN	z59f10.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757963 5' similar to TR.G1055250
7767	20897		4.05	4.0E-11	AF224669.1	NT	G1055250 PHEROMONE RECEPTOR VN4 ;
9831	22836		1.91	4.0E-11	BE149425.1	EST_HUMAN	Homo sapiens mannosidase, beta-A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
10189	23077	38479	1.07	4.0E-11	AI609753.1	EST_HUMAN	h82g12.x1 NCI_CGAP_Brc23 Homo sapiens cDNA clone IMAGE:2105830 3' similar to WP.ZK353.1
12792	25419	31791	4.36	4.0E-11	11545732	NT	CE00385 ;
1510	14541	27503	3.15	3.0E-11	6679077	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
2043	15096		0.92	3.0E-11	AI816033.1	EST_HUMAN	Mus musculus expressed in non-metastatic cells 2, protein (NM23B) (Nme2), mRNA
4374	17398		1.42	3.0E-11	AA309248.1	EST_HUMAN	wj35c006.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2404811 3'
986	14037	26980	1.31	2.0E-11	AI150502.1	EST_HUMAN	EST180120 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' and
1213	14251	27193	4.27	2.0E-11	R24807.1	EST_HUMAN	q36c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752102 3' similar to contains MER10.13
1213	14251	27194	4.27	2.0E-11	R24807.1	EST_HUMAN	MER10 repetitive element ;
1636	14666	27628	3	2.0E-11	L17432.1	NT	y943e12.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
1636	14666	27629	3	2.0E-11	L17432.1	NT	y943e12.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
2815	15804	28802	1.26	2.0E-11	AF087913.1	NT	y943e12.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
3240	16288	28192	8.7	2.0E-11	P10263	SWISSPROT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein
3371	16415	29316	0.9	2.0E-11	AK478617.1	EST_HUMAN	COR3beta (COR3beta) genes, complete cds
4553	17562		0.92	2.0E-11	BE085537.1	EST_HUMAN	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein
4716	17721		0.73	2.0E-11	AL163227.2	NT	Human endogenous retrovirus HERV-P-T47D
5048	18045		1.42	2.0E-11	BE082558.1	EST_HUMAN	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
5125	18121	30963	1.02	2.0E-11	AL163279.2	NT	Im54c09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161936 3'
5162	18155	31002	2.36	2.0E-11	AA307331.1	EST_HUMAN	RC3-BT0316-170200-014-e05 BT0316 Homo sapiens cDNA
6375	19424	32590	1.28	2.0E-11	AW877808.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
							QV2-BT0256-261039-014-a01 BT0256 Homo sapiens cDNA
							Homo sapiens chromosome 21 segment HS21C079
							EST178226 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to alpha-2-macroglobulin
							QV2-PT0073-280300-109-h09 PT0073 Homo sapiens cDNA

Page 228 of 545  
Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6565	19606	32791	1.81	2.0E-11	AA581028.1	EST_HUMAN	nc83h05.t1 NCL CGAP_GC1 Homo sapiens cDNA clone IMAGE:797433 5' similar to SW:PR16_YEAST
7559	20496	33786	0.85	2.0E-11	BF592945.1	EST_HUMAN	P15338 PRE-MRNA SPLICING FACTOR RNA HELICASE PRP16.;
8462	21353		0.72	2.0E-11	P37072	SWISSPROT	797c03.x1 NCL CGAP_GC6 Homo sapiens cDNA clone IMAGE:3442565 3'
							OLFATORY RECEPTOR-LIKE PROTEIN COR6
9764	22698		1.89	2.0E-11	AF028308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
10776	23662	37090	5.29	2.0E-11	Q13806	SWISSPROT	OLFATORY RECEPTOR 611 (OLFATORY RECEPTOR-LIKE PROTEIN OLF1)
10995	23879	37309	0.98	2.0E-11	AW88574.1	EST_HUMAN	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA
10995	23879	37310	0.96	2.0E-11	AW88574.1	EST_HUMAN	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA
11563	24462	37928	1.76	2.0E-11	AA035369.1	EST_HUMAN	2k27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794 3'
11553	24462	37927	1.75	2.0E-11	AA035369.1	EST_HUMAN	2k27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794 3'
11583	24492	37960	1.84	2.0E-11	AA261956.1	EST_HUMAN	zs18b04.t1 NCL CGAP_GC81 Homo sapiens cDNA clone IMAGE:685519 5'
12371	25887		2.11	2.0E-11	AA704186.1	EST_HUMAN	2i77e03.s1 Soares_fetal_liver_spleen_INFLS_ST Homo sapiens cDNA clone IMAGE:460924 3'
12398	25171		2.44	2.0E-11	AW842143.1	EST_HUMAN	RC0-CH0027-210100-011-c01 CH0027 Homo sapiens cDNA
12421	25187	31878	2.51	2.0E-11	BF377659.1	EST_HUMAN	GM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
12806	25429		3.91	2.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
13079	25601		3.36	2.0E-11	11417868	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
699	13759	26875	2.54	1.0E-11	AJ131016.1	NT	Homo sapiens SCL gene locus
810	13863	26801	1.05	1.0E-11	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1245	14281	27223	1.89	1.0E-11	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
1516	14547		1.83	1.0E-11	AF118914.1	NT	Homo sapiens PRO3078 mRNA, complete cds
2051	15093	28068	0.95	1.0E-11	P16268	SWISSPROT	OXYSTEROL-BINDING PROTEIN
2140	15163	28154	4.14	1.0E-11	AF000673.1	NT	Homo sapiens homocitrate 1,2-dioxygenase gene, complete cds
3557	16594	29498	1.22	1.0E-11	BE094316.1	EST_HUMAN	GM0-BN0105-170300-292-d12 BN0105 Homo sapiens cDNA
5515	18594	31442	14.58	1.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
6044	19109	32236	0.75	1.0E-11	BF222646.1	EST_HUMAN	7p57d01.x1 NCL CGAP_PR28 Homo sapiens cDNA clone IMAGE:364945 3' similar to contains MER10.b3
8328	21233		0.46	1.0E-11	AB042297.1	NT	MER10 repetitive element
8780	21710	35056	2.97	1.0E-11	4885546	NT	Homo sapiens P1S gene for 6-pyruvyltetrahydropterin synthase, complete cds
9144	22072	35434	6.62	1.0E-11	R13174.1	EST_HUMAN	Homo sapiens PHD finger protein 2 (PHF2) mRNA
9601	22527	35892	1.26	1.0E-11	BF365119.1	EST_HUMAN	Y793d08.r1 Soares_infant_brain_1N1B Homo sapiens cDNA clone IMAGE:28166 5'
9601	22527	35893	1.26	1.0E-11	BF365119.1	EST_HUMAN	QV4-NN1149-250900-423-a03 NN1149 Homo sapiens cDNA
11732	24634	38116	5.73	1.0E-11	BF690078.1	EST_HUMAN	QV4-NN1149-250900-423-a03 NN1149 Homo sapiens cDNA
12877	25708		2	1.0E-11	Z20377.1	EST_HUMAN	602184807F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295977 5'
							HSAAACADH P, Human foetal Brain Whole tissue Homo sapiens cDNA

Page 229 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2993	16045	25948	0.79	9.0E-12	P20742	SWISSPROT	PREGNANCY ZONE PROTEIN PRECURSOR
10314	23203	36613	1.33	9.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
10314	23203	36614	1.33	9.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
9877	22792		1.22	8.0E-12	BE074720.1	EST_HUMAN	IL5-BT0578-130300-036-G12 BT0578 Homo sapiens cDNA
12469	25215		5.13	8.0E-12	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
4772	17777	30645	1.68	7.0E-12	Q05804	SWISSPROT	34 KD SPIGULE MATRIX PROTEIN PRECURSOR (LSM34)
11789	24710	39201	8.81	7.0E-12	AA704735.1	EST_HUMAN	Z23g01.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:451152 3'
3606	16643		0.81	6.0E-12	AV730554.1	EST_HUMAN	AV730554 HTF Homo sapiens cDNA clone HTFAWF06 5'
4457	17469	30325	11.13	6.0E-12	AA732516.1	EST_HUMAN	n28811.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1302573 3' similar to contains Alu repetitive element;
6852	19691	32884	0.49	6.0E-12	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
9547	22474	35831	1.29	6.0E-12	AF003249.1	NT	Mcrona saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
10007	22824		1.32	6.0E-12	AA847898.1	EST_HUMAN	cd10g11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1367588 similar to contains MIER29.12
1069	14113	27053	1.73	5.0E-12	T08573.1	EST_HUMAN	MER29 repetitive element ;
3449	16493	28397	1.37	5.0E-12	BE047779.1	EST_HUMAN	EST04462 Fetal brain, Striatogene (cat#939206) Homo sapiens cDNA clone HFB8DV33
3791	16822	29709	9.07	5.0E-12	AJ271736.1	NT	t242b06.y1 NCL_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291217 5'
8254	19307	32489	5.65	6.0E-12	AL163278.2	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
6254	19307	32470	5.65	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6787	19801	33012	10.4	5.0E-12	AW874760.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
7382	20032	33326	0.94	5.0E-12	AL040739.1	EST_HUMAN	EST388650 MAGE resequences, MAGN Homo sapiens cDNA
7393	20092	33326	1.15	6.0E-12	AL040739.1	EST_HUMAN	DKFZp434B1615_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B1615 3'
8807	21737	35087	1.26	5.0E-12	AA033745.1	EST_HUMAN	DKFZp434B1615_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B1615 3'
9225	22153		0.8	5.0E-12	AW887037.1	EST_HUMAN	z101g12.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:376718 3' similar to contains L1.13 L1 repetitive element ;
9546	22473		0.61	5.0E-12	AL079581.1	EST_HUMAN	RC1-OT0086-220300-011-B07 OT0086 Homo sapiens cDNA
9653	22579	35951	2.51	5.0E-12	AJ271735.1	NT	DKFZp434J0426_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434J0426 5'
9657	22863	36249	1.23	6.0E-12	P34982	SWISSPROT	Homo sapiens Xq pseudautosomal region; segment 1/2
10768	23654		5.1	5.0E-12	AL163303.2	NT	OLFACTORY RECEPTOR 1D2 (OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E) (OLFACTORY RECEPTOR 17-1) (OR17-4)
10850	23736	37159	0.76	5.0E-12	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C103
263	13359	26274	3.89	4.0E-12	AA700326.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C102
264	13359	26274	4.24	4.0E-12	AA700326.1	EST_HUMAN	z174g11.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
							z174g11.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'

Page 230 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4733	17738	30600	0.75	4.0E-12	AI889884.1	EST_HUMAN	bx28105.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE ;
8067	20990		0.63	4.0E-12	BF445140.1	EST_HUMAN	mad21b03.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3366077 3' similar to contains MER7.b2 MIER7 repetitive element ;
8819	21749		3.74	4.0E-12	AF109907.1	NT	Homo sapiens S104 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
9245	22173	35527	0.95	4.0E-12	AB042815.1	NT	Bos taurus Mth2 mRNA for mitochondrial carrier homolog 2, complete cds
11521	24431	37869	4.68	4.0E-12	AJ229043.1	NT	Homo sapiens 958 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
639	13700	26606	2.95	3.0E-12	AW341683.1	EST_HUMAN	hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR:O14517 O14517 SMRP ;
639	13700	26607	2.95	3.0E-12	AW341683.1	EST_HUMAN	hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR:O14517 O14517 SMRP ;
5315	18299	31151	0.72	3.0E-12	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
5637	18713	31614	1.35	3.0E-12	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
7371	20365	33634	0.47	3.0E-12	BE149692.1	EST_HUMAN	RC1-HT0256-280300-017-c08 HT0256 Homo sapiens cDNA
7829	20788		0.58	3.0E-12	AB042297.1	NT	Homo sapiens PTS gene for 6-pyruvyltetrahydropterin synthase, complete cds
8221	21126		0.48	3.0E-12	AW854328.1	EST_HUMAN	RC3-GT0255-031099-011-h02 GT0255 Homo sapiens cDNA
9651	22577	35948	0.73	3.0E-12	O35453	SWISSPROT	SERINE PROTEASE HEPSIN
11099	24033	37474	3.17	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
11099	24030	37475	3.17	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
1680	14710	27672	1.83	2.0E-12	AW602131.1	EST_HUMAN	IL5-JM0071-120400-065-a05 JM0071 Homo sapiens cDNA
3527	16505	29469	0.93	2.0E-12	87544495	NT	Mus musculus keratin-associated protein 6.2 (Krtap6-2), mRNA
4208	17225	30092	1.22	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA
4528	17537	30093	1.22	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA
5006	18004	30861	0.65	2.0E-12	O70306	SWISSPROT	CNO-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
5006	18004	30862	0.65	2.0E-12	O70306	SWISSPROT	TX15 PROTEIN (T-BOX PROTEIN 15)
5430	18512	31235	0.81	2.0E-12	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
6751	19785		2.64	2.0E-12	AW971857.1	EST_HUMAN	ENDONUCLEASE
7539	20478	33766	3.2	2.0E-12	T08169.1	EST_HUMAN	EST383946 IMAGE reassessment, MAGI Homo sapiens cDNA
7730	20662	33960	1.48	2.0E-12	BE173035.1	EST_HUMAN	EST06060 Infant Brain, Berto Soares Homo sapiens cDNA clone HIBBA13 5' end
7960	20892		0.56	2.0E-12	AW842798.1	EST_HUMAN	MR0-HT0559-200400-015-a08 HT0559 Homo sapiens cDNA
8110	21022	34348	2.4	2.0E-12	11422229	NT	MR2-CNO037-210200-101-b02 CNO037 Homo sapiens cDNA
							Homo sapiens Ac-like transposable element (ALTE), mRNA

Page 231 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9285	22213	35571	0.55	2.0E-12	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYL TRANSFERASE (PROTEIN-UDP ACETYL GALACTOSAMINYL TRANSFERASE) (UDP-GALNAAC:POLYPEPTIDE, N- ACETYL GALACTOSAMINYL TRANSFERASE) (GALNAAC-T)
9848	22955		1.96	2.0E-12	AF196864.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
10491	23379		12.06	2.0E-12	BE165980.1	EST_HUMAN	MR3-HT0497-150200-113-g01 HT0487 Homo sapiens cDNA
10894	23878	37308	0.86	2.0E-12	AI334130.1	EST_HUMAN	Q40702.X1 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:1931835 3' similar to TR:Q13538
12385	25163		2.32	2.0E-12	AL163283.2	NT	Q13538 ORF2: FUNCTION UNKNOWN. ; Homo sapiens chromosome 21 segment HS21C083
127	13232	26148	2.72	1.0E-12	AW627874.1	EST_HUMAN	h90a09.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2970040 3' similar to contains MER18.11 MER18 repetitive element ;
2004	15022		1.28	1.0E-12	AI871728.1	EST_HUMAN	wm5107.x1 NCI_CGAP_UI2 Homo sapiens cDNA clone IMAGE:2439493 3' similar to contains L1.b3 L1 repetitive element ;
3118	16159	28063	0.94	1.0E-12	AF000991.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
3118	16189	28064	0.94	1.0E-12	AF000991.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
3943	16971	29853	46.33	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
3943	16971	29854	46.33	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
6194	19250		1.65	1.0E-12	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
6276	19327		1.98	1.0E-12	O9Y2G7	SWISSPROT	HYPOPHOSPHATASE 1 (HPP1) PROTEIN KIAA0961
6394	19442	32610	0.52	1.0E-12	BF642800.1	EST_HUMAN	EST000008 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1847869 5'
6394	19442	32611	0.52	1.0E-12	BF642800.1	EST_HUMAN	EST000008 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1847869 5'
6811	19844	33054	0.52	1.0E-12	AF229843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds, and unknown gene
7476	20415	33693	1.9	1.0E-12	AF196864.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
7511	20450	33734	13	1.0E-12	AI248533.1	EST_HUMAN	q166a04.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849614 3' similar to gb:U19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.11 MER10 repetitive element ;
7511	20450	33735	13	1.0E-12	AI248533.1	EST_HUMAN	q166a04.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849614 3' similar to gb:U19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.11 MER10 repetitive element ;
9068	21987	35341	0.66	1.0E-12	U66059.1	NT	Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S>

Page 232 of 545  
Table 4  
Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9263	22191	35549	1.45	1.0E-12	AA782323.1	EST_HUMAN	ec26d05.s1 Sirtagene ovary (#937217) Homo sapiens cDNA clone IMAGE:857577 3'
12299	25108	35576	4.45	1.0E-12	AW982164.1	EST_HUMAN	EST374237 MAGE resequences, MAGE Homo sapiens cDNA
12493	25234		1.67	1.0E-12	A1738592.1	EST_HUMAN	w1331h05.x1 NCL CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2392065 3'
12636	25862		2.55	1.0E-12	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
12919	25529		1.49	1.0E-12	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
1078	14122	27059	2.27	9.0E-13	AW082714.1	EST_HUMAN	x561f07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2580805 3' similar to contains MER28.13 MER28 repetitive element 1
3695	16727		1	9.0E-13	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
4024	17051	29942	1.04	9.0E-13	AB029900.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
7659	20592	33890	0.42	9.0E-13	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C063
10126	23019		2.38	9.0E-13	N69553.1	EST_HUMAN	za26b06.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:293651 3'
740	13798	26722	5.28	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
740	13798	26723	6.28	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
1862	14884	27804	3.51	8.0E-13	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nailp) and survival motor neuron protein (smn) genes, complete cds
8690	21621	34963	0.83	8.0E-13	A1884398.1	EST_HUMAN	wm31h09.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
8690	21621	34964	0.83	8.0E-13	A1884398.1	EST_HUMAN	wm31h09.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
10644	23530		3.91	8.0E-13	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
12187	26023	38524	2.6	8.0E-13	U66060.1	NT	Human germline T-cell receptor beta chain TCRBV13S1, TCRBV6S8A2T, TCRBV5S8A3N2T, TCRBV13S6A2T, TCRBV6S9P, TCRBV5S3A2T, TCRBV13S9P, TCRBV6S3A1N1T, TCRBV5S2, TCRBV6S6A2T, TCRBV6S7P, TCRBV13S4, TCRBV6S2A1N1T, TCRBV6S4A2T, TCRBV6S4A1, TCRBV23S1A2T, TCRBV12P
8348	21253	34587	0.59	7.0E-13	A1894398.1	EST_HUMAN	wm31h09.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
8348	21253	34588	0.59	7.0E-13	A1894398.1	EST_HUMAN	wm31h09.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
8812	21742		0.59	7.0E-13	Q66165	SWISSPROT	OLFATORY RECEPTOR-LIKE PROTEIN OLF2
12737	25377		31.57	7.0E-13	BE778223.1	EST_HUMAN	601463265F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866613 5'
12940	25507		2.07	7.0E-13	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYL TRANSFERASE (PROTEIN-UDP ACETYL GALACTOSAMINYL TRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYL GALACTOSAMINYL TRANSFERASE) (GALNAC-T1)
2113	15123	28131	9.96	6.0E-13	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
3367	16411		0.83	5.0E-13	R78338.1	EST_HUMAN	y82f04.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145759 5'

Page 233 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

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3457	16498		1.9	5.0E-13	AA435773.1	EST_HUMAN	z177a12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728350 3' similar to contains Alu repetitive element/contains element MER22 repetitive element ;
7202	20202	33447	0.66	5.0E-13	P08983	SWISSPROT	GAP JUNCTION BETA-1 PROTEIN (CONNEXIN 30) (CX30)
11294	24214	37663	2.58	5.0E-13	P07913	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
1890	14911		2.05	4.0E-13	AW378614.1	EST_HUMAN	PM2-HT0224-221099-001-e11 HT0224 Homo sapiens cDNA
2484	15486		3.04	4.0E-13	AF003529.1	NT	Homo sapiens glycocalyx 3 (GPC3) gene, partial cds and flanking repeat regions
4861	17863		1.15	4.0E-13	AA454054.1	EST_HUMAN	z44807.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795468 5'
5780	18852	31857	5.23	4.0E-13	BE189131.1	EST_HUMAN	PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA
7572	20508	33798	1.3	4.0E-13	AB037750.1	NT	Homo sapiens mRNA for KIAA1329 protein, partial cds
8056	20939	34285	0.93	4.0E-13	AA431529.1	EST_HUMAN	z177g12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782182 5' similar to TR:G452763 G452763 COR1 MRNA ;
8182	21089		1.8	4.0E-13	N44291.1	EST_HUMAN	y03305.r1 Soares melanocyte 2NBM Homo sapiens cDNA clone IMAGE:273080 5' similar to PIR:A32895 A32895 t complex sterility protein - mouse ;
8400	22328	35680	1.27	4.0E-13	AL043810.1	EST_HUMAN	DKF2p434A0128.r1 434 (synonym: htes3) Homo sapiens cDNA clone DKF2p434A0128 5'
10523	23410	36822	4.84	4.0E-13	AI289831.1	EST_HUMAN	q132405.x1 NCL CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1899845 3' similar to contains Alu repetitive element;
11608	24515	37985	1.98	4.0E-13	AA435819.1	EST_HUMAN	z178g10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
11608	24519	37986	1.98	4.0E-13	AA435819.1	EST_HUMAN	z178g10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
12688	25354		5.02	4.0E-13	BE503023.1	EST_HUMAN	h282a05.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3214496 3' similar to contains MER31.1t
181	13283		2.94	3.0E-13	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
890	13943		2.39	3.0E-13	AA430310.1	EST_HUMAN	z188g08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781406 5'
2393	15399	28402	2.22	3.0E-13	AJ271736.1	NT	Homo sapiens Xq pseudoautosomal region, segment 2/2
2501	15503		3.07	3.0E-13	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2713	15707	28702	3.37	3.0E-13	BF372962.1	EST_HUMAN	CM3-FT0100-140700-242-r08 FT0100 Homo sapiens cDNA
3230	16278		2.67	3.0E-13	AA746844.1	EST_HUMAN	ob18d02.s1 NCL CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324035 3'
4604	17612	30472	6.13	3.0E-13	AA430310.1	EST_HUMAN	z188g08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781406 5'
5226	18215	31061	0.65	3.0E-13	BF372962.1	EST_HUMAN	CM3-FT0100-140700-242-r08 FT0100 Homo sapiens cDNA
6730	18903	31896	0.78	3.0E-13	AA134017.1	EST_HUMAN	z188h10.r1 Stratiogene lung carcinoma Q37218 Homo sapiens cDNA clone IMAGE:565316 5' similar to contains THR12 THR repetitive element ;
5730	18803	31897	0.78	3.0E-13	AA134017.1	EST_HUMAN	z188h10.r1 Stratiogene lung carcinoma Q37218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR12 THR repetitive element ;

Page 234 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6223	19278	32432	0.71	3.0E-13	AW005639.1	EST_HUMAN	w283c02.x1 NCI_CGAP_Bin25 Homo sapiens cDNA clone IMAGE:2565890 3' similar to TR:O75139 O75139 KIAA0644 PROTEIN. ;
8463	21394	34735	7.8	3.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
8654	21585	34920	0.78	3.0E-13	AA352487.1	EST_HUMAN	EST60487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to serine protease P100, Reactive factor
8654	21585	34921	0.78	3.0E-13	AA352487.1	EST_HUMAN	EST60487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to serine protease P100, Reactive factor
10694	23590	37010	0.7	3.0E-13	AW935487.1	EST_HUMAN	RC2-DT0007-110100-014-g10 DT0007 Homo sapiens cDNA
11119	24049	37010	3.46	3.0E-13	AI064768.1	EST_HUMAN	HAC538 Human fetal liver cDNA library Homo sapiens cDNA
11492	24395	37845	3.05	3.0E-13	BE083509.1	EST_HUMAN	CM0-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
12028	24870	38373	1.87	3.0E-13	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
160	13250	26178	2.22	2.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
258	13355	26271	1	2.0E-13	U23839.1	NT	Danio rerio fibroblast growth factor receptor 4 mRNA, complete cds
1297	14330	27276	5.69	2.0E-13	AF239710.1	NT	Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11 and complete cds
3049	16101	29004	0.79	2.0E-13	8924119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3049	16101	29005	0.79	2.0E-13	8924119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3325	16371	29272	1.02	2.0E-13	BF431899.1	EST_HUMAN	nab76005.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3'
3564	16601	29505	1.04	2.0E-13	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4203	17221	31199	1.7	2.0E-13	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5378	18360	31199	1.02	2.0E-13	M59318.1	NT	Homo sapiens ala gene
5378	18360	31200	1.02	2.0E-13	M59318.1	NT	Homo sapiens ala gene
6362	19411	32576	4.77	2.0E-13	O06852	SWISSPROT	CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1)
6448	19494	33603	0.44	2.0E-13	X79417.1	NT	S.scrofa rps12 mRNA for ribosomal protein S12
7126	20330	33603	6.66	2.0E-13	X16912.1	NT	Human PFKL gene for liver-type 8-phosphofructokinase (EC 2.7.1.11) exon 2
7407	20105	33340	0.83	2.0E-13	10835072	NT	Homo sapiens N-myristoyltransferase 1 (NMT1), mRNA
7407	20105	33341	0.63	2.0E-13	10835072	NT	Homo sapiens N-myristoyltransferase 1 (NMT1), mRNA
10937	23822	37249	1.93	2.0E-13	6031896	NT	Homo sapiens mab-21 (C. elegans)-like 1 (MAB21L1) mRNA



Page 235 of 545  
Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12453	25203		25.49	2.0E-13	AW892155.1	EST_HUMAN	GM0-NN0001-100300-274-e11 NN0001 Homo sapiens cDNA
311	13403	26320	1.59	1.0E-13	S74126.1	NT	FGF-1 fibroblast growth factor 1 [human, kidney, Genomic, 342 nt, segment 2 of 2]
913	13666	26912	6.04	1.0E-13	AJ007973.1	NT	Homo sapiens LGMD2B gene
1364	14396	27350	1.78	1.0E-13	X87344.1	NT	H. sapiens DNA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
2035	16052	28050	2.8	1.0E-13	AA720574.1	EST_HUMAN	nm21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13
4704	17709	30572	1.95	1.0E-13	BF340987.1	EST_HUMAN	THR repetitive element ;
6713	19749	32953	0.47	1.0E-13	AA090732.1	EST_HUMAN	602038009F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4185666 5'
8489	21420	34757	1.03	1.0E-13	AA577812.1	EST_HUMAN	y1535.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
8489	21420	34758	1.03	1.0E-13	AA577812.1	EST_HUMAN	nm24d01.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu
10592	23479	37106	0.93	1.0E-13	O15481	SWISSPROT	repetitive element contains element MER24 repetitive element ;
10780	23679	37106	0.57	1.0E-13	AF300701.1	NT	MELANOMA-ASSOCIATED ANTIGEN B4 (IMAGE-B4 ANTIGEN)
11818	24739	38230	11.71	1.0E-13	BF108755.1	EST_HUMAN	Mus musculus osteoclastin protein tyrosine phosphatase mRNA, complete cds
12292	25103		1.6	1.0E-13	AV715377.1	EST_HUMAN	7145e10.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER28.b2 MER28 repetitive element ;
12892	25482		2.07	1.0E-13	AJ271735.1	NT	AV715377 DOB Homo sapiens cDNA clone DOBAIE03 5'
353	13440	26353	2.13	9.0E-14	AA781159.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region, segment 1/2
354	13441	26354	2.16	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.t1 MER19 repetitive element ;
2523	15524		5.16	9.0E-14	AW861577.1	EST_HUMAN	aj24c01.s1 Soares testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.t1 MER19 repetitive element ;
2932	15630	28624	1.41	9.0E-14	AJ133127.1	NT	RC4-CT0322-090100-073-d09 CT0322 Homo sapiens cDNA
2932	15630	28625	1.41	9.0E-14	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
2802	15791	28790	7.93	9.0E-14	AB038162.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
3157	16207	29097	6.45	9.0E-14	AW513298.1	EST_HUMAN	Homo sapiens TFF gene cluster for trefoil factor, complete cds
3284	13440	26353	1.01	9.0E-14	AA781159.1	EST_HUMAN	x054h05.x1 NCI_CGAP_UT1 Homo sapiens cDNA clone IMAGE:2707833 3'
3862	16691	29776	8.91	9.0E-14	D14547.1	NT	aj24c01.s1 Soares testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.t1 MER19 repetitive element ;
4870	17870	30734	1.84	9.0E-14	AJ002153.1	NT	Human DNA, SINE repetitive element
3556	16593		1.27	8.0E-14	BE468263.1	EST_HUMAN	Saguinus oedipus gene for seminal vesicle secreted protein semenogelin I
4039	17066		4.12	8.0E-14	R76269.1	EST_HUMAN	hz71c09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213424 3'
							y172e03.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:144786 3'

Page 236 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9980	21339	34674	50.26	8.0E-14	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
10089	22882	36268	3.61	8.0E-14	AA219316.1	EST_HUMAN	z17c10.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:829970 3'
11865	24755		1.47	8.0E-14	BE062668.1	EST_HUMAN	QV2-BT0268-281099.014-a01 BT0268 Homo sapiens cDNA
12044	25320	31822	3.19	8.0E-14	A1888118.1	EST_HUMAN	wc32h08.x1 NCL CGAP_Co3 Homo sapiens cDNA clone IMAGE:2328143 3'
1652	15906		5.71	7.0E-14	AW151673.1	EST_HUMAN	x87e10.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
9476	22404		0.74	7.0E-14	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
388	13472	26390	8.8	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
10337	23226	36641	2.66	8.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
10337	23226	36642	2.66	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
641	13702	26308	5.79	5.0E-14	Q63120	SWISSPROT	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN)
5186	18178	31024	1.07	6.0E-14	AW073791.1	EST_HUMAN	xb03b05.x1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575185 3' similar to contains L1.12 L1
5723	18796	31888	5.15	5.0E-14	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
1150	15893		1.84	4.0E-14	P04928	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
1800	14921	27001	8.26	4.0E-14	AJ007973.1	NT	Homo sapiens LGMD2B gene
3816	16845		0.92	4.0E-14	AA046502.1	EST_HUMAN	xp45f12.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 6'
4384	17407	30273	1.05	4.0E-14	N46328.1	EST_HUMAN	W73c12.s1 Soares_multiple_sclerosis_2NbHMS Homo sapiens cDNA clone IMAGE:278190 3' similar to contains L1.13 L1 repetitive element;
8536	21467		0.73	4.0E-14	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
12849	25968		6.5	4.0E-14	A1888224.1	EST_HUMAN	wtr08c03.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2435332 3' similar to contains Alu repetitive element;
977	14028	26970	1.22	3.0E-14	X85466.1	NT	R.norvegicus mRNA for CP2 protein
5036	18033	30890	0.82	3.0E-14	AW265354.1	EST_HUMAN	xp45f12.x1 NCL CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element; contains element MER repetitive element;
7038	20064	33297	1.03	3.0E-14	A1420786.1	EST_HUMAN	ic91c12.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE.;
7038	20064	33298	1.03	3.0E-14	A1420786.1	EST_HUMAN	ic91c12.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE.;

Page 237 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

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7160	25666		0.56	3.0E-14	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
7379	20373	33642	0.65	3.0E-14	AA386311.1	EST_HUMAN	EST185034 Brain IV Homo sapiens cDNA
9345	22273	35635	1.04	3.0E-14	N42165.1	EST_HUMAN	Y07610.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:270523 5'
11684	18033	30890	8.35	3.0E-14	AW265354.1	EST_HUMAN	xp45f12.x1 NCL_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element; contains element MER9 repetitive element;
12867	25838		2.9	3.0E-14	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
411	13484	26404	2.72	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
411	13484	26405	2.72	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
714	15881	26581	6.49	2.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2411	15415		1.73	2.0E-14	AW372856.1	EST_HUMAN	RC6-BT0377-081289-031-D12 BT0377 Homo sapiens cDNA
2488	15490		1.22	2.0E-14	7657529	NT	Homo sapiens rhadoid tumor deletion region protein 1 (RTDR1), mRNA
2553	15553	28550	3.95	2.0E-14	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2571	15599		1.43	2.0E-14	BE222432.1	EST_HUMAN	hvdg10.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3180738 3' similar to contains Alu repetitive element; contains OFR.t1 OFR repetitive element;
5714	18787	31718	0.96	2.0E-14	BF380661.1	EST_HUMAN	IL2-UT0072-240800-142-D07 UT0072 Homo sapiens cDNA
5815	18887	31998	0.86	2.0E-14	AJ312351.1	EST_HUMAN	ta78h01.x2 NCL_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050225 3' similar to contains L1.13 L1 repetitive element;
5922	18989	32108	2.89	2.0E-14	U01317.1	NT	Human beta globin region on chromosome 11
7210	20210		0.89	2.0E-14	BE000550.1	EST_HUMAN	RC3-BN0072-240200-011-a08 BN0072 Homo sapiens cDNA
7684	20588	33897	1.09	2.0E-14	P56163	SWISSPROT	ZINC-FINGER PROTEIN NEURO-D4
7930	20852	34159	20.73	2.0E-14	BE188761.1	EST_HUMAN	IL2-HT0397-071299-024-D04 HT0397 Homo sapiens cDNA
7930	20852	34160	20.73	2.0E-14	BE188761.1	EST_HUMAN	IL2-HT0397-071299-024-D04 HT0397 Homo sapiens cDNA
10426	23317	36735	0.52	2.0E-14	AJ978795.1	EST_HUMAN	wr59g10.x1 NCL_CGAP_U01 Homo sapiens cDNA clone IMAGE:2492034 3' similar to contains Alu repetitive element;
10900	23785	37211	0.61	2.0E-14	AV741648.1	EST_HUMAN	AV741648 CB Homo sapiens cDNA clone CBFBBF04 5'
11219	24143	37596	4.35	2.0E-14	AW139800.1	EST_HUMAN	UI-H-B11-adv-a-10-Q-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718234 3'
11932	18989	32108	2.69	2.0E-14	U01317.1	NT	Human beta globin region on chromosome 11
12864	25841		2.34	2.0E-14	AF008191.1	NT	Homo sapiens putative G6 protein (GR6) gene, complete cds
13071	15492		1.85	2.0E-14	7657529	NT	Homo sapiens rhadoid tumor deletion region protein 1 (RTDR1), mRNA
1094	14137	27074	1.15	1.0E-14	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1431	14462	27414	7.47	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
1431	14462	27415	7.47	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
2017	15035	28026	7.34	1.0E-14	L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's

Single Exon Probes Expressed in Adult Liver

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2200	15211	28213	4.94	1.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2433	15437	28437	3.4	1.0E-14	AF001689.1	NT	Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds
2986	16038	28942	1.68	1.0E-14	P06227	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
3209	16257	29155	5.6	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3209	16257	29156	5.6	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3955	16983	29867	2.04	1.0E-14	AA682994.1	EST_HUMAN	ae89c12.s1 Striatogene schizo brain S11 Homo sapiens cDNA clone IMAGE:971350 3'
4586	17594	30452	1.79	1.0E-14	AY275862.1	EST_HUMAN	xq39h10.x1 NCL_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2753059 3'
6020	19082	32208	2.03	1.0E-14	AF126145.1	NT	Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
6970	25660	33228	11.73	1.0E-14	11437150	NT	Homo sapiens prominin (mouse)-like 1 (PROML1), mRNA
6970	25660	33227	11.73	1.0E-14	11437150	NT	Homo sapiens prominin (mouse)-like 1 (PROML1), mRNA
1598	14629	27588	1.14	9.0E-15	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, I (PTPRT), mRNA
2186	15197		1.42	9.0E-15	AF198779.1	NT	Homo sapiens transcription factor IGEM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel $\alpha$ -
7917	20841	34143	3.98	9.0E-15	P21416	SWISSPROT	GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P15, P12, P30, P10]
8595	21526	34870	1.34	9.0E-15	BE903569.1	EST_HUMAN	601677750F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960169 5'
13032	29571		1.76	9.0E-15	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
2858	13573		0.94	8.0E-15	BE261482.1	EST_HUMAN	601148632F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3164023 5'
7545	20463	33772	1.41	7.0E-15	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862085 5'
10916	23801		3.03	7.0E-15	AW241959.1	EST_HUMAN	xn77d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700483 3' similar to contains THR12 THR repetitive element;
12349	25141		2.12	7.0E-15	AA284465.1	EST_HUMAN	zs57408.f1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701583 5' similar to gb:U121934 S TEROL
1021	14070	27013	6.96	6.0E-15	AJ271736.1	NT	O-ACYLTRANSFERASE (HUMAN) contains L1.11 L1 repetitive element;
6142	19201	32337	1.26	6.0E-15	X73462.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
6142	19201	32338	1.26	6.0E-15	X73462.1	NT	O.aries mRNA for hair keratin cysteine-rich protein
13100	25615		2.17	6.0E-15	BF432200.1	EST_HUMAN	O.aries mRNA for hair keratin cysteine-rich protein
433	13504	26428	9.56	5.0E-15	AL163303.2	NT	nab81c12.x1 Soares_NSIF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3'
							Homo sapiens chromosome 21 segment HS21C008
2811	15800	28799	1.5	5.0E-15	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
3529	16567		1.06	5.0E-15	AW296817.1	EST_HUMAN	U1-H-BW0-ajb-9-10-0-U1.s1 NCL_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2731219 3'
450	13117	26003	2.65	4.0E-15	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103

Page 239 of 545  
Table 4

## Single Exon Probes Expressed in Adult Liver

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4228	17244	30112	0.73	4.0E-15	AL118598.1	EST_HUMAN	DKFZp761C0810_r1 761 (synonym: hemy2) Homo sapiens cDNA clone DKFZp761C0810 5'
6960	19889	33213	0.8	4.0E-15	AB007970.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript K/AA0501
8365	21289	34621	0.42	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
8365	21289	34622	0.42	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
11501	21289	34621	2.11	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
11501	21289	34622	2.11	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
4313	17327		8.61	3.0E-15	N89452.1	EST_HUMAN	LY1142F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone LY1142 5' similar to ANF(CARDIODILATIN)
5038	18035		0.83	3.0E-15	P92485	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5
5160	18153	30988	0.72	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
5160	18153	31000	0.72	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
7125	20329		1.41	3.0E-15	Q64625	SWISSPROT	GLUTATHIONE PEROXIDASE RY2D1 PRECURSOR (ODORANT-METABOLIZING PROTEIN RY2D1)
7656	20500	33887	3.12	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
7656	20500	33888	3.12	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
10436	23325		2.25	3.0E-15	AA807128.1	EST_HUMAN	oc36a07.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1351764 3' similar to contains MIER19.11
11234	24160	37609	1.79	3.0E-15	AB026898.1	NT	MER19 repetitive element ;
12652	29869		1.81	3.0E-15	AJ271735.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
269	13364	26280	3.97	2.0E-15	AF223391.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
369	13473	26391	5.38	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
389	13473	26392	5.38	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1552	14583		1.2	2.0E-15	8923201	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3588	16605	29508	1.37	2.0E-15	AF223391.1	NT	Homo sapiens hypothetical protein FLJ20212 (FLJ20212) mRNA
3588	16605	29509	1.37	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4155	17176	30049	0.94	2.0E-15	AW235469.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4738	17741		3.24	2.0E-15	AI806335.1	EST_HUMAN	wp0705x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2741621 3' similar to contains L1.43 L1 repetitive element ;
							O61043 NINEIN. ;

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6423	19470	32844	0.99	2.0E-15	BE562352.1	EST_HUMAN	601344253F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677268 5'
6423	19470	32845	0.99	2.0E-15	BE562362.1	EST_HUMAN	601344253F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677268 5'
7473	20413		1.26	2.0E-15	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf16 gene and C11orf17 gene
7647	20581	33878	2.18	2.0E-15	AA704195.1	EST_HUMAN	z177e03.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3'
7793	20722	34025	5.1	2.0E-15	W05064.1	EST_HUMAN	z178d10.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:288675 5' similar to WP:P44F4.8 CE02227 TRANSPOSASE ;
8394	21239	34571	0.87	2.0E-15	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
9463	22391	35753	2.89	2.0E-15	D14547.1	NT	Human DNA, SINE repetitive element
9622	22548	35918	0.67	2.0E-15	AA397758.1	EST_HUMAN	z177g08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 6'
9822	22548	35919	0.87	2.0E-15	AA397758.1	EST_HUMAN	z177g08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
9939	22844	36233	1.59	2.0E-15	AW379465.1	EST_HUMAN	CM0-HT0244-201099-078-a12 HT0244 Homo sapiens cDNA
9939	22844	36234	1.69	2.0E-15	AW379465.1	EST_HUMAN	CM0-HT0244-201099-078-a12 HT0244 Homo sapiens cDNA
11278	24188		5.05	2.0E-15	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12975	16605	29508	2.5	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
12975	16606	29509	2.5	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2824	15913		3.57	1.0E-15	A1689884.1	EST_HUMAN	b28d05.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13639 Q13639
3059	16108	29014	1.18	1.0E-15	BE043584.1	EST_HUMAN	MARNER TRANSPOSASE ;
3168	16235	29130	1.3	1.0E-15	P06547	SWISSPROT	Rk40s02.y1 NCL_CGAP_Ov34 Homo sapiens cDNA clone IMAGE:2999162 5'
5372	18354	31194	0.71	1.0E-15	6753875	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6632	19672	32888	1.54	1.0E-15	T95763.1	EST_HUMAN	Mus musculus factor in the germline alpha (Figla), mRNA
7353	20349		1.92	1.0E-15	BE074217.1	EST_HUMAN	ye40a10.s1 Soares_fetal_liver_spleen_INFLS Homo sapiens cDNA clone IMAGE:120234 3' similar to contains
7390	20088	33324	0.76	1.0E-15	P39057	SWISSPROT	MER6 repetitive element ;
8810	21740	35099	0.86	1.0E-15	AL163280.2	NT	QV3-BT0569-270100-074-g05 BT0569 Homo sapiens cDNA
8991	21920	35275	5.15	1.0E-15	A1200976.1	EST_HUMAN	DYNEIN BETA CHAIN, CILIARY
8991	21920	35276	5.15	1.0E-15	A1200976.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
9591	22517	35879	0.57	1.0E-15	AL163207.2	NT	q168f05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
9594	22520	35883	1.37	1.0E-15	4507208	NT	q168f05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
9789	22753	36135	1.04	1.0E-15	Q39575	SWISSPROT	Homo sapiens spermidine synthase (SRM) mRNA
							DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM

Page 241 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10158	23049	36449	0.98	1.0E-15	AA864653.1	EST_HUMAN	oh37c03.s1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:1459972 3' similar to contains L1.13 L1 repetitive element;
11287	24181	37831	3.1	1.0E-15	AF044083.1	NT	Homo sapiens major histocompatibility locus class III region
13036	25717	31665	9.74	1.0E-15	AI783944.1	EST_HUMAN	l31c05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219912 3' similar to contains Alu repetitive element;
4431	17442		1.03	9.0E-16	BF689487.1	EST_HUMAN	602120192F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277422 5'
4625	17631	30495	1.33	9.0E-16	4503168	NT	Homo sapiens cut (Drosophila)-like 1 (CCAAAT displacement protein) (CUTL1) mRNA
11431	24347	37792	1.85	9.0E-16	F08698.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23105
3424	16466	29372	0.73	7.0E-16	Y10196.1	NT	Homo sapiens PHEX gene
5900	18989	32087	0.71	7.0E-16	4885120	NT	Homo sapiens chemokine (C-C motif) receptor 8 (CCR8) mRNA
7727	20659	33956	1.44	7.0E-16	O88807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
7727	20659	33957	1.44	7.0E-16	O88807	SWISSPROT	(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
12994	25798		24.09	7.0E-16	T94149.1	EST_HUMAN	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
2155	15167		9.99	6.0E-16	AW972611.1	EST_HUMAN	y628c12r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:119082 5'
3932	16950	29843	1.05	6.0E-16	AF224669.1	NT	EST384702 IMAGE resequences, MAGL Homo sapiens cDNA
2728	15722	28718	2.6	5.0E-16	AA992176.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
11952	24796	38236	3.63	5.0E-16	BF217368.1	EST_HUMAN	ol80c04.s1 Soares_t04_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1623078 3' similar to contains element L1 repetitive element;
13066	25592		14.26	5.0E-16	11418127	NT	601855734F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4104129 5'
2254	15264		1.24	4.0E-16	AB001523.1	NT	Homo sapiens GTP binding protein 1 (GTPBP-1), mRNA
2402	15407	28410	1.45	4.0E-16	AW797188.1	EST_HUMAN	Homo sapiens gene for TMEM1 and PWP2, complete and partial cds
2402	15407	28411	1.45	4.0E-16	AW797188.1	EST_HUMAN	QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA
3517	16555	29456	5.72	4.0E-16	Q16653	SWISSPROT	QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA
4240	17253	30122	8.21	4.0E-16	BE083875.1	EST_HUMAN	MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR
4240	17253	30123	8.21	4.0E-16	BE083875.1	EST_HUMAN	PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
5063	18060		1.01	4.0E-16	AV730833.1	EST_HUMAN	PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
5293	18278	31128	1.1	4.0E-16	P08548	SWISSPROT	PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
8172	21079	34409	35.21	4.0E-16	AL163284.2	NT	AV730833 HTF Homo sapiens cDNA clone HTFAXE09 5'
9835	22741	36122	0.86	4.0E-16	11423191	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11668	24572	38048	1.66	4.0E-16	AV730030.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
12447	26200		12.89	4.0E-16	C05947.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10024 (FLJ10024), mRNA
						EST_HUMAN	AV730030 HTF Homo sapiens cDNA clone HTFAWA03 5'
						EST_HUMAN	C05947 Human pancreatic islet Homo sapiens cDNA clone hbc63555

Table 4

## Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12457	25205	31851	1.62	4.0E-16	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
137	13239	26158	1.41	3.0E-16	AW022862.1	EST_HUMAN	U445c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
137	13239	26159	1.41	3.0E-16	AW022862.1	EST_HUMAN	U445c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
488	13559		1.2	3.0E-16	AL046445.1	EST_HUMAN	DKFZp434P037_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434P037 5'
498	13568		2.08	3.0E-16	AF135446.1	NT	Homo sapiens TSX (TSX) pseudogene, exon 5
1471	14502	27463	1.15	3.0E-16	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
3017	16069	28970	4.45	3.0E-16	P03200	SWISSPROT	ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220]
4008	17035	29925	0.74	3.0E-16	T08169.1	EST_HUMAN	EST06060 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBBA13 5' end
4041	17068		0.65	3.0E-16	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
4042	17069		1.07	3.0E-16	U03887.1	NT	Human BXP20 gene
5056	18053	30906	1.12	3.0E-16	AV661393	EST_HUMAN	AV661393 GLC Homo sapiens cDNA clone GLCGSA01 3'
5460	18541		0.97	3.0E-16	AA077255.1	EST_HUMAN	7B10F02 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B10F02
5811	18683	31992	1.49	3.0E-16	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
9216	22144	35498	3.69	3.0E-16	AI002835.1	EST_HUMAN	am8h05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains THR.b2 THR repetitive element;
10402	23291		0.81	3.0E-16	BF690617.1	EST_HUMAN	602246538F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332032 5'
10619	23605	36939	4.38	3.0E-16	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
13086	25939	31374	2.1	3.0E-16	AL043268.2	EST_HUMAN	DKFZp434L1623_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L1623 5'
898	14048		1.44	2.0E-16	AL183279.2	NT	Homo sapiens chromosome 21 segment HS21C079
2409	15413		1.01	2.0E-16	AA621761.1	EST_HUMAN	af06d04.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1030855 3'
2739	15732		1.15	2.0E-16	J03061.1	NT	Human SSAV-related endogenous retroviral LTR-like element
4274	17288	30155	1.36	2.0E-16	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
4594	17602	30458	1.32	2.0E-16	AI208733.1	EST_HUMAN	qg56i03.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1839197 3' similar to contains MER29.13
7045	20071	33305	0.9	2.0E-16	Q31125	SWISSPROT	MER29 repetitive element;
8176	21083	34415	0.85	2.0E-16	AI470723.1	EST_HUMAN	HISTIDINE-RICH PROTEIN KE4
							U19e11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141708 3' similar to contains element
							MER33 repetitive element;
8545	21476	34818	2.1	2.0E-16	AI732837.1	EST_HUMAN	nz47f06.x6 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:1290947 similar to TR:O54849 O54849
8736	21666	35011	0.73	2.0E-16	BE858026.1	EST_HUMAN	HYPOTHETICAL 42.9 KD PROTEIN. [2] TR:O08905 contains MER7.11 MERY repetitive element;
8736	21666	35012	0.73	2.0E-16	BE858026.1	EST_HUMAN	7f82h09.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3303521 3'
							7f82h09.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3303521 3'



Page 243 of 545  
Table 4

## Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5091	22020	35376	0.97	2.0E-16	AW877214.1	EST_HUMAN	GM4-PT0034-180200-506-a01 PT0034 Homo sapiens cDNA
9091	22020	35377	0.97	2.0E-16	AW877214.1	EST_HUMAN	GM4-PT0034-180200-508-a01 PT0034 Homo sapiens cDNA
196	13294	26207	1.57	1.0E-16	AF200716.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
403	13516		26.08	1.0E-16	AA628592.1	EST_HUMAN	af39g11.31 Soares_tad_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1034084 3' similar to contains ORF 12 OFR repetitive element ;
1987	15005	27993	3.12	1.0E-16	BF327942.1	EST_HUMAN	QV0-BN0148-070700-293-a10 BN0148 Homo sapiens cDNA
5923	18950	32109	0.88	1.0E-16	AF153864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
6703	19739		21.98	1.0E-16	U45983.1	NT	Homo sapiens COR8 chemokine receptor (CMKBR8) gene, complete cds
6856	19888	33102	3.03	1.0E-16	Q02779	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 10 (MIXED LINEAGE KINASE 2) (PROTEIN KINASE MST)
7985	19739		6.4	1.0E-16	U45983.1	NT	Homo sapiens COR8 chemokine receptor (CMKBR8) gene, complete cds
9823	22729	36111	1.05	1.0E-16	AW875651.1	EST_HUMAN	QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA
3802	18833	29719	3.35	9.0E-17	AW900048.1	EST_HUMAN	GM1-NIN1003-200300-153-a01 NN1003 Homo sapiens cDNA
7025	20051		1.95	9.0E-17	A1992964.1	EST_HUMAN	t922e11.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2106624 3' similar to contains MER28.12
8685	21617		3.72	9.0E-17	AW160257.1	EST_HUMAN	MER28 repetitive element ;
10720	23606		2.59	9.0E-17	AF200719.1	NT	xg49g12.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2630950 3' similar to contains OFR 12 OFR repetitive element ;
1045	14089		1.75	8.0E-17	AW880701.1	EST_HUMAN	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
3962	16900		0.91	8.0E-17	AL163280.2	NT	QV0-OT0032-080300-155-d01 OT0032 Homo sapiens cDNA
5775	25632	31951	3.95	8.0E-17	BE172081.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
7651	20585		1.75	8.0E-17	AV730759.1	EST_HUMAN	MR0-H10559-060300-003-e04 HT0559 Homo sapiens cDNA
8210	21115	34445	0.47	8.0E-17	6753651	NT	AV730759 HTF Homo sapiens cDNA clone HTFAQB07 5'
1477	14508		2.48	7.0E-17	6753097	NT	Mus musculus dynein, axon, heavy chain 11 (Dnahc11), mRNA
5506	18595		3.34	7.0E-17	AF216650.1	NT	Mus musculus apolipoprotein B editing complex 2 (ApoBec2), mRNA
							Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternatively spliced
6984	20011	33243	8.58	7.0E-17	AF229843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
216	13315	26233	7.16	6.0E-17	AW983880.1	EST_HUMAN	RC1-HN0003-220300-021-b04 HN0003 Homo sapiens cDNA
6589	19809	32794	2.28	6.0E-17	AW662772.1	EST_HUMAN	h81d04.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2678695 3' similar to contains L1 t2 L1 repetitive element ;
444	13111	25997	3.31	5.0E-17	IT64110.1	EST_HUMAN	yc05h08.11 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:79839 5'
8024	20840	34255	3.01	5.0E-17	IT61043.1	EST_HUMAN	yd26b04.1 Soares fetal liver spleen (NFLS) Homo sapiens cDNA clone IMAGE:109327 5'
3703	19735	29625	1.47	4.0E-17	AA643697.1	EST_HUMAN	h96605.e1 NCI_CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1068628 3'

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9900	22898	36272	1.15	4.0E-17	AW129185.1	EST_HUMAN	x120e04.x1 NCL_CGAP_K168 Homo sapiens cDNA clone IMAGE:2618622 3' similar to contains Alu repetitive element; contains MER19.b1 MER19 repetitive element ;
11924	24786	38266	2.06	4.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
12381	25161		2.18	4.0E-17	AI073546.1	EST_HUMAN	ov45e04.x1 Soares_1estis_NHT Homo sapiens cDNA clone IMAGE:1640286 3' similar to TR:Q16530 Q16530 PMS3 MRNA ; contains MER10.12 MER10 repetitive element ;
2110	15123	28127	1.14	3.0E-17	AW119123.1	EST_HUMAN	x489c09.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2804784 3'
3237	16295		1.46	3.0E-17	P36410	SWISSPROT	MAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG
3710	16742	29631	1.43	3.0E-17	BE326522.1	EST_HUMAN	hw05b04.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181999 3'
3710	16742	29632	1.43	3.0E-17	BE326522.1	EST_HUMAN	hw05b04.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181999 3'
8844	21774	35121	1.36	3.0E-17	N68451.1	EST_HUMAN	zai14b02.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:292491 3' similar to contains p TR5.13 PTR5 repetitive element ;
10224	23115	36516	5.18	3.0E-17	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10868	23764	37160	0.71	3.0E-17	BF327012.1	EST_HUMAN	GV3-BN0047-270700-283-a12 BN0047 Homo sapiens cDNA
10868	23754	37181	0.71	3.0E-17	BF327012.1	EST_HUMAN	GV3-BN0047-270700-283-a12 BN0047 Homo sapiens cDNA
12348	25140		3.48	3.0E-17	11417966	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
373	13460	26376	2.95	2.0E-17	AI270080.1	EST_HUMAN	q163a05.x1 NCL_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1659822 3' similar to contains Alu repetitive element ;
374	13460	26375	2.08	2.0E-17	AI270080.1	EST_HUMAN	q163a05.x1 NCL_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element ;
1015	14065		1.18	2.0E-17	AA722932.1	EST_HUMAN	zg81d04.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:399751 3'
2471	15474	28473	2.23	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2471	15474	28474	2.23	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2972	18024	28924	8.35	2.0E-17	P12036	SWISSPROT	NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H)
5551	18629	31506	1.75	2.0E-17	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
5551	18629	31507	1.75	2.0E-17	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
6516	19560		1.76	2.0E-17	AF055086.1	NT	Homo sapiens MHC class 1 region
6766	19800		1.57	2.0E-17	AL134881.1	EST_HUMAN	DKFZp762J0610.t1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762J0610 5'
8356	21261	34595	0.73	2.0E-17	AB037839.1	NT	Homo sapiens mRNA for KIAA1418 protein, partial cds
8662	21563	34932	1.39	2.0E-17	Q95159	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF3
8026	21954	35312	1.13	2.0E-17	AA300640.1	EST_HUMAN	EST13504 Testis tumor Homo sapiens cDNA 5' end similar to similar to glycogenin
10382	23271	36694	1.95	2.0E-17	BE298988.1	EST_HUMAN	600944690F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960615 5'
10415	23304	36721	3.28	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
10415	23304	36722	3.28	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
10752	23638	37071	5.43	2.0E-17	D13391.1	NT	Human CYP19 gene for aromatase cytochrome P-450, promoter region (containing two cis-acting transcriptional regulatory elements)
10867	23763	37178	0.84	2.0E-17	P98063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10867	23763	37179	0.84	2.0E-17	P98063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10892	23777	37203	0.73	2.0E-17	A1798902.1	EST_HUMAN	we94b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
10892	23777	37204	0.73	2.0E-17	A1798902.1	EST_HUMAN	we94b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
10892	23777	37204	0.73	2.0E-17	A1798902.1	EST_HUMAN	we94b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
774	13831	26764	3.41	1.0E-17	P08183	SWISSPROT	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)
1737	14764		2.2	1.0E-17	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
1792	14818	27787	4.78	1.0E-17	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2128	15141	28144	2.12	1.0E-17	P02461	SWISSPROT	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
2359	15365	28368	4.28	1.0E-17	U79410.1	NT	Homo sapiens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B
3627	16663		1.21	1.0E-17	AF224688.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
4235	17251		9.56	1.0E-17	R09942.1	EST_HUMAN	(UBE2D3) genes, complete cds
5397	18379		1.12	1.0E-17	AA299037.1	EST_HUMAN	yf3de07.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA 5' end similar to similar to retrovirus-related pd
6729	19765		0.97	1.0E-17	AW468468.1	EST_HUMAN	he38e05.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2921312 3' similar to contains Alu repetitive element; contains LTR8.t1 LTR8 repetitive element;
6946	19975	33197	1.67	1.0E-17	A185942.1	EST_HUMAN	qe55b05.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
6946	19975	33199	1.67	1.0E-17	A185942.1	EST_HUMAN	qe55b05.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
7448	20389	33659	1.21	1.0E-17	Q16831	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
9154	22082	35440	1.25	1.0E-17	BE062744.1	EST_HUMAN	QV0-BT0263-101299-072-d07 BT0263 Homo sapiens cDNA
10511	23398	38810	0.94	1.0E-17	AW996538.1	EST_HUMAN	QV3-BN0046-220300-120-c10 BN0046 Homo sapiens cDNA
11850	24700	38192	2.05	1.0E-17	Q28824	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE (MLCK) [CONTAINS: TELOKIN]
10030	22930		3.62	9.0E-18	A1472167.1	EST_HUMAN	l83d03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2148389 3'
3852	18881	29766	1.47	8.0E-18	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
369	13456	26369	22.74	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
369	13456	26370	22.74	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
7847	20774	34075	1.08	7.0E-18	AW387542.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN);
12818	13456	26369	6.38	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S

Page 246 of 545  
Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12818	13456	26370	6.38	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:U20868 60S RIBOSOMAL PROTEIN L4 (HUMAN);
3338	16384	28283	1.27	6.0E-18	X71791.2	NT	Rattus norvegicus partial GdnRPh-1 gene for gila-derived neuroprotease nexin I, enhancer region
4880	17862		4.52	6.0E-18	P52181	SWISSPROT	PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE (TISSUE TRANSGLUTAMINASE) (TGASE C) (TGC)
8825	21755		2.35	6.0E-18	11428165	NT	Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sapiens) (LOC63446), mRNA
8922	21852	35207	0.77	6.0E-18	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
9635	22561	35930	0.59	6.0E-18	AI008256.1	EST_HUMAN	RC-BT165-020499-014 BT166 Homo sapiens cDNA
9635	22561	35931	0.59	6.0E-18	AI008256.1	EST_HUMAN	RC-BT165-020499-014 BT166 Homo sapiens cDNA
11772	24672	38160	1.99	6.0E-18	X87344.1	NT	H. sapiens DNA, DMB, HLA-Z1, IFF2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
12579	25261	31840	2.74	6.0E-18	U87929.1	NT	Human acylate hydratase (ACO2) gene, exon 4
1175	14215	27154	15.33	5.0E-18	AI280214.1	EST_HUMAN	qm65g11.x1 Soares_plicenta_8to6weeks_2NBHP8b9W Homo sapiens cDNA clone IMAGE:1893688 3' similar to contains Alu repetitive element;
5455	18536	31378	1.08	5.0E-18	AF087913.1	NT	Human endogenous retrovirus HERV-P-T47D
9279	22207	35664	6.21	5.0E-18	BE143312.1	EST_HUMAN	MR0-HT0161-221099-002-c06 HT0161 Homo sapiens cDNA
11416	24332	37780	3.86	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
11416	24332	37781	3.86	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
12701	25356		11.85	5.0E-18	AW867182.1	EST_HUMAN	MR1-SN0035-060400-001-g11 SN0035 Homo sapiens cDNA
13006	25556		36.99	5.0E-18	AV650547.1	EST_HUMAN	AV650547 GLC Homo sapiens cDNA clone GLCCGA02 3'
129	13233	28149	1.4	4.0E-18	BE044076.1	EST_HUMAN	hc36r04.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3 MER29 repetitive element ;
129	13233	28150	1.4	4.0E-18	BE044076.1	EST_HUMAN	hc36r04.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3 MER29 repetitive element ;
1746	14772	27742	9.56	4.0E-18	AA821814.1	EST_HUMAN	np24f11.s1 NCL_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M28328 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
2216	18227	28231	1.09	4.0E-18	Q06430	SWISSPROT	N-ACETYLACTOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (N-ACETYLGLUCOSAMINYLTRANSFERASE) (L-BRANCHING ENZYME) (IGNT)
2216	18227	28232	1.09	4.0E-18	Q06430	SWISSPROT	N-ACETYLACTOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (N-ACETYLGLUCOSAMINYLTRANSFERASE) (L-BRANCHING ENZYME) (IGNT)
5548	18626	31501	2.33	4.0E-18	AI017555.1	EST_HUMAN	cu23e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
5548	18626	31502	2.33	4.0E-18	AI017555.1	EST_HUMAN	cu23e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'

Page 247 of 545  
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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8428	21360		0.70	4.0E-18	AA746811.1	EST_HUMAN	rx64a08.s1 NCL_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1266998 similar to contains L1.12 L1 repetitive element ;
11443	24359	37809	6.22	4.0E-18	AA371807.1	EST_HUMAN	EST83633 Pituitary gland, subtracted (prolactin/growth hormone) II Homo sapiens cDNA 5' end similar to EST containing O family repeat
874	13927	26875	6.61	3.0E-18	AA814196.1	EST_HUMAN	662311.1.s1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1924581 3' similar to SW:RS5_HUMAN
958	14008	26953	3.14	3.0E-18	BE088634.1	EST_HUMAN	P46782 40S RIBOSOMAL PROTEIN S6 ;
4030	17057	29946	1.2	3.0E-18	AL163247.2	NT	GM0-BT0690-210300-298-g07 BT0690 Homo sapiens cDNA
7142	20250	33502	4.81	3.0E-18	BE001671.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
11364	24292	37725	1.52	3.0E-18	BF218660.1	EST_HUMAN	PM0-BN0081-100300-001-b08 BN0081 Homo sapiens cDNA
12822	25441		7.17	3.0E-18	AW022015.1	EST_HUMAN	601884856F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103652 5'
270	13365	26281	2.52	2.0E-18	AW838820.1	EST_HUMAN	df31h12.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485126 5'
1180	14220		63.41	2.0E-18	BE256097.1	EST_HUMAN	QY1-L T0036-150200-070-e07 L T0036 Homo sapiens cDNA
3108	16218	29108	1.39	2.0E-18	Q39575	SWISSPROT	601114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5'
6596	18872		4.98	2.0E-18	AA868610.1	EST_HUMAN	DYNEIN GAMMA CHAIN FLAGELLAR OUTER ARM
5698	18769	31694	3.12	2.0E-18	D14547.1	NT	ak53407.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409652 3' similar to TR:O14577
5696	18769	31695	3.12	2.0E-18	D14547.1	NT	O14577 BAC CLONE RG114A06 FROM 7Q31, COMPLETE SEQUENCE ;
6093	19164		1.94	2.0E-18	BF347229.1	EST_HUMAN	Human DNA, SINE repetitive element
6406	19454	32626	1.02	2.0E-18	X60459.1	NT	602021164F1 NCL_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4156670 5'
6406	19454	32627	1.02	2.0E-18	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
6530	19574	32756	0.86	2.0E-18	BF352940.1	EST_HUMAN	Human IFNAR gene for interferon alpha/beta receptor
6573	19614	32800	3.18	2.0E-18	AW665853.1	EST_HUMAN	IL3-HT0619-220700-222-C12 HT0619 Homo sapiens cDNA
7840	20768	34071	0.61	2.0E-18	AA457619.1	EST_HUMAN	h194g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979984 3' similar to contains
8726	21656	35002	0.54	2.0E-18	BE439524.1	EST_HUMAN	MER19.12 MER19 repetitive element ;
10550	23436	36856	1.34	2.0E-18	AW151673.1	EST_HUMAN	aa99d11.11 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838485 5' similar to TR:G61634 G61634 POLYPEPTIDE PR77 ;
10550	23436	36857	1.34	2.0E-18	AW151673.1	EST_HUMAN	HTM1-160F1 HTM1 Homo sapiens cDNA
11412	24328	37777	2.3	2.0E-18	AW470791.1	EST_HUMAN	x67e10.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12 MER10 repetitive element ;
							x67e10.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12 MER10 repetitive element ;
							ha33408.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.53 THR repetitive element ;

Page 248 of 545  
Table 4  
Single Exon Probes Expressed in Adult Liver

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12154	24993	38492	3.93	2.0E-18	AW151299.1	EST_HUMAN	xg47e09.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2630728 3' similar to contains MER8.b2
12517	14220		8.71	2.0E-18	BE256087.1	EST_HUMAN	MER8 repetitive element;
4523	17532		0.98	1.0E-18	T95406.1	EST_HUMAN	601114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5'
5540	18819	31470	2.61	1.0E-18	AV653405.1	EST_HUMAN	ye43g05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120536 5' similar to contains L1 repetitive element;
5762	18835	31938	2.19	1.0E-18	D00059.1	NT	AV653405 GLC Homo sapiens cDNA clone GLODK11 3'
5762	18835	31939	2.19	1.0E-18	D00059.1	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
6725	19761	32968	1.24	1.0E-18	AL163280.2	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
9010	21939	35295	1.23	1.0E-18	AI148288.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
10411	23300	38718	3.07	1.0E-18	U91328.1	NT	oz68d09.x1 Soares_senescent_fibroblasts_NbHSP Homo sapiens cDNA clone IMAGE:1680593 3' similar to contains L1.t1 L1 repetitive element;
12475	25220	31856	6.48	1.0E-18	AF003529.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
567	13636	26647	3.3	9.0E-19	AA281981.1	EST_HUMAN	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
568	13636	26547	3.05	9.0E-19	AA281981.1	EST_HUMAN	z111406.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
8431	21363		4.15	9.0E-19	F08888.1	EST_HUMAN	MER19 repetitive element;
9248	22174	35528	2.66	9.0E-19	AL163203.2	NT	z111406.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
9248	22174	35529	2.86	9.0E-19	AL163203.2	NT	MER19 repetitive element;
11567	24476	37943	4.48	9.0E-19	AB032989.1	NT	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
12258	13636	26547	17.41	9.0E-19	AA281981.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
1074	14118		1.17	8.0E-19	AW974902.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
8727	21657	35003	1.17	8.0E-19	BE158938.1	EST_HUMAN	Homo sapiens mRNA for KIAA1143 protein, partial cds
2260	15270	28276	1.48	7.0E-19		NT	z111406.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
6727	19763	32970	2.23	7.0E-19	AF092080.1	NT	MER19 repetitive element;
7681	20616	33914	0.65	7.0E-19	P26444	SWISSPROT	EST387007 MAGE resequences, MAGN Homo sapiens cDNA
12388	25952		1.49	7.0E-19	AA705694.1	EST_HUMAN	MRO-HT0404-210200-001-g06 HT0404 Homo sapiens cDNA
3848	16875		1.12	6.0E-19	AW852930.1	EST_HUMAN	Homo sapiens DEAD(H) (Asp-Glu-Ala-Asp/His) box polypeptide 6 (RNA helicase, 54kD) (DDX6) mRNA
4574	17582	30444	1.41	6.0E-19	P34986	SWISSPROT	Rattus norvegicus cpi151 mRNA, partial cds